GENETIC RESOURCES UNIT

Annual Report for 1996 and 1997

About ICARDA and the CGIAR

Established in 1977, the International Center for Agricultural Research in the Dry Areas (ICARDA) is governed by an independent Board of Trustees. Based at Aleppo, Syria, it is one of 16 centers supported by the Consultative Group on International Agricultural Research (CGIAR).

ICARDA serves the entire developing world for the improvement of lentil, barley and faba bean; all dry-area developing countries for the improvement of on-farm water-use efficiency, rangeland and small-ruminant production; and the West and Central Asia and North Africa region for the improvement of bread and durum wheats, chickpea, and farming systems. ICARDA's research provides global benefits of poverty alleviation through productivity improvements integrated with sustainable natural-resource management practices. ICARDA meets this challenge through research, training, and dissemination of information in partnership with the national agricultural research and development systems.

The results of research are transferred through ICARDA's cooperation with national and regional research institutions, with universities and ministries of agriculture, and through the technical assistance and training that the Center provides. A range of training programs is offered extending from residential courses for groups to advanced research opportunities for individuals. These efforts are supported by seminars, publications, and specialized information services.

CGIAR

The CGIAR is an international group of representatives of donor agencies, eminent agricultural scientists, and institutional administrators from developed and developing countries who guide and support its work. The CGIAR receives support from a wide variety of country and institutional members worldwide. Since its foundation in 1971, it has brought together many of the world's leading scientists and agricultural researchers in a unique South-North partnership to reduce poverty and hunger.

The mission of the CGIAR is to promote sustainable agriculture to alleviate poverty and hunger and achieve food security in developing countries. The CGIAR conducts strategic and applied research, with its products being international public goods, and focuses its research agenda on problem-solving through interdisciplinary programs implemented by one or more of its international centers, in collaboration with a full range of partners. Such programs concentrate on increasing productivity, protecting the environment, saving biodiversity, improving policies, and contributing to strengthening agricultural research in developing countries.

The World Bank, the Food and Agriculture Organization of the United Nations (FAO), the United Nations Development Programme (UNDP), and the United Nations Environment Programme (UNEP) are cosponsors of the CGIAR. The World Bank provides the CGIAR System with a Secretariat in Washington, DC. A Technical Advisory Committee, with its Secretariat at FAO in Rome, assists the System in the development of its research program.

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International Center for Agricultural Research in the Dry Areas
P.O. Box 5466, Aleppo, Syria
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This report was written and compiled by program scientists and represents a working document of ICARDA. Its primary objective is to communicate the season's research results quickly to fellow scientists, particularly those within West Asia and North Africa, with whom ICARDA has close collaboration. Owing to the tight production deadlines, editing of the report was kept to a minimum.

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1. GENETIC RESOURCES ACTIVITIES

1.1. Introduction and highlights

This report represents work carried out at the Genetic Resources Unit (GRU) of ICARDA in the seasons 1995-96 and 1996-97. During this two-year period the GRU continued its normal activities of germplasm collection, acquisition, characterization, preliminary evaluation, and in-depth evaluation in collaboration with ICARDA's Germplasm Program (GP) scientists and the NARS. Research on methodology for *in situ* conservation and other support research also formed an important component of GRU's activity. In addition, further development of documentation of genetic resource holdings, short-term and long-term conservation of germplasm, and distribution of germplasm sub-samples to users was also carried out. All the above mentioned activities were accomplished despite the loss of staff members. The loss in the staffing of the Genetic Resources Unit are also partially responsible for the production of this combined Annual Report for the two seasons instead of separate ones in the past.

The monthly precipitation, air temperature, and frost events for the season 1995-96 are reported in **Tables A1, A2, and A3**, respectively in the Appendix, page 214. The monthly precipitation, air temperature, and frost events for the season 1996-97 are reported in **Tables A4, A5, and A6**, respectively, also in the Appendix, page 215.

The number of accessions (accs.) in ICARDA's genetic resources collections increase each year. At the end of December 1997 they totalled 115,808. The status of these holdings for December 1997 are given in the following tables:

Table A7 in the Appendix, page 216, gives the status of ICARDA germplasm collections by origins for the three mandate crop types, viz., cereals, food legumes and forage legumes, for December 1997.

Table A8 in the Appendix, page 218, gives the status of ICARDA cereal collections alone by origin for December 1997.

Table A9 in the Appendix, page 220, gives the status of ICARDA food legume collections alone by origin for December 1997.

Table A10 in the Appendix, page 222, gives the status of ICARDA forage legume collections alone by origin for December 1997.

Collecting germplasm to augment and fill the gaps in the gene bank's collection in one of the most important activity of GRU. The following tables provide details of the cereal collecting missions by species (for country codes see Barley Germplasm Catalog III 1998):
Table A11 in the Appendix, page 225, lists durum wheat (*Triticum durum*) landrace collecting missions from 1983 to 1994.
Table A12 in the Appendix, page 226, lists missions for collecting "other cultivated wheats" (mostly obsolete forms) from 1983 to 1994.
Table A13 in the Appendix, page 227, lists missions conducted for collecting wild *Triticum* spp. from 1983 to 1997.
Table A14 in the Appendix, page 228, lists missions conducted for collecting *Aegilops* spp. from 1983 to 1997.

Germplasm exploration, collection and acquisition
In 1996 and 1997, the collecting effort in countries of the West Asia and North Africa (WANA) region and beyond continued but on a reduced scale than in previous years. The position of a cereal curator has not been filled and hence very few exploration missions for new wheat and barley genetic resources could be launched after 1995. However, ICARDA's holdings for wheat and barley genetic resources, including wild progenitors, are now fairly comprehensive and hence collecting efforts have been scaled down and also reflect the current budgetary constraints. The collection of food and forage legumes continued, as in previous years, and several gaps in ICARDA's genetic resources collections of these species were filled, thanks to special project funding from Australia. Table 1 gives details of the 2,112 accs. added to ICARDA's holdings through collection and acquisition during 1996 and 1997. The major results and new findings of some of these collecting missions during the two years are summarized below. More information is reported in **Section 1.2.**

1) Survey and collection trips in northern and central Syria during 1996 revealed the alarming extent and the causes of genetic erosion in wheat wild progenitors. There is an urgent need to conserve representative populations of wild progenitors of cultivated wheats, i.e., *Triticum urartu, T. baeoticum, T. dicoccoides, Aegilops speltoides* and *Ae. tauschii* in their natural habitat (*in-situ*). It is envisaged that the newly-funded Global

Environment Facility (GEF) project, which includes Syria, Jordan, Lebanon and Palestine, will be able address this urgent need for action. For more information see **Section 1.2.1.**

2) The basaltic regions in Homs, Hama and Idleb provinces of central Syria were thoroughly surveyed for wild wheat relatives and progenitors in 1997. The mission yielded a total of 61 new bulk samples for *ex situ* conservation in ICARDA and at ARC Douma gene banks, and 393 single-plants for genetic diversity studies of natural populations of wild wheats and for in-depth evaluation and utilization. Populations of wild *Triticum* species, the main target of the mission, were found on 11 sites out of the total 18 collected. The finding of the wild diploid wheat, *T. baeoticum*, on the Homs-Hama basaltic plateau is important. The discovery of a *T. araraticum* population, on a site near Kafr Nabil, extends the geographical distribution of the species in the western part of the Near East arc to the south by 100 km. The presence of *Ae. speltoides*, the donor of the durum and bread wheat B genome, on low-rainfall sites (260-320mm) indicates that this species, which usually prefers high-rainfall conditions, may develop ecotypes adapted to dry environments. Habitat destruction by over-grazing is the major cause of rapid genetic erosion of wild *Triticum* populations in the surveyed region and the process is rapid and ubiquitous. For a full report of this mission see **Section 1.2.2.**
3) The survey of rangelands in the Oujda region of Morocco resulted in the collection of 385 accessions from at least 60 species. The most frequent rangeland plant collected was *Stipa* spp. Other rangeland plants collected were *Helianthemum* spp., *Herniaria* spp., *Paronychia argentea*, *Peganum harmala*, *Plantago* spp., *Schismus barbatus* and *Thymus* spp. Another important rangeland plant *Artemisia* spp., was found frequently but could not be collected as it sets seed in the autumn. For more details see **Section 1.2.3.**
4) Ethiopian landraces still form the basis of most crops. For ICARDA conditions, Ethiopia is one of the best potential sources of new and rare gene combinations in both pulses and cereals. Two collection missions took place in 1997, one in January and

the second in October. The collection mission in January 1997 concentrated on lupins, lathyrus and lentils, and crops at or near harvest during that period of the year. In all of 311 samples were collected during 12 days of collection and 1,880km were covered from Addis Ababa, the capital, to Gondar in the North. Whilst most collections were from field-sown crops, market samples in towns were also targeted. More details of this mission see **Section 1.2.4.**

5) During the October 1997 mission to Ethiopia emphasis was given to the collection of peas and faba beans. Another prime aim of the mission was to revisit some key lupin sites in the Lake Tana region from which *Ascochyta* resistance has been isolated. In all 225 samples were collected to which were added the 42 market samples collected during the January mission. See **Section 1.2.5.** for more information.
6) In an earlier mission to Bangladesh in 1995, six accs. of faba bean (*Vicia faba*) were collected. The mission in 1997 was planned to provide a more thorough sampling of the genetic diversity of farmer landraces of faba bean from areas not represented in present collections in Bangladesh and ICARDA. In all 29 accs. were collected. This germplasm is also expected to provide unique germplasm with extreme earliness and possible tolerance to higher temperatures during flowering. For more details see **Section 1.2.7.**
7) **Section 1.2.9.** reports an important multi-crop collection mission conducted in June 1996 in Ecuador. A total of 205 populations of faba bean, lentil, pea, *Lathyrus* and barley were collected at 103 sites from farmers and from local village markets at intervals of 10-20km along the Andean mountain route in Ecuador at elevations of 2300 to 3500m asl. By collecting over a range of altitudes, lateness in the sources of resistance to chocolate spot in the Andean region may be sampled. One acc. each of local *Lathyrus sativus* and *L. cicera* were found at a remote farm and were collected. The farmer related that he used these food legumes for soups and that they had been handed down each generation in his family since the time the Spanish conquests. These two landrace varieties were not encountered again at any other site and were not previously known to exist in Ecuador. Three accs. of

Vicia articulata were found. These were referred to locally as black lentils. In the past, *V. articulata* was cultivated in Spain as a substitute for lentil.

8) A genetic resources collecting mission was conducted in Spain during June-July 1997. It covered mostly the rural communities of Castilla-León, Extremadura and Andalucía provinces. There were four major ecological environments: mountain grasslands, grassland steppes, pasture-grounds, and forests. The aim of this mission was to upgrade germplasm of grain, forage and pasture legumes from these regions. Sixty-five sites were sampled and a total of 363 accs. of pasture, forage and grain legumes were collected. All the species collected grow wild in the Iberian Peninsula; in paddocks, pastures and the characteristic Mediterranean evergreen oak "dehesa" (pasture ground). For more details of this interesting mission see **Section 1.2.10.**
9) **Section 1.2.11.** provides a short report of the faba bean germplasm collection to China in 1996. This was a specially funded international collection mission to collect landraces of faba bean in rural areas of Sichuan and Yunnan provinces of China. The Yunnan plateau was particularly targeted since it has the widest range of crop genetic resources diversity in China. This region of China is characterized by diverse physiography, climate and natural vegetation that often result in rapid changes in the environment over short distances. Mountains and rivers cut across the province, which has eight distinct climatic zones. Yunnan has a long history of human settlement and agricultural activities and hence possesses potential for collection and conservation. In all, 68 sites (34 in Yunnan and 34 in Sichuan) were collected in these two provinces. A total of 34 faba bean landraces were collected from Yunnan administrative region and the same number were collected from Sichuan administrative region. These faba bean accs. showed a large variation for hundred seed weight. The accs. from Yunnan were with a larger one-hundred seed weight than those from Sichuan. All accs. were with equina seeds, except one from Yunnan which was of the major type.

Table 1. Germplasm introduced at GRU-ICARDA in 1996 and 1997

Crop	Collections by GRU		From other sources		Total	
	1996	1997	1996	1997	1996	1997
Barley	56	7	-	238	56	245
Wild *Hordeum*	3	23	1	21	4	44
Durum wheat	-	2	-	680	-	682
Bread wheat	-	5	83	20	83	25
Wild *Triticum*	8	23	-	-	8	23
Aegilops spp.	29	28	2	164	31	192
Cereals	**96**	**88**	**86**	**1123**	**182**	**1211**
Chickpea	10	57	3	-	13	57
Wild *Cicer*	-	-	-	-	-	-
Lentil	58	26	71	3	129	29
Wild *Lens*	-	3	-	2	-	5
Faba bean	176	166	87	3	263	169
Food legumes	**244**	**252**	**161**	**8**	**405**	**260**
Medicago	-	-	-	-	-	-
Vicia	33	35	-	-	33	35
Lathyrus	21	83	-	-	21	83
Pisum	27	25	-	498	27	523
Forage legumes	**81**	**143**	**-**	**498**	**81**	**641**
GRAND TOTAL	**421**	**483**	**247**	**1629**	**668**	**2112**

Germplasm multiplication, characterization and evaluation

A total of 2,049 bread wheat (*Triticum aestivum*) landrace accs., received or collected from different countries, were characterized during the 1995-1996 season. A large set of 1,266 wheat wild relatives (population and progenies) of *T. dicoccoides* (365 entries),

T. urartu (349), *T. baeoticum* (502) and *T. timopheevi araraticum* (50) collected from Jordan and Turkey were planted for preliminary evaluation in the 1995-1996 growing season in the post-quarantine area at Tel Hadya. The main objective of this study was to characterize the germplasm in the eco-geographical condition of northern Syria. In addition, 167 accessions of wild barley (*Hordeum spontaneum*) originating from Jordan (46 acc.), Palestine (89 acc.) and Turkey (32 acc.) were planted at Tel Hadya during 1995-1996 growing season. Three cultivated barley (Tadmor, Harmal and Roho) and two wild barley (ICWB 181541 & 181542) were included in the study as systematic checks. A total of 118 accessions of *Aegilops* spp. from Jordan (73), Syria (4), and Turkey (41) were characterized also during 1995-96 season. The details of samples multiplied, characterized and evaluated is given in Table 2.

During 1996-97 a second set of 2,162 bread wheat landraces received as donations or were collected from different countries was planted in the same manner as in 1995-1996. Three wheat varieties, Cham 6, Mexipak and Sonalika were included in the evaluation as systematic checks. As in the previous season, a collection of 473 accessions of *Aegilops* spp. collected or received from different countries was planted for characterization at Tel Hadya. Three *Aegilops* checks with known characteristics, *Ae. vavilovii* (400067), *Ae. triuncialis* (400021), and *Ae. biuncialis* (400831) were used as systematic checks in this study.

The characterization and evaluation of food and forage legumes was as follows: During the 1996-97 season a total of 2,295 lentil landraces and ICARDA breeding lines were evaluated in an unreplicated augmented design with one systematic (ILL 4000) and two random (ILL 4401 and ILL 5582) checks, with a block size of 23 plots. There were 25 descriptors on which data was recorded. Summary statistics revealed that the largest variation for quantitatively scored descriptors was for SPP and PPP with CVs over 60%. This was followed by the yield descriptors SYLD, BYLD, STYLD, HI and HSW, all with CVs over 40%. The means of the accs. for SYLD and STYLD were lower, than the three checks, by 16.6 % and 20.0%, respectively. For other quantitative traits the means were similar to the three check means.

The entire *Medicago lacinata* (196 accs.), and *M. littoralis* (246 accs.) germplasm collections were tested in the 1995-96 season and the entire *M. orbicularis* (649 accs.) and *M. scutellata* (127 accs.) germplasm collections were tested in the 1996-97 season. All trials

were evaluated in augmented nurseries using one systematic check (IFMA 7858 *M. polymorpha* var. *vulgaris*), and two random checks (IFMA 811, *M. rigidula* and IFMA 2600, *M. rotata*). Most *M. lacinata* accs. were from the western Mediterranean area (64 from Morocco, 43 from Spain and 27 from Tunisia). Most *M. littoralis* accs. were also from the western Mediterranean area (47 from Libya, 40 from Morocco, 40 from Tunisia and 23 from Algeria. From west Asia the largest number of *M. littoralis* accs. were from Cyprus (25) and Turkey (18). The largest numbers of M. orbicularis accs. were from west Asia (177 from Syria, 90 from Jordan and 84 from Turkey. There were also large number of *M. orbicularis* accs. from Algeria (89), Spain (37), Italy (36), and Tunisia (23). The largest number of *M. scutellata* accs. were from Syria (25), Jordan (24), Italy (15), Turkey (11) and Cyprus (10). Data on 12 descriptors was recorded. Details are given in **Section 1.3.6.**

During the 1995-96 season 700 accs. of five *Vicia* species were evaluated as follows: *V. hybrida* (142 accs.), *V. lutea* (81 accs.), *V. monantha* (110 accs.), *V. palaestina* (95 accs.) and *V. villosa* (272 accs.). Most *V. hybrida* accs. were from Syria (73) and Turkey (43), most *V. lutea* accs. were from Italy (25) and Turkey (20), most *V. monantha* accs. were from Algeria (48) and Syria (30), most *V. palaestina* accs. were from Syria (71) and most *V. villosa* accs. were Turkey (62), Hungary (47), Italy (37) and Morocco (22). Details are given in **Section 1.3.7.**

In 1996-97 season 700 accs. collected in North Africa of six *Vicia* species were evaluated: *V. narbonensis* (9 accs.), *V. lutea* (9 accs.), *V. monantha* 15 accs.), *V. sativa* (197 accs.) *V. villosa* (24 accs.) and V. ervilia (46 accs.). These accs. were mostly from Morocco and Tunisia. Details in **Section 1.3.8.**

Section **1.3.9.** describes the evaluation of *Lathyrus* spp. collected in North Africa in previous years. During the 1996-97 season 74 accs. comprising of six *Lathyrus* spp. were evaluated: *L. aphaca* (4 accs.), *L. articulatus* (39 accs.), *L. ciciera* (10 accs.), *L. ochurs* (17 accs.) *L. sativus* (2 accs.) and *L. tingitanus* (2 accs.). These accs. were mostly from Morocco and Tunisia and their collection and characterization was supported through the project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" funded by the Australian Center for International Agricultural Research (ACIAR). Collection was in collaboration with the Centre for Legumes for Mediterranean Agriculture (CLIMA).

Table 2. Germplasm multiplication, characterization and evaluation in 1995-96 and 1996-97 (combined figures)

	Multiplied	Characterized &/or evaluated	
Crop	**(accs.)**	**(accs.)**	**(traits)**
Barley	632	-	-
Wild barley	-	167	16
Durum wheat	708	-	-
Bread wheat	747	4283	16
Wild wheat	419	1857	18
Cereals	**2506**	**6307**	-
Chickpea	1568	-	-
Wild *Cicer*	310	-	-
Lentil	1671	2299	34
Wild *Lens*	450	-	-
Faba bean	1857	113	25
Food legumes	**5856**	**2412**	-
Medicago	792	1280	18
Vicia	3031	1109	58
Lathyrus	2795	129	-
Trifolium	3670	-	-
Pisum	631	-	-
Others	874	-	-
Forage legumes	**11793**	**2518**	-
GRAND TOTAL	**20155**	**11237**	-

Germplasm management

The GRU at ICARDA, which is holding the mandate crop germplasm collections in trust under the auspices of the FAO, continued through

germplasm collection, acquisition, characterization, documentation and distribution, to contribute to the global effort of conserving and utilizing plant genetic biodiversity.

For example, during 1996 and 1997, a total of 4,583 cereal and legume samples were added to the genebank through collections by GRU-ICARDA staff in cooperation with national programs. These new additions raised the Center's gene bank holdings to 115,808 accs. (Table 3).

Table 3. Summary of status of ICARDA collections by origin (December 1997)

	Cereals	Food legumes	Forage legumes	Total
WANA	37418	17387	20945	75750
Other countries	18197	9605	9079	36881
Unknown origin	728	1539	910	3177
TOTAL	**56343**	**28531**	**30934**	**115808**

During 1996 and 1997 more than 40,186 and 34,109 seed samples were distributed from ICARDA's genebank to users, respectively (Table 4). Moreover, 6,295 and 8,068 accs. were despatched for safety duplication to various centers in 1966 and 1997, respectively. For more details see **Section 1.6.3.**

Genetic resources conservation support research

Amplified fragment length polymorphism (AFLP) analysis of 18 genotypes of six accessions of wild wheat *Triticum urartu* Tum. ex Gand., across of their habitat region in South and North Syria, supported the distribution previously determined using agro-morphological characters and biochemical characterization. UPGMA and principal coordinate analysis of the AFLP data revealed two distinct clusters corresponding to the six accs. In addition, analysis of

molecular variance confirmed the results obtained by GENSTAT statistical analysis program. AFLP analysis on individual genotypes of *T. urartu* showed variability among the regions and the populations with four primer combinations suggesting they are members of distint accs. A report of this research, which is being conducted in cooperation with University of Bristol, UK, is given in **Section 1.4.1.**

Also, genetic diversity in an *ex situ* collection of *T. urartu* Tum ex Gand. was studied using random primers and the polymerase chain reaction (PCR). Random amplified polymorphic DNA (RAPD) technology was applied to fifteen single plant progenies which are derived from single-plants of three Syrian *T. urartu* natural populations. Electrophoretic analysis of the amplification products revealed the presence of polymorphism in *T. urartu*. Pairwise comparisons of polymorphic amplification products were used to generate Jaccard's similarity coefficients. These were used to construct a dendrogram using the unweighted pair-group method with arithmetic averages (UPGMA). The UPGMA analysis did not indicate a clearly defined geographical pattern of the DNA polymorphism. A report of this research is given in **Section 1.4.2.**

A study on the use of DNA markers in assessing biodiversity in barley (*Hordeum* spp.) was carried out in collaboration with scientists from Tishreen University, Latakkia, Syria, and the GP (**Section 1.4.3.**). A total of 315 accessions were analyzed using single plant per acc. The Random Amplified Polymorphic DNA (RAPD) technique was used for this study with three Operon primers: OPG-08, OPK-16 and OPS-09. This technique proved to be a useful tool for the detection and evaluation of variability within a barley core collection. The results showed a high level of genetic variability between accessions. Samples collected from certain areas revealed unique banding patterns as well as patterns which were in common with other areas from where germplasm was collected.

Development of synthetic hexaploid wheats is reported in **Section 1.4.4.** and some statistical analysis of ICARDA's barley collection is reported in **Section 1.4.5.**

In situ conservation research was continued in collaboration with the Agricultural Research Center (ARC) Douma, Syria. Experiments with self-regenerating populations of wheat wild progenitors were

planted in 1994 at Yahmoul ARC Research Station in Aleppo Province, northern Syria and in 1995 in other two research stations in the south of the country (see **Section 1.4.6.**).

The Seed Health Laboratory (SHL) also carried out research to improve techniques for the detection of various plant diseases prevalent in the region. For example, *Pyrenophora graminea* has a detrimental effect on barley yield and its components in Northern Syria. Also, during the 1996-97 seasons the Seed Health Laboratory in cooperation with the Virology Laboratory (GP), produced a polyclonal antiserum for virulent Syrian isolates of *Pseudomonas syringae* pv. *pisi*, the casual agent of bacterial blight of pea. The prepared antiserum is made available for use by seed health laboratories of the various national programs in WANA countries. This is reported in **Sections 1.4.7., 1.4.8.** and **1.4.9.**

Germplasm management: conservation and distribution

In 1996 and 1997, 21,038 accs. of cereals, food and forage legumes were multiplied for storage (Table 2). Also, during 1995-96 and 1996-97 a total of 6,596 and 7,201 accs., respectively, were tested for viability in the germination room of GRU. Those with low viability (< 85%) were identified for rejuvenation in the next available season. During 1996 and 1997 a total of 3,099 new accs. of ICARDA mandate crops were deposited in the long-term cold room which is maintained at a constant temperature of -20°C. Serving users of genetic resources in the main aim of the GRU and during 1996 and 1997 a total of 74,355 accs. were distributed (Table 4). Out of this total, 27,515 were used for carrying out GRU's own tasks of viability testing, rejuvenation, characterization and evaluation (**Section 1.6.**).

One of the major highlights of 1997 was the Rhizobium diversity conservation at ICARDA. A total of 1,512 accs. of *Rhizobium ciceri*, *R. leguminosarum*, *R. meliloti* and *R. trifolii* accs. are now included in the ICARDA Rhizobium database, which contains both passport and evaluation data. The database is now maintained at GRU and will be periodically updated. Geographic origin of ICARDA rhizobial collections is mostly in countries of West Asia and North Africa (WANA).

Table 4. GRU distribution of ICARDA's germplasm to users during 1996 to 1997

Crop	1996	1997	Total
Barley	5162	3650	8812
Wild *Hordeum*	259	208	467
Bread wheat	1927	1971	3898
Durum wheat	1050	521	1571
Other cult. *Triticum* spp.	144	169	313
Wild *Triticum* spp.	553	255	808
Aegilops spp.	946	427	1373
Cereals	**10041**	**7201**	**17242**
Chickpea	4392	3791	8183
Wild *Cicer* spp.	514	601	1115
Lentil	1255	2709	3964
Wild *Lens* spp.	166	538	704
Faba bean	270	86	356
Faba bean BPL	62	500	562
Food legumes	**6659**	**8225**	**14884**
Medicago	184	47	231
Vicia	483	2710	3193
Lathyrus	576	485	1061
Trifolium	385	190	575
Other	913	378	1291
Forages	**2541**	**3810**	**6351**
Total	**19241**	**19236**	**38477**
GRU's own work	14650	12865	27515
Total	**33891**	**32101**	**65992**
Safety duplication	6295	8068	8363
Grand Total	**40186**	**40169**	**74355**

Documentation of genetic resources

The GRU's database was set up on a ICARDA-wide network so all scientists can readily search for the required information. In 1997 the CGIAR's SINGER project was completed and put into operation. At the heart of SINGER lies the Network Operation Center (NOC) with the central server storing the data transferred from all Centers dealing with genetic resources. Over 500,000 accs. maintained in the CGIAR centers are now included in the SINGER database, which is available on Internet. ICARDA has contributed the passport and evaluation data of 111,740 accs. The database-generated summary of origins of accs. at ICARDA gene bank as of December 1997 is given in Table 5.

The world's longest established major germplasm collection is maintained at the Nicolay Ivanovich Vavilov Scientific Research Institute of Plant Industry (VIR), St. Petersburg, Russia. Initiation of the GRDC/CLIMA/ICARDA project on the preservation and utilization of the unique pulse and cereal genetic resources of the N.I. Vavilov Institute necessitated an access to VIR's crop databases in order to select the genetic resources accs. for further research. During 1996 and 1997 contacts with VIR scientists dealing with the germplasm documentation and databases were established through exchange of visits and correspondence. As a result computerized data from VIR's database can now be queried on ICARDA's network. These proved very fruitful and subsequent collaboration should lead to periodical exchange of updated records of germplasm collections between the cooperating Centers for optimal utilization of genetic resources collections.

A database of microbial genetic resources in CGIAR Centers was initiated in ICARDA in 1997. This project attempts also to initiate the process leading to the development of a strategy and standards for microbial collection and conservation at CGIAR centers, placement of the CGIAR microbial collections under the auspices of FAO, and the development of a CGIAR policy on collections and distribution in line with the Convention on Biological Diversity (CBD). In October 1997, GRU-ICARDA hosted the project's workshop attended by the representatives from other CGIAR Centers, viz., the International Institute for Tropical Agriculture (IITA); the International Livestock Research Institute (ILRI); International Rice Research Institute (IRRI); and ICARDA. For more information on SINGER and other genetic resources documentation systems projects see **Section 1.5.**

Table 5. Database-generated summary of origins of accs. at ICARDA genebank (as of December 1997)

Germplasm type	WANA countries		Other countries		Unknown origin		Total
Barley	10461	45.6	12179	53.1	283	1.2	22923
Wild *Hordeum*	1613	92.9	97	5.6	27	1.6	1737
Durum wheat	14954	75.1	4433	23.7	230	1.2	18717
Bread wheat	7199	91.1	680	8.6	27	0.3	7906
Other *Triticum* spp.	222	46.4	141	29.5	115	24.1	478
Wild *Triticum* spp.	1411	97.2	19	1.3	21	1.4	1451
Aegilops spp.	2458	78.5	648	20.7	25	0.8	3131
Total cereals	**37640**	**66.4**	**18338**	**32.3**	**843**	**1.3**	**56343**
Chickpea	7648	78.3	1884	19.3	230	2.4	9762
Wild *Cicer*	262	99.2	1	0.4	1	0.4	264
Lentil	4313	55.6	3413	44.0	33	0.4	7759
Wild *Lens*	417	90.1	46	9.9	-	-	463
Faba bean	2258	50.9	2144	42.6	328	6.5	5030
Faba bean BPL	2189	41.7	2117	40.3	947	18.0	5253
Total food legumes	**17387**	**60.9**	**9605**	**33.7**	**1539**	**5.4**	**28531**
Medicago	6427	82.9	1178	15.2	148	1.9	7753
Vicia	3875	69.7	1655	29.8	28	0.5	5558
Pisum	1129	26.4	2573	60.2	569	13.3	4271
Lathyrus	1566	51.5	1466	48.2	7	0.2	3039
Trifolium	3723	81.2	795	17.3	68	1.5	4586
Alfalfa	322	49.5	278	42.7	51	7.8	651
Avena	19	3.5	526	96.5	-	-	545
Other forages	3884	85.7	608	13.4	39	0.9	4531
Total forages	**20945**	**67.7**	**9079**	**29.3**	**910**	**2.9**	**30934**
GRAND TOTAL	**75750**	**65.4**	**36881**	**31.8**	**3177**	**2.7**	**115808**

Seed Health Laboratory (SHL)

The SHL operates under the supervision of Dr Ahmed El-Ahmed. The work of the SHL in observation of quarantine regulations for in-coming and out-going seeds is reported in **Section 2.1.** and **Section**

2.2. The SHL fully met its objectives in ensuring the safe movement of germplasm during the two season, and in addition conducted research on the effect of *Pyrenophora graminea* on barley yield and its components in Northern Syria. The study objected to assess the effect of infection with *P. graminea* on barley yield and its components of two barley cultivars "Roumi" and "Faiz". During the 1996-97 seasons the seed health laboratory in cooperation with the Virology laboratory (GP), produced a polyclonal antiserum for virulent Syrian isolates of *Pseudomonas syringae* pv. *pisi*, the casual agent of bacterial blight of pea. In addition, 201 accs. of pea, collected from 17 countries and preserved in ICARDA's gene bank, were screened in 1997 under artificial inoculation for resistance to a mixture of 4 virulent Syrian isolates of *P. syringae* pv. *pisi*. The research component of SHL's work in development of new methods of detection of pathogens can be found in **Sections 1.4.7., 1.4.8.** and **1.4.9.**

Training and international cooperation

There was considerable increase in training activities at GRU during 1996 and 1997. As compared to only 52 trainees in 1994 and 1995, 112 trainees (an increase of over 100%) attended a total of 14 training courses. A number of short courses were conducted by GRU staff jointly with those of IPGRI and GP of ICARDA. An in-country training course on "Genetic Resources of Grain Legumes" was organized jointly in cooperation with IPGRI and IAV Hassan II in Morocco during February-March 1997. A specialized training course on "Faba Bean Improvement - with Emphasis on Host Plant Resistance" was organized jointly by GP and GRU in March-April 1997. The SHL staff conducted two training courses in Iran on "General Seed Technology" and "Seed Quality Control".

In addition to the above, individual training in various aspects of genetic resources conservation work, including the use of electrophoretic techniques, was also provided to NARS scientists. More details are provided in **Section 3.1.** The SHL played a significant role in providing individual training. For instance, during 1996 and 1997 one scientist each from Syria, Algeria and Jordan were trained in "Seed Health Testing and Field Inspection" techniques (see **Section 3.2.**)

Details of research carried out within the frame-work of the special project on "**Enhancing wheat productivity in stress environments utilizing wild progenitors and primitive forms**" at the Department of Agrobiology and Agrochemistry, University of Tuscia, Viterbo, Italy, is reported in **Section 1.4.10.** This collaborative research work was conducted by Elena Iacono under the supervision of Professor Enrico Porceddu.

Research on "**Measurement of biodiversity within the genus *Lens***", funded by Overseas Development Agency (ODA), UK, [Project R5578(H)] and conducted jointly with GRU-ICARDA and the University of Birmingham, UK, is reported in Sections **1.4.11.** and **1.4.12.** This work was carried out by Ms Morag Ferguson under the supervision of Dr Larry Robertson.

The collection of plant genetic resources from centers of diversity has been a major aim of a cooperative project funded by Australian Center for International Agricultural research (ACIAR) as a restricted core grant to ICARDA. In this project ICARDA and the Center for Legumes in Mediterranean Agriculture (CLIMA) are equal partners in the collection of legume plant genetic resources from the Mediterranean region and in assisting its transfer to host countries like Pakistan, Bangladesh and Ethiopia which generally lack the resources to exploit germplasm from outside their own countries. The collection, conservation, and distribution of genetic resources under this international cooperative project is reported in several sub-sections of **Section 1.2.**

Genetic resources related activity

A International Symposium on the "**Origins of Agriculture and Domestication of Crop Plants in the Near East**" was organized largely through the initiative of GRU scientists and held at ICARDA 10-14 May, 1997. There were just over 60 registered participants from diverse disciplines from more than 23 countries. Over 30 papers and posters were presented. This was the first international meeting of its kind to be held in the West Asia and also the first one at an international center, ICARDA. The Symposium was part of the celebrations to commemorate 20 years of ICARDA's work in the region. This Symposium was dedicated to the work of Professor Jack R. Harlan in recognition of his efforts at understanding crop evolution

and the origins of agriculture. During his long and distinguished career Harlan received several honors and prizes. He was presented (*in absentia*) with a lifetime achievement award at the Symposium. A "Book of Abstracts" was produced by the GRU and published by ICARDA. For more details about this Symposium and the full proceedings volume see **Section 4.**

Publications and staff list

As in the past years, the GRU continued to maintain its high rate of scientific publications in 1996 and 1997. There were 37 publications in all as follows: Books (2), Journal papers (10), Book chapters (8), Conference presentations (12), and Newsletter articles (5).

A complete list of these publications produced by GRU staff and their co-authors is reported under **Section 5.** The GRU staff-list as in December 1997 is under **Section 6.** The acknowledgements and the appendixes appear at the very end of this report.

J. Valkoun and GRU staff

1.2. New germplasm collected/introduced during 1996 and 1997

1.2.1. Collection of cereal wild progenitors in Syria in 1996

During the 1995 collection mission to Gaziantep Province, Turkey (GRU Annual Report 1994 and 1995, Section 1.2.1.), a population of *Triticum araraticum* Jakubz. was found 10km north of the Syrian border. As the species has not been found in Syria and there were reports on new *Triticum urartu* sites in the north of the country (G. Willcox, pers. comm.), a survey and collection mission was undertaken in 1996 in cooperation with the Agricultural Research Center (ARC), Douma, to learn more about the present status and geographical distribution of wild *Triticum* spp. and other wheat wild relatives in northern Syria. Three populations of *T. araraticum* were found in Aleppo Province. Two of these were mixed with *Triticum dicoccoides*. One site, a relatively undisturbed hard limestone rocky slope, was identified for possible *in situ* conservation in future because of its high plant species diversity. The first finding of *T. araraticum* in Syria extends the geographical distribution of the species in the western part of the Near East arc further southwest. New *T. dicoccoides*, *T. urartu* and *Triticum baeoticum* Boiss sites were identified and samples collected in Aleppo and Raqq'a provinces. Also, four new *Aegilops tauschii* sites were discovered between Ain Al-Arab almost at the Turkish border and Al-Koum deep in the Syrian desert. In total, the mission yielded 40 bulk and 165 single-plant samples of cereal wild progenitors and relatives.

J. Valkoun, B. Humeid (GRU-ICARDA) and Kh. Obari (ARC, Douma, Syria)

1.2.2. Explorations for cereal wild progenitors in Syria in 1997

An exploration mission to central Syria, covering the provinces of Hama, Homs and Idleb was mounted in June 1997. The objective of this mission was to find and sample habitats of wild *Hordeum* and *Triticum* spp. A survey of the geographical distribution of wild *Triticum* spp. in central provinces of Syria was conducted in order to

Table 6. Geographical location and description of collection sites in Syria

Site no.	Province	Longitude	Latitude	Altitude	Rainfall
1	Homs	E 36° 29'	N 34°49'	780	700
2	Homs	E 36° 28'	N 34°49'	500	680
3	Homs	E 36° 34'	N 34°51'	390	450
4	Homs	E 36° 44'	N 34°53'	430	450
5	Homs	E 36° 40'	N 34°53'	395	400
6	Homs	E 36° 36'	N 34°54'	360	430
7	Homs	E 36° 33'	N 34°53'	345	450
8	Homs	E 36° 38'	N 34°54'	360	450
9	Homs	E 36° 40'	N 34°56'	370	400
10	Hama	E 36° 38'	N 34°58'	360	400
11	Homs	E 36° 51'	N 34°57'	470	320
12	Hama	E 37° 00'	N 35°02'	600	300
13	Hama	E 36° 42'	N 35°01'	340	350
14	Idleb	E 36° 54'	N 35°34'	420	260
15	Idleb	E 36° 53'	N 35°34'	420	260
16	Idleb	E 37° 01'	N 35°33'	390	240
17	Idleb	E 36° 33'	N 35°36'	560	480
18	Idleb	E 36° 26'	N 35°37'	720	530

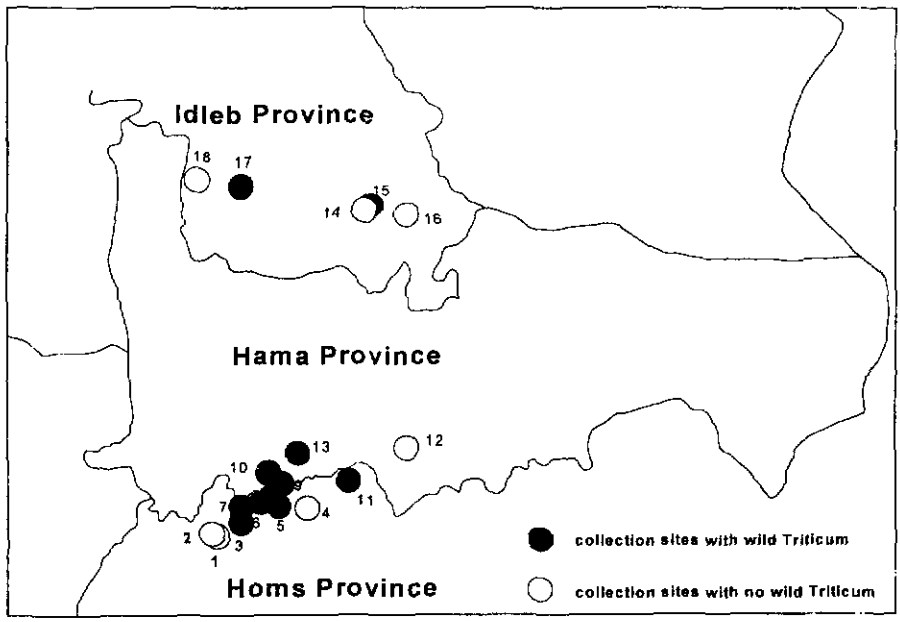

Fig. 1. Map showing collection sites of wild cereal progenitors in Hama, Homs, and Idleb provinces of Syria

to fill the gaps in the current knowledge on the occurrence of wild wheats in the target region, which is poorly represented in the wild *Triticum* spp. genepool at ICARDA as well as ARC Douma. It was possible to assess the extent of genetic erosion in natural populations of wheat and barley wild relatives, as well as, identify sites suitable for *in situ* conservation of wheat and barley wild relatives. Collection site data are briefly summarized in Table 6 and site locations are shown in Fig. 1.

The collection team commenced by exploring an extensive basaltic area west and south-west of Homs. However, no wild cereal species were found in this area. Most of the land was cultivated and comprised of field borders and roadsides, which were heavily over-grazed. Even the soil texture was not typical for wild *Triticum* spp. Prevalence of perennial grasses indicated high rainfall. Subsequently, the team went to the north and sampled natural populations of *Aegilops biuncialis, Ae. triuncialis* and *Ae. peregrina,* and one population of wild barley, *Hordeum spontaneum* in a hilly area in the vicinity of Sharaqliyah. A wild wheat, *Triticum dicoccoides,* population was found at the south-western margin of a large basaltic plateau, which extends west of the Homs-Hama national highway. This population was growing among irrigated crop fields, at some distance from the villages, on stony field borders and uncultivated patches where it was somewhat protected against over-grazing. The soil was a typical vertisol, the preferred habitat of wild wheats. Except for this finding, the entire region was heavily over-grazed, and not a single wild wheat plant was found in the nearby grazing land on stony hills.

Next a complete exploration of the basaltic plateau west of the Homs-Hama highway was conducted. It turned out that the whole region may provide suitable habitats for *T. dicoccoides*. Its presence or absence depends on the degree of over-grazing and stone removal from field borders and stony patches within the fields. Most of the area is irrigated and all land is cultivated. Consequently, the only refuge left for the wild wheat is roadsides, stony field borders and heaps of stones and stony patches within the fields themselves. The habitats in the vicinity of villages are heavily over-grazed. Thus, the wild wheat populations could survive only in areas far removed from

these villages. The close genetic proximity of the wheat wild progenitor, *T. dicoccoides*, with cultivated durum and bread wheats at the field borders results in occasional production of spontaneous hybrids. This seems to be a fairly frequent event, as eight such hybrids (or introgressed forms) were sampled from different sites and the germplasm so abundant that not all the hybrids found were collected in a single day.

Usually the hybrid products had spikelets with more than two grains as in cultivated wheat but the rachis was brittle like in *T. dicoccoides*. One can surmise, that locally grown landraces of durum wheat, e.g., "Abbasiyeh", have accumulated a number of *T. dicoccoides* genes by occasional inter-crossing and subsequent introgression. On the other hand, local wild wheats may not be so `wild' if the gene flow has taken place in both directions. A total of six *T. dicoccoides* populations were sampled (sites 5 to 10 in Tables 6 and 7, and Fig. 1), together with associated eight hybrid forms and two cultivated durum wheat populations. This germplasm may be a valuable material for molecular studies of gene introgressions between the wheat wild progenitor and cultivated wheats and thus throw light on certain as yet unexplained aspects of the origin of modern wheats.

The areas east of the Homs-Hama highway were also thoroughly explored to ascertain, as to how far wild wheats penetrate in to the low-rainfall zone. At collection Site 11 (Fig. 1) the decisive detrimental effect of over-grazing, particularly by small ruminants, on the natural populations of wheat and barley wild relatives could be clearly discerned. This site was part of a reforestation area with abundance of annual grasses, *Aegilops* spp. and *Hordeum spontaneum*, in particular. Four *Aegilops* spp., *speltoides, kotschyi, vavilovii* and *geniculata* were present. *H. spontaneum* produced a massive stand which resembled a cultivated barley `field' in the lower part of the protected area, and several small sub-populations of *T. dicoccoides* were also found scattered in the upper part. This rich biodiversity of cereal wild relatives was in striking contrast with the surrounding unprotected area, which was either cultivated or intensely over-grazed, and depleted of any wild species of interest.

Table 7. List of species of wild relatives of cereals collected in Syria

Genus	Species	No. of samples collected Bulks	SP*	Collected from sites
Hordeum	*spontaneum*	15	-	2,3,4,5,6,7,8,9,11,12,13, 14,16,17,18
Triticum	*dicoccoides*	10	301	3,5,6,7,8,9,10,11,13,17
Triticum	*urartu*	3	44	13, 15, 17
Triticum	*baeoticum*	1	15	13
Triticum	*araraticum*	1	25	17
Aegilops	*speltoides* var. *speltoides*	3	-	11,14,17
Aegilops	*speltoides* var. *ligustica*	1	-	14
Aegilops	*searsii*	1	-	14
Aegilops	*kotschyi*	3	-	11,12,16
Aegilops	*vavilovii*	2	-	11,14
Aegilops	*crassa*	1	-	16
Aegilops	*biuncialis*	3	-	1,17,18
Aegilops	*triuncialis*	2	-	1,2
Aegilops	*columnaris*	2	-	17,18
Aegilops	*peregrina*	2	-	1,2
Aegilops	*geniculata*	1	-	11
x *Triticum* hybrids		-	8	5,6,7,8
Total		**61**	**393**	**18 sites**

* SP = single-plant

Further along this route, the area around Salamiyeh was too dry and the soils were poor. Therefore, only those species well-adapted to marginal conditions, such as, *H. spontaneum* and *Ae. kotschyi* were found and collected (Site 12, Fig. 1). The inspection of the basaltic hills north of the Salamiyeh-Hama road revealed a similar scenario. The team then returned to the northern margin of the basaltic plateau, which had been sampled previously. The search near Bisrin village paid off, as not only *T. dicoccoides*, but also two wild diploid wheats, *T. urartu* and *T. baeoticum*, were found (Site 13, Fig. 1). This indicates that the basaltic plateau west of Homs-Hama highway is rich not only in *T. dicoccoides* but may still harbor remnant populations of the two wild diploid wheats.

There has been a large gap in the geographical distribution of wild diploid wheats, both *T. urartu* and *T. baeoticum*, extending from the north of Aleppo Province to Ba'albek in Lebanon. They were found to occur near Hama and with an extensive area with *T. dicoccoides* stands west of the Homs-Hama highway, indicate that the geographical distribution of wild wheats is not as discontinuous as reported by Jack Harlan and Daniel Zohary back in 1966.

The next area to be explored was the extensive basaltic region located in a low-rainfall zone east of Ma'aret Numan. Surprisingly, a site (No. 14, Fig. 1) was discovered to be rich in *Ae. speltoides*, (both var. *speltoides* and var. *ligustica*) in 260-270mm zone which is much further than other reported sites mostly in the high-rainfall zones. Closer inspection of the site yielded two other drought-adapted *Aegilops* spp.; *vavilovii* and *searsii*. The latter is an entirely new discovery for northern Syria, and northern part of the Near East arc as a whole. Its occurrence was supposed to be limited to central Palestine, the western mountain ranges of Jordan, and in south-western Syria and Lebanon. The northernmost geographical distribution previously reported was at least 200 km south of this site, near Ba'albek in the Beka'a valley. Some 2km east from Site 14, a small, but morphologically diverse *T. urartu*, population was found on both sides of the road (Site 15, Fig. 1). Again, this finding updates our knowledge of the present geographical distribution of the species. It also confirms that, *T. urartu* is the most drought-tolerant wild wheat, adapted to stressful environments which range from the extreme cold of Mt. Lebanon at altitudes over 1800m asl to the heat of low-lands at margins of the Syrian desert.

The mission continued further eastward but despite a thorough search all around, no other wild wheats could be found in that season. *Ae. crassa, Ae. kotschyi* and *H. spontaneum* were collected in a very dry Site 16 (about 240mm annual rainfall). Due to the fact that the dry rangelands in the eastern part of the basaltic area were heavily over-grazed, as were the field borders and stony patches in the higher rainfall area, the team moved to a very different basaltic region west of Ma'aret Numan. An extremely interesting site, 2km south of Kafr Nabil, was discovered. This site comprised a mixed fig and olive tree plantation with a large number of wild wheat and *Aegilops* spp.

growing at the base of the stony walls and around heaps of basalt stones within the enclosure. Three wild *Triticum* and three *Aegilops* spp. were found on the site together with *H. spontaneum*. The most exciting discovery was the presence of *Triticum araraticum*, a species which used to be considered a typical element of the eastern part of the Near East arc. In 1996, for the first time in Syria, *T. araraticum* was found near the base of the Saint Simeon Citadel ruins by the joint ICARDA-ARC exploration mission. The discovery at the Kafr Nabil site extends the geographical distribution of the species in the western part of the Near East arc some 100 km to the south. The presence of *T. urartu* and *T. dicoccoides* is new for that part of Syria and, again, fills the gap in our knowledge of the species' geographical distribution.

The basaltic low-land area near Jisr ash Shughour did not, in spite of an intensive search throughout the area, yield any wild wheats because of a high disturbance factor. The entire region is either intensively cultivated or heavily over-grazed stony patches. No suitable habitat for wild wheats remains intact in this area.

Recommendations for future action

The basaltic regions in Homs, Hama and Idleb Provinces with potential habitats for wild *Triticum* spp., have been sufficiently covered during this mission. However, hard-limestone areas with vertisols, which may also be a good habitat for these species, were not covered. Therefore, it is recommended that another mission should be conducted in future to focus on the hard-limestone areas in the 250-650mm rainfall zone. A project proposal relating to on-farm conservation of wild *Triticum* spp. in Homs, Hama and Idleb provinces should be developed urgently to stop the destruction of these genetically important populations, which represent a bridge between large wild wheat regions in southern Syria and west Beka'a in Lebanon, and south-eastern Turkey. The project, if approved, should focus without delay on stony field borders and stony patches within fields, as well as strips at the stony walls in fruit tree plantations as possible habitats of the target species in the agricultural landscape.

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1.2.3. Survey of biodiversity of rangelands of Oujda region, Morocco in 1997

A joint mission to survey the rangelands of the Oujda region of Morocco for plant biodiversity was carried out in cooperation with Institut de la National Recherche Agronomique (INRA), Centre Régional de la Recherche Agronomique, Oujda, Morocco, and the Natural Resources Management Program (NRMP) of ICARDA.

The main objectives of this mission were: (1) to survey, collect and catalog the biodiversity of the rangelands of the Oujda region in the rural communes of El Ateuf, Ouled Mohammed, Ouled Ghzyal, Merija and Beni Mathar; (2) using the catalog of the available biodiversity in this region to provide a baseline for future work on rangeland rehabilitation in this area; (3) to record eco-climatological data for collection sites for eco-geographic analysis of the distribution of rangeland species; and, (4) to provide germplasm with edaphic adaptation to harsh conditions for future research and, rangeland rehabilitation in this and other regions.

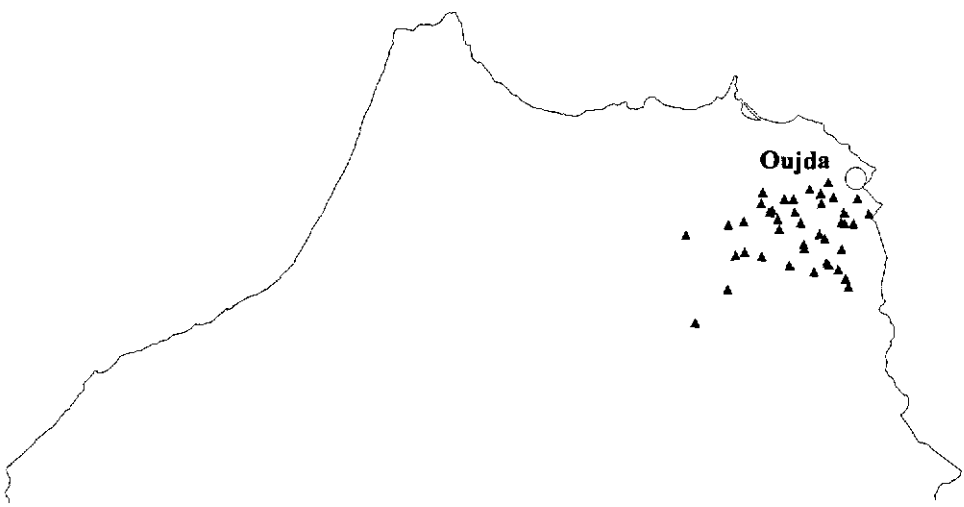

Fig. 2. Collection sites of rangeland species in Oujda, Morocco

The collection route covered a total of 2200 km and rainfall regions of 180 to 500 mm. In all, 43 sites were collected (Fig. 2). Samples were collected at intervals of 10-15 km, along a collection route which cover the above mentioned rural communes. Approximately 50 plants were sampled per species to adequately sample the variation available and to provide sufficient seed to allow splitting of samples two ways. Emphasis was given to collecting full passport data and sufficiently identifying each collection site geographically and ecologically. The global positioning system (GPS) units were used to accurately fix collection sites. Climatic data were obtained from published records. Elevation was measured during sampling using an altimeter. Soil samples were taken from the top 30 cm at the sites to provide mechanical analysis and tests of pH, $CaCO_3$, soil color, available phosphorus and total nitrogen. This will allow the studies of the eco-geographical distribution of range species.

In addition to the collection of germplasm, 100-step (approx. 100m) transects were taken at each collection site to measure the relative frequencies of each rangeland species. This data will be used for studies on biodiversity of rangelands. Relative frequencies will be used to calculate species diversity at each site by using the Shannon Weaver species diversity index. The co-relationship between species diversity and ecological data will be studied.

In all, 385 accs. from at least 60 species were collected (Table 8). In the area of the collection, the most frequent rangeland plant collected was *Stipa* spp. (51 accs. of 4 species). Other important rangeland plants collected were *Helianthemum* spp., *Herniaria* spp., *Paronychia argentea*, *Peganum harmala*, *Plantago* spp., *Schismus barbatus* and *Thymus* spp. Another important rangeland plant Artemsia spp., was found frequently but was not collected as it sets seed in the autumn. In areas brought to cultivation where there was protection from grazing, species of vetch and medic species were collected which are likely to yield useful germplasm for replacement of fallow in the agricultural zone of the Taouirirt-Tafoughalt development project which started in 1997.

Seed of collected ecotypes was divided into two equal parts. One part was left at INRA for the use of the national program, and the other taken to ICARDA for multiplication and conservation.

Germplasm collected will be freely available for all bonafide users once the seed are multiplied. ICARDA will introduce the germplasm collected during this mission into the collections maintained at ICARDA's gene bank. As for all material collected and conserved by ICARDA-GRU, the sub-samples or derivatives of the present material will be distributed under the terms of a Material Transfer Agreement (MTA), which describes the conditions for the use of the material.

Passport data is in the process of being computerized and put into the ICARDA germplasm collection database. Soil has been deposited for analyses at the Département du Milieu Physique, INRA, Rabat, Morocco. Once this is completed, the data will be added to the ICARDA germplasm database. Data on rainfall and temperatures for the collection sites needs to be completed and added to the ICARDA germplasm database.

Other species for collection

Certain species do not normally set seed during the period of the collection mission but mature during the autumn (e.g., *Artemisia* spp., *Atriplex* spp., *Noaea mucronata*). It would be important to collect these plants in the region covered in future.

Other areas for collection

This collection only covered some rural communities of Oujda, Taourirt and Jerada provinces. There is a need to collect in other rural communities rurales in Oujda and also in the provinces of Bouarfa and Figuig.

Evaluation and utilization

The germplasm collected will be multiplied and characterized for potential use in rangeland rehabilitation. The vetch and medic germplasm collected may have the most immediate use to replace fallow in the agricultural zone of the Taouirirt-Tafoughalt development project, which started in 1997, and therefore require multiplication and evaluation in this region.

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Table 8. Forage and other species collected in Morocco, 1997

Botanical Name	No.	Botanical Name	No.
Adenocarpus bacquei	1	*Lotus corniculatus*	4
Aristida spp.	2	*Lygeum spartum*	5
Artemisia herba alba	3	*Medicago laciniata*	5
Asphodelus microcarpus	7	*Medicago aculeata*	2
Asphodelus spp.	1	*Medicago polymorpha*	2
Astragalus hamosus	3	*Medicago truncatula*	10
Atractylis serratuloïdes	3	*Melilotus sulcata*	7
Atriplex glauca	1	*Mentha pulegium*	3
Bromus rigidus	24	*Noaea mucronata*	7
Coronilla scorpioides	6	*Onobrychis crista-galli*	1
Cynodon dactylon	2	*Paronychia argentea*	12
Dactylis glomerata	8	*Peganum harmala*	19
Erodium spp.	1	*Plantago albicans*	17
Festuca elatior	3	*Plantago lanceolata*	3
Festuca elatior	3	*Rosmarinus officinalis*	1
Filago spathulata	3	*Rosmarinus tournefortii*	5
Globularia alypum	1	*Schismus barbatus*	17
Helianthemum hirtum	17	*Scorpiurus sulcata*	6
Helianthemum lippii	8	*Stipa barbata*	4
Herniaria fontanesii	18	*Stipa parviflora*	21
Herniaria spp.	6	*Stipa retorta*	10
Hippocrepis unisiliquosa	1	*Stipa tenacissima*	16
Hordeum murinum	1	*Thymelaea microphylla*	1
Hordeum spp.	6	*Thymus algeriensis*	3
Juniperus oxycedrus	1	*Thymus hirtus*	24
Lathyrus clymenum	1	*Trigonella monspeliaca*	5
Lathyrus spp.	2	*Vicia monantha*	18
Launea acanthoclada	1	*Vicia* spp.	1
Launea arborescens	2	*Ziziphus lotus*	2
Lavatera cretica	9	Unknown spp.	7

1.2.4. Collection of plant genetic resources in Ethiopia-I in 1997

The collection of plant genetic resources from Ethiopia has been a major aim of the project funded by Australian Center for International Agricultural Research (ACIAR) as a restricted core grant to ICARDA. In this project ICARDA and the Center for Legumes in Mediterranean Agriculture (CLIMA) are equal partners in the collection of legume plant genetic resources from the Mediterranean region and in assisting its transfer to host countries like Pakistan, Bangladesh and Ethiopia. These countries generally lack the financial and infrastructural resources to exploit germplasm from outside their own boundaries.

Over 90 percent of Ethiopia's population depend on agriculture for their food supply. Small subsidence farmers plant old landraces which they themselves have developed through selection over several decades. These farmer-developed landraces still form the basis of most crop germplasms. For environmental conditions for which ICARDA's germplasm is targeted, Ethiopia is one of the best potential sources of new and rare gene combinations in both pulses and cereals.

The collection mission in January, one of two planned for 1997, had been postponed for two years as Ethiopia, in line with many other North African countries, has developed its policy towards use of their genetic resource base by other countries. In particular the sharing of any economic benefits from commercialization of genetic resources has been a contentious issue. Formal agreements are now necessary and a major requirement of an agreement is that ICARDA and CLIMA ensure that potentially valuable germplasm for Ethiopia from their own collections is lodged with the National Collection of Ethiopia. The joint project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" with CLIMA funded this mission and the ACIAR supported it.

The collection in January 1997

The initial collection was concentrated on legumes belonging to lupin, lathyrus and lentil species; the crops which are at or near harvest time in January each season. A subsequent trip to collect faba bean and peas was scheduled for late November. Staff of the Biodiversity Institute (BDI) accompanied the mission and were the key to its success for collecting 311 lines in 12 days (Table 8 and Fig. 3). Whilst most samples were collected in the field, samples were also

collected from farmers' markets in the towns on the route. Market samples, however, were only taken when the specific village or farming region of origin could be identified.

In all, 1880 km were covered from around Addis Ababa to Gondar in the North. Because of the priority placed on lupins, the more sandys soils of the region surrounding Lake Tana were the subject of special attention during this mission. Basalt is the most common base rock often producing heavy textured but fertile soils with pH usually around 6. Pulses collected from such soils should possess adaptation to low pH *per se*.

Table 9. Species collected in Ethiopia in January 1997

Species	**Accs.**
Cicer arietinum	59
Carthamus tinctorius	1
Eragrostis tef	1
Hordeum vulgare	7
Lathyrus sativus	68
Lens culinaris	26
Lens ervoides	1
Lupinus albus	69
Medicago polymorpha	8
Pisum sativum	20
Quizotia abyssinica	1
Scorpiuris muricatus	1
Trifolium species	4
Trigonella foenum-graecum	7
Triticum diccocum	3
Triticum durum	1
Triticum aestivum	5
Vigna ungulata	1
Vicia faba	23
Total	**311**

In the future, the collection of *Rhizobium leguminosarum* from faba bean and chickpeas on the acid and less well drained soils will be of particular interest. An extension of this project should plan for more collecting missions in Ethiopia and postgraduate studies in Perth, Western Australia, using the Ethiopian strains.

Lupins

In all, 69 white lupin (*Lupinus albus*) accs. were collected from the Lake Tana region. They included mostly relatively large samples from farmers' crops. The soils were typically red-brown light sandy loams. During this time of the year, lupins were almost the exclusive pulse crop sown in the region. The Ethiopian farmers, over time, have clearly recognized lupins as the superior crop on such soils. The lupins were strongly selected not only for the non-shattering trait but also for a high biomass. The lupin stubble after harvest and the seed are key parts of the animal feed system and tall lupins are favored over short ones. The seed is soaked to remove harmful alkaloids and then roasted for human comsumption. The same lupins in ground form is also fermented into a strong heady liquor.

In such a high rainfall subtropical climate, it is expected that evolution of disease resistance should also have been a feature in contributing to the success of lupins as a crop in the region. The populations will consequently be introduced at the earliest opportunity into the anthracnose screening program. Early indications, with only two accs. available, show that Ethiopia is likely to be a good source of resistance (see Table 9).

The lupins, like other pulse crops in Ethiopia, are grown in rotation with oil seeds and cereal crops. Clearly the farmers appreciate the benefits of legumes in rotation. They have developed a farming system with an impressively high proportion of legume crops, in fact as high as encountered in Western Australia, where the proportion of legumes is higher than anywhere else in the world.

***Lathyrus sativa* (grasspea)**

In contrast to reports from elsewhere in the world, the area of Lathyrus is actually on the increase in Ethiopia. This is partly related to the extensive tracts of very heavy soils that are poorly aerated when wet, and the broad valleys subject to incipient waterlogging.

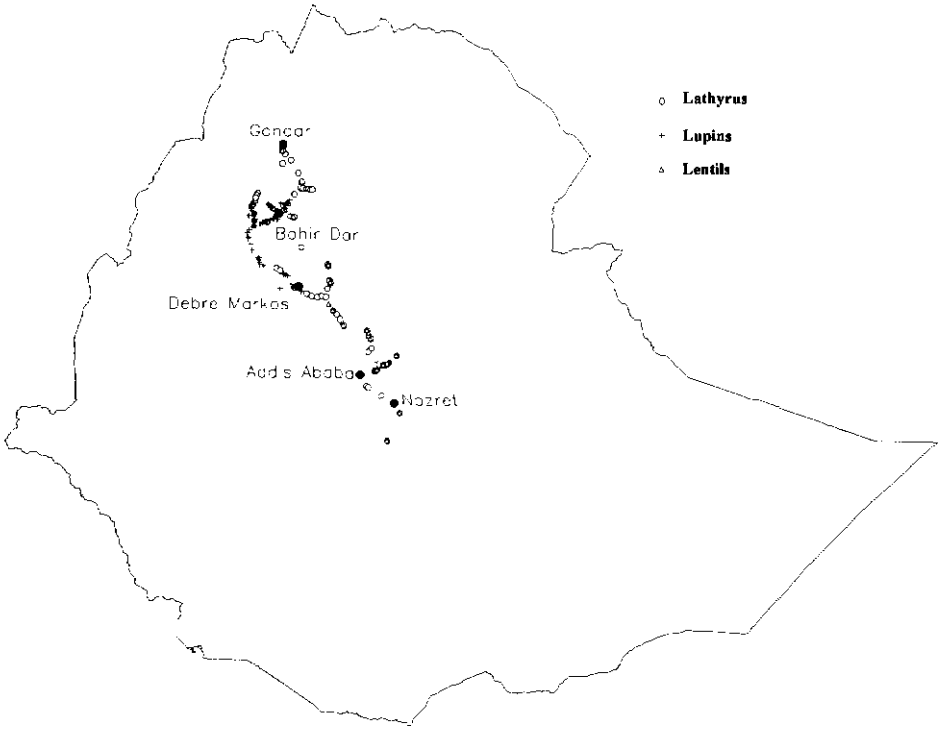

Fig. 3. Collection sites for lathyrus, lupins and lentils in Ethiopia

The farmers have recognized that *Lathyrus* is a more user-friendly crop than lentil or chickpeas on such soils and one that is easier to manage and less prone to diseases. The increase in the area is despite the dangers of lathyrism caused by the free amino acid ODAP (oxalyl diamino propionic acid). Though the people have clearly learned to live with this problem and try to minimize the dangers during the food preparation, it was disturbing to see young children chewing and eating the green pods. CLIMA has introduced 59 low ODAP lines at the BDI. These will be assessed for production against local controls. This large collection of 68 landraces will give us a much clearer picture of the maturity needs for the N and S highlands of Ethiopia and the inherent variation in ODAP content.

Lentils

Although 26 lines of lentils were collected, extensive planting of lentils was common only around Addis Ababa. Small nursery plots for

home consumption was not uncommon in the northern provinces. Lentils are, thus, not a major crop in area terms although a quite important (and tasty) adjunct to the national vegetarian dishes served on Wednesdays and Fridays in line with orthodox Christian religious practice,

Lentils, like chickpeas, are grown on only the best-drained parts of the heavy clay loam soils. They are almost exclusively the small seeded red lentils. They differ somewhat, however, from the pilose small seeded red types found in Nepal and Northern India, and represent a distinctive population. Maturity-wise they are early and this trait should be useful in the search for drought avoidance as moisture becomes scarce as the season progresses. Their main value however will be in the accumulation of disease resistance genes in the populations rather than a direct benefit. The fact that the crops are exclusively hand-harvested means that there has been no selection for plant height uniformity required for machine harvest of lentils.

Chickpeas

The chickpeas were all of the desi type with a large range of seed size and color amongst them. In all, 59 large samples were collected. Their early maturity will be advantageous for disease resistance, especially to *Ascochyta* blight. Hence, earliness was a criteria for the collections.

Chickpea crops were relatively widespread on the heavier and occasionally alkaline soils. Where the crop was extensive and matured enough, sub-samples selected for height and biomass were made. Likewise, in the town and village markets, samples were selected for larger seed size and a bright, light orange seed color.

The chickpea accessions, along with the faba beans and peas, remained with the BDI as they were not covered by the then current collection agreement. They will, however, be listed amongst the species for the collection mission in following November.

In the future, there is to be an expanded effort into kabuli chickpea also. The early maturing lines with *Fusarium* wilt resistance would be a priority amongst introductions from ICARDA.

Faba beans and peas

Only 43 market samples of faba beans and peas were available. The fact that faba beans were typically from acid soils will be of interest to the Western Australia programs, as well as that they very often

grown on poorly aerated oils. The beans are of a high biomass, tall type but strongly selected for a high pod number. They are moderate to small in seed size. The earliness and vigor are likely to be valuable characters for breeding programs.

Pea germplasm collected was both the green forage-type and the larger culinary-type. The later collection mission in November 1997 concentrated on both types and their ecology.

A MOU has been completed between the Biodiversity Institute, ICARDA and CLIMA. An essential part of this, from the Ethiopian point of veiw, is that potentially useful genotypes are donated to Ethiopia in line with the numbers being expatriated. It will also be important to develop mutually beneficial research projects with Ethiopian researchers. This will involve research and training assistance.

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1.2.5. Collection of plant genetic resources in Ethiopia-II in 1997

Agricultural research is being re-oriented in Ethiopia to bring plant research under a single organization. It is, at present, devolved amongst the IAR (Institute of Agricultural Research) and various Agricultural University faculties. A decision on the appointment of a Director of the new umbrella organization EARO (Ethiopian Agricultural Research Organization) had not been made at the time of the second mission in October 1997. It was understood that the BDI, however, will remain independent.

The formalities required to be undergone for collection and exchange of plant genetic resources had been lengthened considerably since our last visit in January 1997, effectively requiring a separate and precisely defined MOU for each mission. A brief meeting with the previous Director of BDI and now Minister for Agriculture, Dr Seyfu Ketema, confirmed their commitment to the project but he stressed once again the necessity of movement of germplasm into the national collection from the foreign partners. In this context lupins, low ODAP lathyrus, *Brassica napus* cultivars, and Kabuli Chick peas have or will soon be shipped to Ethiopia from ICARDA and CLIMA.

A commitment to transfer recently characterized chocolate spot (*Botrytis fabae*) and rust resistant faba bean germplasm to Ethiopia was also made. These lines, which come mostly from very recent collections in Ecuador, should be extremely valuable to Ethiopia as rust and chocolate spot are the major disease threats to the species in the country.

Faba beans and peas

The prime aim of the October 1997 mission was to collect faba bean and pea germplasm and to revisit some key lupin sites in the Lake Tana area from which *Ascochyta* resistance had been isolated. In all, 225 samples were collected (Table 10 and Fig. 4) to which the 42 market samples collected during the January mission would be added. The success of the mission was in no small way due to the diligence and efficiency of the Ethiopian counterparts in the team. They are highly experienced and made the trip a pleasurable as well as a rewarding experience.

The genetic resource base of peas in the BDI collection at Addis Ababa, Ethiopia, currently stands at 1,490. Out of these 997 are local landraces which no doubt are a valuable genetic resource. Peas and faba beans were common in the highlands, especially in the cooler higher regions. The best collections were usually obtained above 2400 m asl. The locality of Debre Behan and the highlands east of Gondar toward Tigre were particularly rich in diversity of these two food legumes. Further collection in both areas and in Tigre itself remains a priority. The crops were almost invariably grown as mixtures and separated by the farmers at harvest. This combination has a lot of logic in the control of black spot, in that the peas remain erect supported by the faba beans and have far less diseases than in high density pure pea crops. The farmers appear to have developed a system which improves seed yield at least of the peas. Faba beans usually dominated the mixture. They were small to medium sized beans coupled with vigorous large seeded green kernel - white seeded peas. Ms Aynebeba Ademu has made, in the Addis-Debre bean locality, 25 collections and isolates using funds provided by CLIMA. She intends to expand the collection next year and the BDI is likely to have the role of maintenance of the rhizobium genetic resource base under the new arrangements.

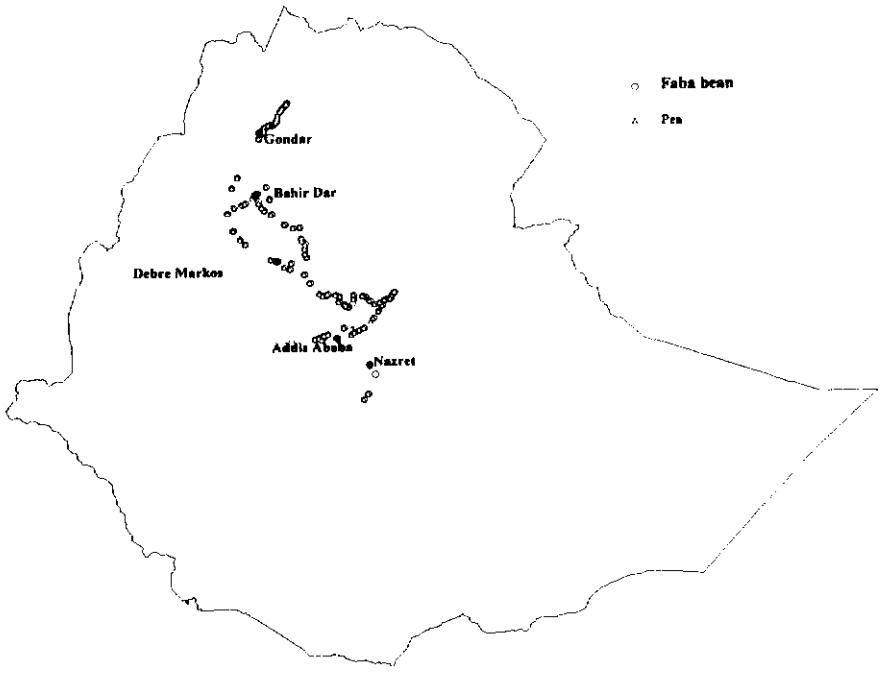

Fig. 4. Faba bean and peas collection sites in Ethiopia in 1997

Table 10. Summary of germplasm collections in Ethiopia in 1997

Species	Jan. 1997	Oct. 1997
Pisum sativum	20	108
Vicia sativa	22	112
Lens ervoides	-	2
Lupinus albus	-	3

Lupins

Lupins were common in the Lake Tana area as noted before. They were found to be far more common in the Debre Marcos regions than previously recorded and more collections were justified, as they were too green (immature) for collection in the previous mission. With the

Table 11. ***Lupinus albus*** **- Sites of anthracnose-resistant lupins collected in Ethiopia in 1997**

Site No.	Exact location	Province	ICARDA No.	Sample No.	Coordinates	Alt.
29	Yinesa Kidanam, 12km from Bahir Dar to Dangila	Gojam	118333	065	E37 18.55, N11 31.38	1900
31	Cebrabo; 15km from Bahir Dar to Dangila	Gojam	118335	067	E37 18.05, N11 29.87	2020
50	Zengelma Erbo; 7km from Bahir Dar to Gondar	Gondar	118364	096	E37 27.44, N11 37.14	1950
94	Gebar Duda; 23.3km from Bahir Dar to Chimba	Gojam	118441	173	E37 13.80, N11 38.83	1930
95	Yigadil-deta Mariam 24.2km from Bahir Dar to Chimba	Gojam	118442	174	E37 13.41, N11 39.18	1930
98	30km from Bahir Dar to Chimba	Gojam	118445	177	E37 11.19, N11 41.31	1900
142	Yewal; 233km from Bahir Dar to Dahe Mohor	Gojam	118496	228	E37 33.93, N10 25.07	2380
130	Kurb; 135km from Bahir Dar to Dahe Mohor	Gojam	118484	216	E37 02.95, N10 49.65	2600
131	Brodi; 139.5km from Bahir Dar to Dahe Mohor	Gojam	118485	217	E37 03.23, N10 47.89	2600
132	Quala; 143km from Bahir Dar to Dahe Mohor	Gojam	118486	218	E37 03.31, N10 45.83	2400
109	Simala; 27km from Dember to Kungzila	Gojam	118456	188	E36 55.37, N11 34.63	2000

aid of hand-held the GPS units, it was possible to locate the actual collection sites of lupins collected earlier this year. These samples had proven to be anthracnose resistant (sites 29 and 31). The farmers involved were happy to provide supplementary samples from their seed stores. Subsequent to this mission, further anthracnose testing in Perth has isolated a further range of sites with resistance. There are at least ten sites (Table 11 and map) providing a substantial degree of resistance to anthracnose. This germplasm will certainly be a great acquisition to the redevelopment of the white lupin export industry in Australia. Crossbreeding with low alkaloid lines has already commenced and could well provide a new crop option for both Australia and Ethiopia.

Grasspea

Grasspea (*Lathyrus sativus*) remains the dominant legume on the poorly drained black clay soils where it is grown in rotation with tef (*Eragrostis tef*) and noog (*Guizotia abyssinica*). There has been a serious outbreak of Lathyrism reported in the local press in the North. It is associated with drought conditions and intake of grasspea higher than normal. An effort should be made to acquire the Indian germplasm for evaluation in Ethiopia and to retest the best of the crosses with the Canadian lines selected in the IAR program. Some additional low ODAP material from Pakistan and Bangladesh should be available, from within the project, for evaluation in Ethiopia next year.

Wild relatives

Mr Berhane Gebre Mariam, the senior officer accompanying the collection mission, has a special interest in wild relatives of chickpea and lentils. He has carefully recorded about 20 locations of *Cicer echinatum* and *Lens ervoides* for later collection as they mature out of phase with the cultivated species. These would be ideally suited to post-graduate studies which he would like to undertake. They are a priority for ICARDA collection as they are poorly represented in world collections. The project should be able to provide some financial assistance toward their collection.

Noog

Noog, *Guizotia abyssinica*, is a potentially very valuable oil seed. It is said to be high in mono unsaturated fatty acids. An oil sample was

taken for analysis. Samples of the seed are however needed for oil content analysis especially of landraces from the higher altitudes. It grows on the whole range of soil types encountered during the collection but most interestingly it is widely used in rotation with grasspeas on some of the heavy poorly drained black soils. Presumably it also has some tolerance of poor drainage. This point is well worth checking as canola performs poorly under such conditions. and potentially noog is a complementary oil seed.

Equipment and funding, for undertaking germplasm collections, were supplied to BDI within the framework of the project project. In addition to the GPS unit provided in January, the project also supplied an altimeter and pH kits to BDI during the second mission in October. Sample bottles for the rhizobium collection and operating costs for the rhizobium research work have also been supplied to BDI by CLIMA from the project budget. In addition to covering the collection costs and vehicle hire, remaining funds due to BDI from ICARDA will be disbursed when the seed shipments are secure, to cover post collection costs associated with the Institute's share of the collection. The joint project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" funded this mission with CLIMA and the ACIAR project supported it.

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1.2.6. Collection of *Lathyrus* and *Vicia* spp. in Syria in 1996 and 1997

Collection missions were conducted in Lattakia and Tartous provinces in 1996, and in Homs, Hama and Tartous provinces in 1997 to complete coverage of the *Vicia* and *Lathyrus* spp. collections in these areas. Sixty-nine accs. of *Vicia* and *Lathyrus* were collected from 33 sites in the two years (Fig. 5). In all, 31 accs. of *Lathyrus* and 38 accs. of *Vicia* spp. were added to the germplasm collections of ICARDA (Table 12). Also, one acc. of *Lupinus* was collected.

The basaltic regions east of the Homs and Hama provinces were surveyed to assess the penetration of wild *Vicia* and *Lathyrus* in to the moisture-stressed rainfed zones of these provinces. This area had natural populations of *Vicia* and *Lathyrus* spp. but was over-grazed by

small ruminants. The area around Salamiyhe was too dry for *Vicia* and *Lathyrus* and the soils were poor. Inspection of the basaltic hills north of Salamiyhe and Hama gave similar results.
The team then sampled natural populations of *Vicia sativa*, *Vicia monantha* and *Lathyrus aphaca*.

The basaltic plateau west of Homs province proved to be a suitable habitat for *Vicia* and *Lathyrus* spp. However, there was over-grazing, and stone removal from field borders and stony patches within the fields. Also, most of the area is irrigated and all arable land is already under cultivation. Consequently, the only refuge left for the wild *Vicia* spp. and *Lathyrus* spp. was roadsides, stony fields, borders and heaps of stones and stony patches within the fields. The team located and sampled *Vicia sativa*, *Vicia peregrina*, *Vicia hybrida*, *Lathyrus basalaticus* and *Lathyrus hierosolymitanus*. The southern part of Homs province and the southern margin of basaltic plateau are heavily over-grazed and the soil poor. The team sampled populations of *Vicia sativa*, *Vicia monantha*, *Lathyrus cicera*, *Lathyrus blepharicarpus* and *Vicia narbonensis*. Little was collected in the basaltic area west of Hama province since the whole region is either cultivated fields or heavily over-grazed uncultivated stony patches, not suitable for wild *Vicia* and *Lathyrus* spp. The only germplasm found was that of *Vicia perigrina* and *Lathyrus aphaca*.

In conclusion, the drier areas showed severe over-grazing, and *Vicia* and *Lathyrus* spp. were mostly found only among field borders, stony patches and the roadsides.

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1.2.7. Collection of faba bean germplasm in Bangladesh in 1997

In an earlier mission during 1995 (see GRU Annual Report for 1994 and 1995) it was discovered that in the central provinces of Bangladesh there was a limited production of faba bean (*Vicia faba*) under harsh conditions. At that time only six accs. of faba bean could be collected (Fig. 6). The present mission was planned to provide a more thorough sampling of the genetic diversity of farmers' landraces of faba bean from areas not represented in the present collections in Bangladesh and ICARDA.

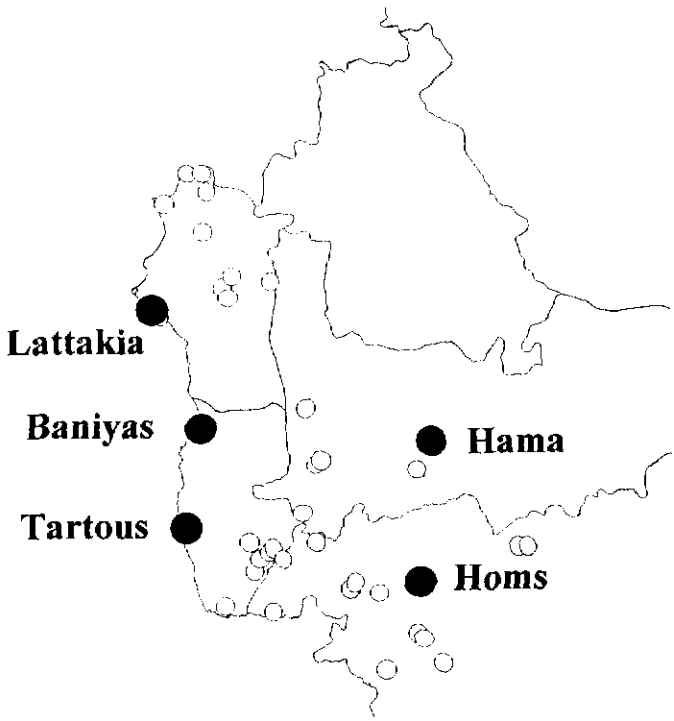

Fig. 5. Collection sites of *Lathyrus* and *Vicia* in Syria in 1996 and 1997

In all, 29 accs. were collected (Table 13, Fig. 6). This material will be screened for resistance to heat and other abiotic stresses at ICARDA. However, during the first multiplication of the faba bean accs. collected during the 1995 mission at Tel hadya, it was observed that the Bangladeshi material was extremely early. Thus, it not only possesses heat tolerance genes as well as it possibly avoids terminal heat stress close to maturity time because of the earliness.

The 1997 collection mission was conducted between 25 and 28 March. At each collection site full passport data was recorded. Existing climatological data will be obtained on the geographical location of each collection site through use of a global positioning system (GPS) hand-held units. The climatological data will include rainfall, and minimum and maximum temperatures during the growing season.

Table 12. *Lathyrus, Lupinus* and *Vicia* germplasm collected in Syria 1996 and 1997

Species	No. of accs.
Lathyrus aphaca	6
Lathyrus basalaticus	1
Lathyrus blepharicarpus	4
Lathyrus cicera	1
Lathyrus hierosolymitanus	6
Lathyrus ochrus	2
Lathyrus spp.	11
Lupinus spp.	1
Vicia ervilia	2
Vicia hybrida	4
Vicia monantha	5
Vicia narbonensis	1
Vicia palaestina	2
Vicia peregrina	4
Vicia sativa	7
Vicia sativa subsp. *nigra*	3
Vicia sativa subsp. *sativa*	2
Vicia villosa	4
Vicia villosa subsp. *dasycarpa*	1
Vicia spp.	3
Total	**70**

Table 13. Faba bean accs. collected in the three provinces of Bangladesh in 1995 and 1997

Province	1995	1997	Total
Dhaka	1	15	16
Manikgani	1	9	10
Tangail	4	5	9
Total	**6**	**29**	**35**

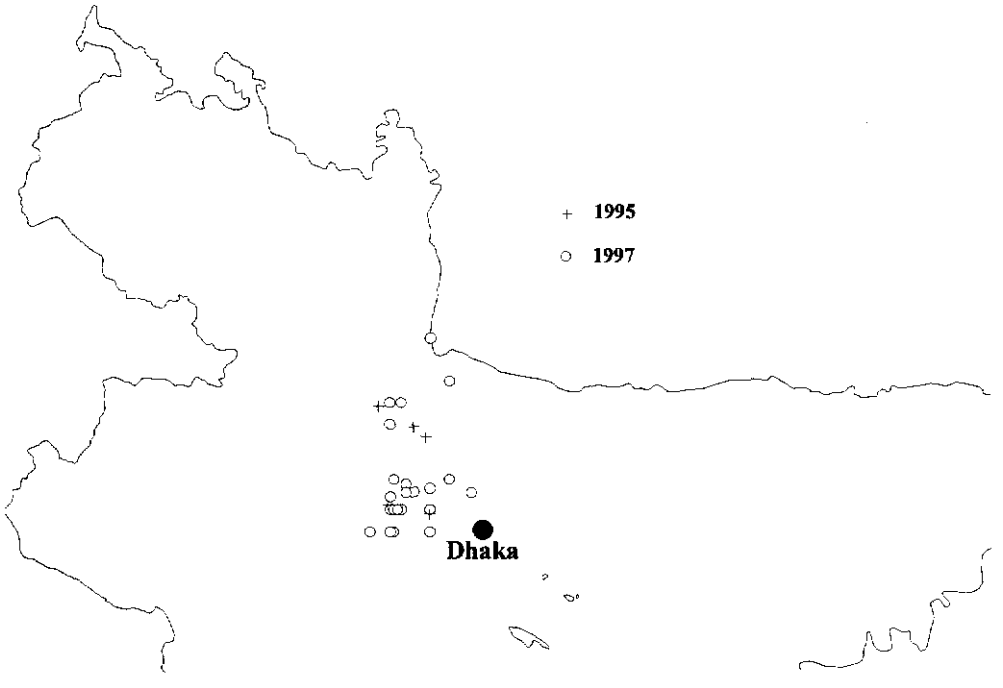

Fig. 6. Collection sites of faba bean accs. in Bangladesh during 1995 and 1997

Faba bean germplasm was collected at 23 sites in 1997 (Fig. 6) and from three provinces (Table 13). This germplasm is expected to provide unique genes for extreme earliness and tolerance to higher temperatures during flowering, a condition they are being produced under in Bangladesh. The faba bean germplasm may be unique in its characteristics as it is outside the range of environments the crop is normally grown in. This first ever collection of faba bean in Bangladesh may prove to be valuable germplasm for several important traits in addition to earliness and heat tolerance.

This mission was funded by the joint project With CLIMA "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" and supported by ACIAR project.

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1.2.8. Collection and conservation of food legumes in Pakistan in 1996

A collection mission in Pakistan was conducted by GRU-ICARDA for lentils, lathyrus, faba bean, and peas during 1996, since there existed several gaps in ICARDA's collections of these crops which needed to be filled. The mission was conducted jointly with Plant Genetic Resources Institute (PGRI) of the National Agricultural Research Centre (NARC); Agricultural Research Council (ARC), Islamabad; The Pulses Program of NARC, Pakistan; and CLIMA, Perth, Australia.

This mission was conducted within the frame-work of the ICARDA/CLIMA collaborative project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" funded by ACIAR to support the collection, conservation and utilization of genetic resources of forage and grain legumes in the Western Mediterranean Region. In addition to the Western Mediterranean Region, this project also aims to: (i) provide support for conservation of genetic resources of Ethiopia and Pakistan and (ii) to promote germplasm exchange between these countries and the Western Mediterranean region. This collection mission has been funded by the above mentioned project to provide: (i) adequate sampling of lentil, lathyrus, faba bean, and pea from the provinces of Punjab and Sindh of Pakistan and (ii) a basis for a survey of the socio-economic factors related to the production and consumption of these pulses.

Lentil (*Lens culinaris*) is the second most important pulse in terms of area and production in Pakistan, followed closely by field pea (*Pisum sativum*). The area of faba bean is small but wide-spread, mostly in kitchen gardens, and holds a wealth of genetic diversity. The area of *Lathyrus sativus* (local name: khesari) is not reported in FAO statistics but it is significant.

While there has been some collection of khesari and lentil in Pakistan, researchers have recognized the need for further collections to increase the genetic variability available for crop improvement programs. In the ICARDA world collections of lentil and lathyrus before this mission, there were only 215 accs. of lentil and 25 of lathyrus from Pakistan. Of the lentil, 45 are from Sindh province and

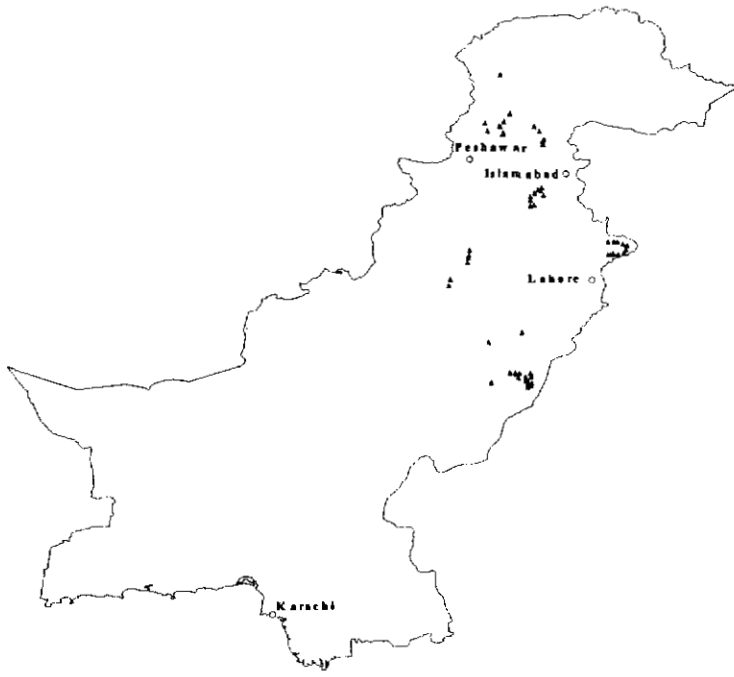

Fig. 7. Distribution of legume collecting sites in Pakistan in 1996

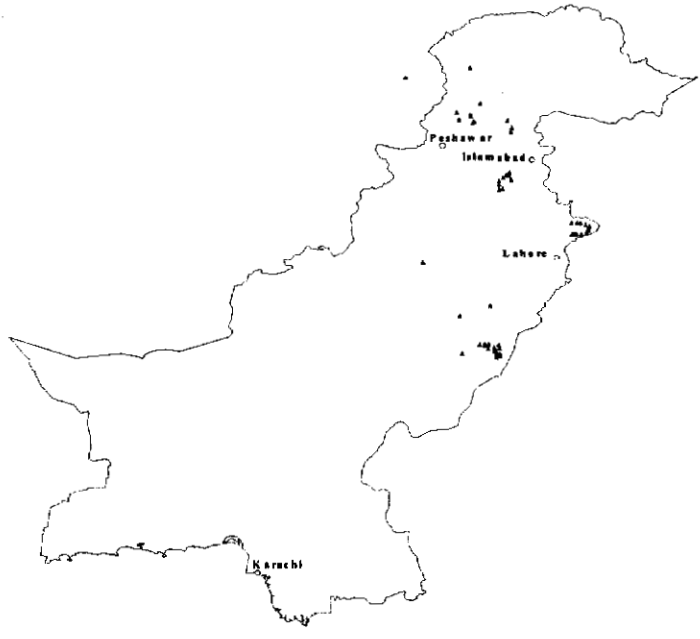

Fig. 8. Distribution of lentil collection sites in Pakistan in 1996

only 12 from Punjab province. There are only 34 accs. of faba bean with all coming from Balochistan province, and there are only 15 accs. of pea.

The collections

The mission was conducted from March 27 through April 6, 1996. Population samples of landraces were collected of lentil, pea, chickpea and lathyrus from farmers at intervals of 10-20 km along a collection route which covered areas not represented in present collections of these crops in Pakistan and ICARDA. However, because Sindh province was off limits to the team, the lathyrus collection was relatively little. No faba bean was found along the route taken due to the same reason. Hence the Northwest Frontier Province (NFP) was added to the mission's itinerary.

Approximately 50 plants, selected at random, were sampled per landrace to adequately collect the available variation and to provide sufficient seed to allow splitting of the samples two-ways. Populations of the landraces were sampled from standing crop in the field, threshing floors, and where necessary, from farmer's stores. Emphasis was given to collecting full passport data including identification of each collection site geographically and ecologically. At each collection site a hand-held GPS unit was used to obtain latitude and longitude. Obtaining climatological data will be facilitated by the use of these coordinates. The climatological data will include rainfall, and minimum and maximum temperatures during the season. Soil pH was recorded for each site.

A total of 107 accs. of different types of legumes were collected from Punjab and the NFP (Table 14, and Fig. 7). The majority of the accs. were of lentil (Fig. 8). Small numbers of chickpea (9 desi- and 1 kabuli-type) and of lathyrus and pea were also collected. Also some accs. of forage *Vicia* and *Medicago* and other pasture species were also collected.

Germplasm handling, documentation and evaluation

The collected seed material was divided in equal parts, one half kept in Pakistan and the other taken to ICARDA for multiplication, evaluation and germplasm conservation. After multiplication at ICARDA, seed was sent to CLIMA for introduction into the Australian genetic resources system.

Table 14. Legume germplasm accs. collected in Pakistan in 1996

Genus species	subtaxa/type	No. of accs.
Cicer	*arietinum* desi	9
Cicer	*arietinum* kabuli	1
Lathyrus	*sativus*	1
Lathyrus	*setifolius*	2
Lens	*culinaris*	52
Medicago	*laciniata*	1
Medicago	*polymorpha* var. *vulgaris*	2
Medicago	*tornata*	9
Phaseolus	*vulgaris*	1
Pisum	*sativum* subsp. *sativum*	5
Trigonella	*foenum-graceum*	2
Trigonella	*monantha*	1
Vicia	*johannis*	1
Vicia	*monantha*	3
Vicia	*sativa* subsp. *nigra*	16
Vicia	*sativa* subsp. *sativa*	1
Total		**107**

ICARDA introduced the germplasm resulting from this mission into the collections maintained at GRU, under the auspices of the FAO and, under the requirements of the CBD. ICARDA will make it freely available with the restriction to recipients that they not take variety protection rights on, nor will patent any naturally occurring genes from the germplasm provided. ICARDA also stipulates that parties

receiving this germplasm will also require the same conditions on any further distributions to third parties. CLIMA agrees to the same conditions as ICARDA for introduction of the collected germplasm into the Australian genetic resources conservation system.

The ACIAR-funded genetic resources project also supports evaluation and conservation of the germplasm collected through this and other possible missions in the future. Any evaluation data of this germplasm resulting from ICARDA or CLIMA trials will be made available to the national program of Pakistan.

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1.2.9. Collection and conservation of faba bean and barley in Ecuador in 1996

The main objectives of this exploration mission were as follows: 1. Collection and conservation of faba bean germplasm with chocolate spot (*Botrytis fabae*) resistance from the Andean mountain region of Ecuador. This region has provided the best sources of resistance for chocolate spot, ILB 438 and ILB 938, which were used to develop resistant varieties in Europe, Egypt and Australia; 2. Collection of barley, the other important crops in the farming systems in use in the Andean mountains; and 3. Collection of other grain legumes found in the Ecuador Andean mountain range.

The explorations and collections were conducted in cooperation with the Departmento Nacional de Recursos Fitogeneticos y Biotechnologia (DENAREF), the Instituto Nacional de Investigaciones Agropecuarias (INIAP), Quito, Ecuador and CLIMA.

The best sources of resistance to chocolate spot and rust have been selected exclusively from germplasm received from the Andean region of Peru, Ecuador, and Colombia. However, there are relatively few accs. of faba bean from Ecuador, considering the major importance of the chocolate spot resistance found there (97 accs. including re-selections previous to this mission). And hence a collection mission was launched to increase the genetic base of resistance to these important pathogens of faba bean (*Vicia faba*).

Fig. 9. Distribution of faba bean collection sites in Ecuador

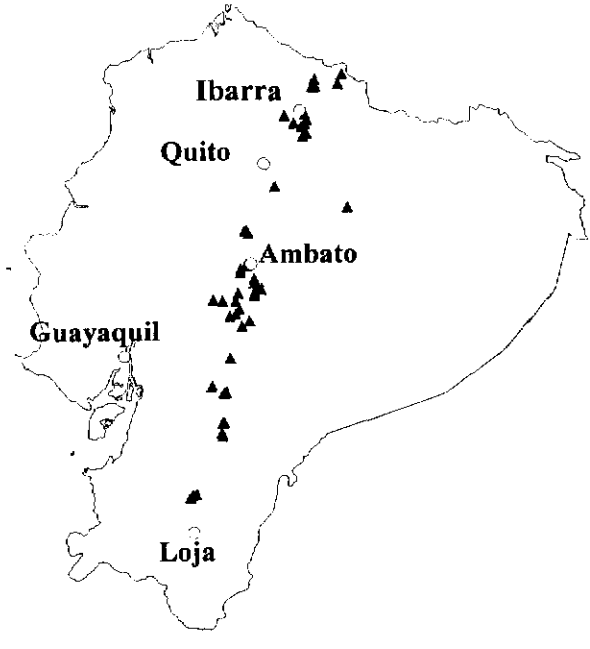

Fig. 10. Distribution of barley collection sites in Ecuador

Table. 15. Germplasm collected in Ecuador in 1996

Taxa	No. acc.
Hordeum vulgare	57
Lathyrus cicera	1
Lathyrus sativus	1
Lens culinaris	6
Pisum sativum	23
Vicia articulata	3
Vicia faba	108
Vicia sativa subsp. *nigra*	2
Vicia sativa subsp. *sativa*	3
Vicia spp.	1
Total	**205**

The Andean region of South America has an environment highly conducive for the development of chocolate spot. The rainfall is high, and the weather cool during the entire growing season. This leads to a strong natural selection pressure for resistance to this disease which can cause entire crop losses in susceptible varieties.

The Australian Grains Research and Development Corportation (GRDC) has previously funded the re-initiation of screening faba bean germplasm for disease resistance at ICARDA. This collection mission was funded from the above mentioned project to provide a source of new germplasm for disease screening at ICARDA to develop additional sources of resistance to chocolate spot and rust.

The present mission was conducted from 18 June to 1 July 1996. Populations of faba bean, lentil, pea, lathyrus and barley were collected at 103 sites from farmers and from local village markets at intervals of 10-20 km along the Andean mountain route in Ecuador

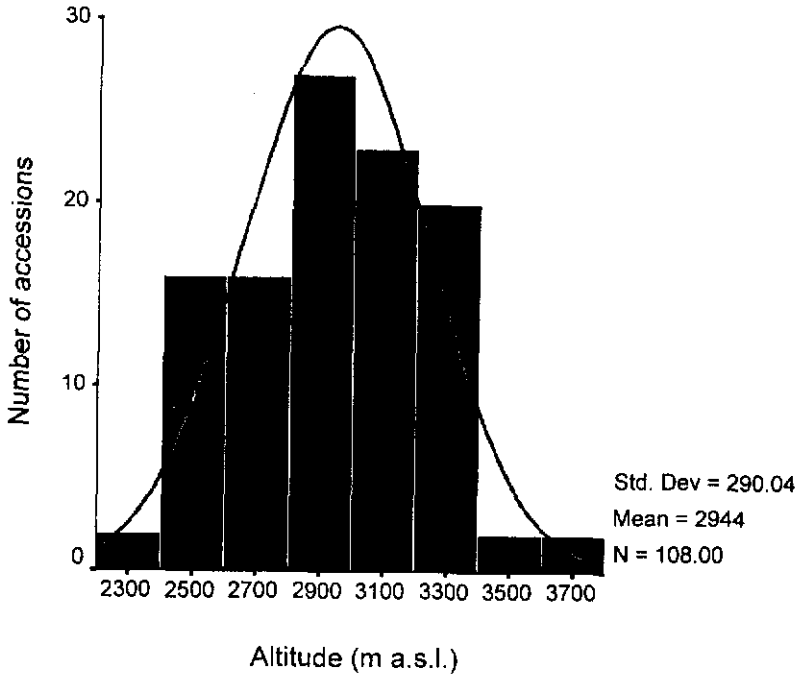

Fig. 11. Distribution of altitude(m) of faba bean collection sites in Ecuador

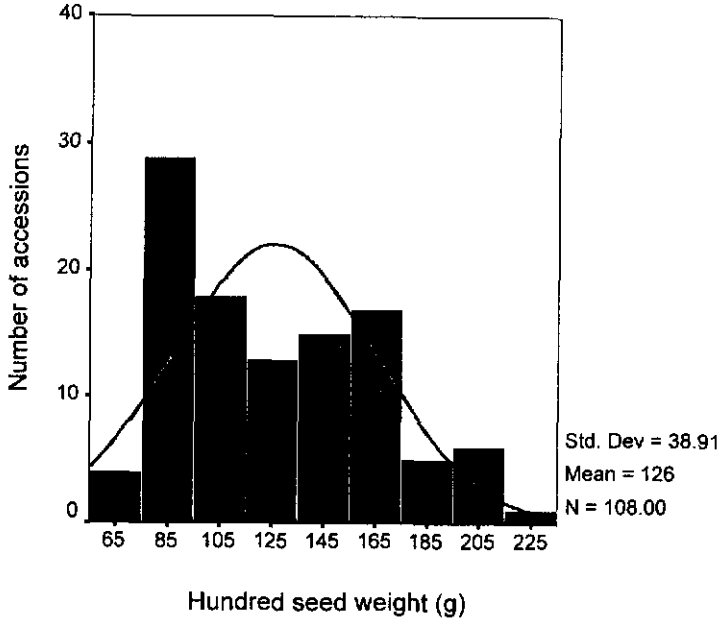

Fig. 12. Distribution of 100-seed weight(g) of faba beans collected *in Ecuador*

Table 16. Multi-crop collections by province for Ecuador in 1996

Province/Crop	No. of accs.
Azuay	**24**
Barley	6
Peas	4
Faba bean	13
Vicia spp.	1
Bolivar	**16**
Barley	2
Lentil	2
Peas	2
Faba bean	10
Canar	**21**
Barley	6
Peas	3
Faba bean	12
Carchi	**37**
Barley	8
Peas	7
Faba bean	20
Vicia spp.	2
Chimborazo	**32**
Barley	13
Lentil	1
Peas	2
Faba bean	13
Vicia spp.	3
Cotopaxi	**10**
Barley	4
Lathyrus spp.	2
Faba bean	2
Vicia species	2
Imbabura	**18**
Barley	6
Lentil	1
Peas	2
Faba bean	8
Vicia spp.	1
Loja	**8**
Barley	2
Lentil	1
Faba bean	5
Pichincha	**14**
Barley	3
Faba bean	11
Tungurahua	**25**
Barley	3
Lentil	1
Peas	3
Faba bean	14
Grand Total	**205**

(Fig. 9 and Fig. 10). Faba bean was collected from areas at elevations of 2300 to 3500m asl (Fig. 11). By collecting over a range of altitudes, the problems of lateness in the sources of germplasm with resistance to chocolate spot in the Andean region may be solved.

Approximately 50 plants were sampled per landrace to adequately collect the available variation and to provide sufficient seed to allow sharing of the samples two ways. Seed was taken from the crop standing in the field, threshing floors, farmers stores and from local markets. Emphasis was given to collecting full passport data and sufficiently identifying each collection site geographically and ecologically by taking the latitude and longitude using a handheld GPS unit. The coordinates will be used to identify climatological data for the collection sites.

For the two major components of the Andean mountain cropping system in Ecuador, faba bean and barley, 108 and 57 accs., respectively, were collected (Table 15). Germplasm from 10 provinces throughout the Andean mountain region of Ecuador was sampled (Table 16 and Fig. 9 and Fig. 10). Other grain legumes collected included lentil (6 accs.) and pea (23 accs.). One acc. each of unique *Lathyrus sativus* and *L. cicera* landraces were discovered at a remote farm and were collected. The farmer related that he used these for making soups. He proudly claimed that both these varieties were family heirlooms which had been handed down each generation since the time of the Spanish conquests. These two landrace varieties were not found at any other site and were not previously known to exist in Ecuador. Three accs. of *Vicia articulata* were found. These were referred to locally as black lentils. In the past, *V. articulata* was also cultivated in Spain as a substitute for lentil.

The accs. of faba bean collected provided diverse seed size (Fig. 12), shape, and color, and would be of great value in developing durable resistance for chocolate spot disease for different agroecological conditions. These have been evaluated for disease resistance. Results are available in Section 1.4.13. of this report.

Seed collected of ecotypes were divided in to equal halves. One half was left at INIAP and the other taken to ICARDA for multiplication, distribution, germplasm conservation, evaluation. Germplasm collected will be freely available for all bona fide users

subject to the usual conditions mentioned in previous reports. Passport data has been computerized and put into the ICARDA germplasm collection database.

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1.2.10. Collection of pasture and forage legumes in Spain in 1997

A genetic resources collecting mission was conducted in Spain from the 24 June to 6 July, 1997. It covered mostly the rural communities of Castilla-León, Extremadura and Andalucía provinces. The aim of this mission was to upgrade germplasm of grain, forage and pasture legumes from these regions. The mission was made possible by the provision of funding by the ACIAR, and cooperation between ICARDA and the Instituto National de Investigaciones Agrarias (INIA), Madrid, Spain, and CLIMA. The linking of research in the Mediterranean countries with that of ICARDA has ensured a continuum of genetic resources for countries around the Mediterranean through a long-term and strategic program of collection, conservation and exchange.

Herbaceous legume species occur in every continent; however, the Mediterranean region is a rich centre of diversity for many leguminous species which have also been developed in temperate Australia, e.g., *Trifolium*, *Medicago*, *Lupinus* and *Vicia* spp. However, the Mediterranean basin is very highly populated and is increasingly being developed through building activity. Consequently, it is one of the areas most at risk in terms of genetic erosion of its endemic crop and forage plants as new varieties replace the old and cropping intensifies.

Both people and animals are increasing the pressure on the available land in the rural regions. This has serious ramifications for the world's plant genetic resource base because of intensification of cultivation. Cropping destroys the seed bank and places additional grazing pressure on the few plants that may survive in the pastures.

Genetic erosion is the most serious problem confronting man in developing crop and pasture resources. Leguminous crop and forage species are high on the list of those most at risk from the intensification of cropping and grazing currently taking place in the

Mediterranean region. Of the species still available, it is the large seeded legumes such as *Vicia, Lens, Lathyrus* and *Lupinus,* which are most seriously endangered. However, many *Medicago* and *Trifolium* species have been assessed as having high potential for agricultural use and being at risk of genetic erosion, have been given a high collection priority by the EP/GR forage working group for collection, conservation and forage development.

The western Mediterranean region has widely diverse environments and has the largest available population of leguminous plants suited to the milder climates of southern Australia. The area is a valuable source of species, some, like *Lathyrus* species, are little used in agriculture, many may be valuable pasture or crop plants. Some such as the serradellas are used in agriculture, but have much greater variability than available in Australia. Their preservation is essential, not only to the countries themselves, but also to other countries, like Australia, dependent on the region for a continued flow of germplasm. Southern Australia has depended heavily on the Mediterranean region for its leguminous pasture and crop plants and many are direct introductions. However, collections for some genera have been very limited and have not been specifically targeted at specific adaptive traits, such as acid tolerance, drought or salt tolerance.

ICARDA in North Africa and European countries of the Mediterranean individually, backed by IPGRI, fully appreciate the value of conservation. Spain has developed an impressive genetic resources conservation national program, the Centro de Recursos Fitogeneticos (CRF), and supported the project with CLIMA and ICARDA in line with its policies of constantly seeking opportunities to increase its gene bank.

The objectives of this mission were to: 1) survey, collect and catalogue the legume biodiversity of the provinces of Andalucia, Valladolid and Salamanca and the administrative region of Extramadura; 2) to take eco-climatological data for collection sites for eco-geographic analysis of the distribution of rangeland species; and 3) to collect soil samples to aid in the characterization of factors related to the distribution of the target species in Spain.

Fig. 13. Distribution of collection sites in Spain in 1997

Fig. 14. Distribution of *Ornithopus* collection sites in Spain

An itinerary was prepared in joint consultation taking into consideration several factors, such as, diversity of habitats from mountain to sea level, several soil types and weather types, the list of preferred species for collection, information in the Floras, environment and weather data, cultural uses, the indigenous knowledge of the counterparts and other experts.

Sixty-five sites were visited in seven provinces in three Spanish autonomous communities (Castilla-León, Extremadura and Andalucía). The collection sites (Fig. 13) were all located in the western part of Spain.

A total of 363 accessions of pasture, forage and grain legumes was collected (Table 15). The majority of the accessions were of *Trifolium* species. There were also a large number of accessions of *Vicia* species. Additionally, a large number of *Ornithopus* accessions were collected (Fig. 14). These will now be discussed in relation to their ecological distribution.

All the species collected grow wild in the Iberian Peninsula; in paddocks, pastures and the characteristic Mediterranean evergreen oak "dehesa" (pasture ground). Also, along the roadsides and sometimes in and around cultivated habitats near settlements. There were four major ecological environments:

Mountain grasslands

Mountain grasslands were visited during the initial phase of the mission. These were near *Guardo* and *Cervera* municipalities, in the northern part of *Palencia* province. The regions are on the south face of the Cantabric Mountain Range. The Mountains reach 2,500 m asl, but pastures grow between 1200 to 800 m altitude only. With an annual mean temperature of 9°C and 1068 mm mean rainfall, the climate-type is a cold-temperate Mediterranean. In the western part water-division of rivers *Carrión* and *Pisuerga* means that irrigation is possible, and soils are classified as cuarcites and ferruginous sandstone, whereas in the east part there were alkaline soils on limestone rock.

These pastures are permanent and are used general for beef cattle grazing in spring and autumn, and are harvested in summer and near the settlements. Sometimes they are associated with poplar trees mainly in the *Carrión* river side. They are collectively used

pasturelands, joined with rocky areas and slopes, but have a high cattle-feed quality.

The vegetation consists mainly of grasses and clovers, which are slowly being replaced by cultivated grassland. It is possible to find in them pasture legume species such as those belonging to the genus *Trifolium*: *T. repens, T. micranthum, T. fragiferum, T. alpinum, T. campestre, T. michelianum, T. isthmocarpum, T. striatum* and other genera such as *Vicia* and *Medicago*.

Grassland steppes

Mainly located on the plateau of central Spain, the grasslands are flat, arid areas, with a climate classified as temperate Mediterranean or dry Mediterranean, with long cold winters, and hot, dry summers and strong thermic oscillation. In general, these areas are used for dryland farming of cereals. Sheep feed on the stubble. Interesting species grow wild in fallow lands, landmarks and roadsides.

During the mission, these areas were found in *Tierra de Campos,* region of *Palencia* province. It has 9°C of mean temperature, 600mm mean annual precipitation and limestone soils with alkaline pH. Here a *Medicago sativa* ecotype is found to be growing, together with other pasture legume species such as *Vicia monantha*, *Astragalus hamosus*, *Melilotus sulcata*, *Coronilla emerus*, and some dry-land *Trifolium*, e.g., *T. angustifolium*.

Interesting species were also found in grassland steppes of *Salamanca* province (around Almenara, Ledesma, Alba de Tormes, region of Peñaranda de Bracamonte), on granites, slates or sands, and with similar climate. Populations of *Vicia*: *V. villosa, V. sativa, V. lutea, Lupinus* spp., *Astragalus hamosus, Biserrula pelecinus,* and dry-land clovers, e.g., *T. angustifolium, T. glomeratum, T. arvense, T. tomentosum* were found and their seed collected.

Pasture-ground: "dehesa"

The "dehesa" is the characteristic Mediterranean evergreen oak pasture ground improved for forest and animal production. They are located primarily in southwest Spain. The trees are leafy, mainly *Quercus ilex* and *Quercus suber* which provide 5-20% of the cover. The herb substrate is formed by grasses and legumes are grazed extensively by cattle and small ruminants.

The land use is rotational, i.e., one year with part of the land

cultivated for stockfeed for low grass production months and to control shrub proliferation. And, in the following two to eight years, the land is left fallow and native pastures are allowed to grow. They are gazed by native beef cattle of the varieties: retinta, morucha, serrana or avileña, and some of them by fighting bulls, merino sheep, and by Iberian landrace herds of black pigs in southern Salamanca, Badajoz, northern Sevilla and Huelva. Acorns are used for supplementary animal feed from October to December each year.

This ecosystem lies over silica and sandstone soils in the Western part of Salamanca province (region of Campo de Ledesma, Vitigudino, Fuente de S. Esteban, Ciudad Rodrigo), and has a dry Mediterranean climate. There is pasture ground also in the wet Mediterranean areas of north side Central range, in the south of the province. There, it was possible to find populations of *Lathyrus*, *Vicia*, *Lupinus*, *Biserrula* and *Lotus*, also, *Ornithopus sativus, O. compresus* (distribution of *Ornithopus* species shown in Fig. 14), *Trifolium repens, T. cherleri* and *T. subterraneum.*

Extremadura Community is covered by this kind of land use. There can be distinguished a limestone area with *Astragalus*, *Scorpiurus*, *Lathyrus*, *Medicago*, and some species of *Trifolium* such as, *T. bocconei*, *T. campestre*, *T. arvense*, *T. angustifolium*, *T. glomeratum*, *T. stellatum* and *T. tomentosum* located around Almendralejo town and Villafranca de los Barros. There is another neutral to acid area near Jerez de los Caballeros, Fregenal de la Sierra, Llerena, Barcarrota and Olivenza where *Astragalus*, *Coronilla*, *Lotus*, *T. subterraneum*, *T. glomeratum*, *T. campestre*, *T. tomentosum*, *T. arvense*, *T. scabrum* and *T. striatum* are found. All of these areas were visited during collecting mission. In the courses of streams, wet valleys and highest rainfall areas of Llerena, Jerez de los Caballeros and Fregenal, one could find *Trifolium repens*, *T. resupinatum* and *T. fragiferum.*

Sites also visited were the "dehesas" over granite or slates in los Pedroches and Sierra Morena, regions in Córdoba; and in the Northern ridge of mountains in Sevilla: Constantina, Cazalla de la Sierra, Real de la Jara and El Pedroso villages. From there, some samples of *Scorpiurus sulcatus*, *Scorpiurus vermiculatus*, *Ornithopus compressus*, *O. sativus*, *Trifolium glomeratum*, *T. campestre*, *T. stellatum*, *T. scabrum*, were collected.

Forest

This is land with tree cover of more than 20%, or shrubs upto 60%. Its use is mainly for hunting, as well as forest industry and grazing by goats. However, it is becoming extinct. In the herbaceous layer, some interesting species can be found. Continental Mediterranean climate areas were visited. The regions of los Pedroches, La Sierra (near Sierra Morena mountains) and La Penibética mountain range in Córdoba province, and the northern ridge of mountains in Sevilla. These have 16 to 18°C mean annual temperature and 550 to 950mm of annual rainfall, but are very different in lithology: Sierra Morena is siliceous and South-eastern Cordoba (called La Penibética) is over loam and limestone.

The majority of the trees are *Quercus ilex, Quercus suber* and wild *Olea europaea* with pastures rich in clovers. These are grazed from October to May. Shrubs found in La Sierra and los Pedroches are *Cistus ladanifer, Erica arborea, Daphne gnidium, Pistacea lentiscus with T. tomentosum, T. arvense, T. lappaceum,* etc. *Quercus coccifera, Pistacea terebinthus*, and species of *Genista* or *Citysus* grow in the shrub-forest around Priego, Cabra, Rute and the other villages of La Penibética. Some populations of *Scorpiurus sulcatus, Medicago sativa, Trifolium campestre* and *T. angustifolius* can be found here.

The pine-forest over sand called Coto de Doñana (the protected natural area between Huelva and Sevilla) were also visited. It has a maritime Mediterranean climate, with 16.7°C mean temperature and 632mm annual rainfall. It is not grazed, because it is a National Park, but there are some populations of *Trifolium* in the path-sides and gorges.

The collected germplasm was divided into two equal parts. One part was kept at INIA and the other taken to ICARDA for multiplication and long-term conservation. After multiplication at ICARDA, seed will be sent to CLIMA for introduction into the Australian germplasm system. Passport data has been computerized and put into the ICARDA germplasm collection database.

L.D. Robertson (GRU-ICARDA), C. Francis (CLIMA), C. de la Cuadra, (CRF-INIA, Spain), C. Crespo (SIA-Salamanca, Spain), F. González (CIDT-Badajoz, Spain), F. Temprano (CIDA-Seville, Spain), and T. Moreno (CIDA-Córdoba, Spain)

Table 15. Germplasm of pasture, forage and grain legumes collected in Spain during 1997

Taxa	No. of accs.
Astragalus hamosus	4
Astragalus spp.	1
Biserrula pelecinus	10
Coronilla emerus	1
Lathyrus aphaca	1
Lathyrus clymenum	5
Lathyrus spp.	4
Lotus angustissimus	1
Lupinus albus	2
Lupinus angustifolius	7
Lupinus hispanicus	4
Medicago lupulina	2
Medicago sativa	4
Melilotus sulcata	1
Ornithopus compressus	34
Ornithopus sativus	4
Scorpiurus sulcata	6
Scorpiurus vermiculatus	3
Trifolium angustifolium	32
Trifolium arvense	20

Table 15 (Cont'd).

Taxa	No. of accs.
Trifolium aureum	4
Trifolium bocconei	3
Trifolium campestre	23
Trifolium cherleri	10
Trifolium fragiferum	1
Trifolium glomeratum	15
Trifolium hirtum	1
Trifolium incarnatum	1
Trifolium lappaceum	3
Trifolium monantum	1
Trifolium pratense	10
Trifolium repens	14
Trifolium resupinatum	2
Trifolium scabrum	10
Trifolium spp.	31
Trifolium spumosum	2
Trifolium stellatum	18
Trifolium striatum	6
Trifolium subterraneum	5
Trifolium tomentosum	9
Trigonella monspeliaca	1
Trigonella polyceratia	1
Vicia ervilia	3
Vicia lutea	16
Vicia monantha	1
Vicia sativa	18
Vicia spp.	1
Vicia villosa	7
Total	**363**

1.2.11. Faba bean germplasm collection in China in 1996

This was a specially funded international collection mission to collect landraces of faba bean in rural areas of the Sichuan and Yunnan provinces of China. The cooperating institutions were: Institute of Crop Germplasm Resources (ICGR), Chinese Academy of Agricultural Sciences (CAAS), Beijing, China; Zeijiang Academy of Agricultural Sciences (ZAAS), Zhejiang, China; Yunnan Academy of Agricultural Sciences, (YAAS), Sichuan, China; Sichuan Academy of Agricultural Sciences, (SAAS), Chengdu, Sichuan, China; GRU-ICARDA; New South Wales Agriculture, Tamworth Centre for Crop Improvement, Tamworth, Australia; and the University of Adelaide, Department of Plant Science, Waite Agricultural Research Institute, Glen Osmond, Australia.

The Yunnan plateau was particularly targetted since it has the widest range of crop genetic resources diversity in China. This region of China is characterized by diverse physiography, climate and natural vegetation that often result in rapid changes in the environment over short distances. Mountains and rivers cut across the province, which has eight distinct climatic zones. Yunnan has a long history of human settlement and agricultural activities and hence possesses a tremendous potential for germplasm collection and conservation.

The collection was conducted in the provinces of Yunnan and Sichuan between 9 April and 19 April 1996, inclusive. In all, 68 sites (33 in Yunnan and 34 in Sichuan) were collected in these two provinces (Fig. 15) at intervals of approximately 20 km along a collection route which partially covered the two regions (emphasis given on areas where faba bean was known to be grown). About 50 plants per population were sampled to adequately gather the variation within landraces and to provide sufficient seed to allow splitting of samples two ways. Seed was collected from the crop standing in the field, from stocks and from farmers' stores, where necessary.

Emphasis was given to collecting full passport data and sufficiently identifying each collection site geographically and ecologically. The global positioning system (GPS) units were used to accurately fix collection sites. Data on county, village, latitude, longitude, soil pH, topography and altitude was gathered at each site.

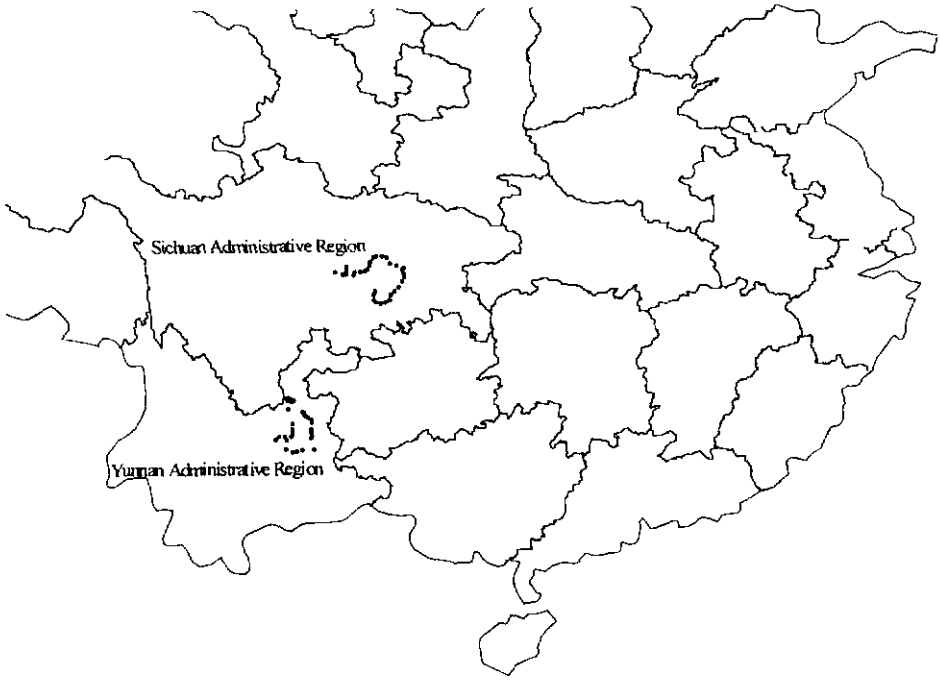

Fig 15. Distribution of faba bean colection sites in China

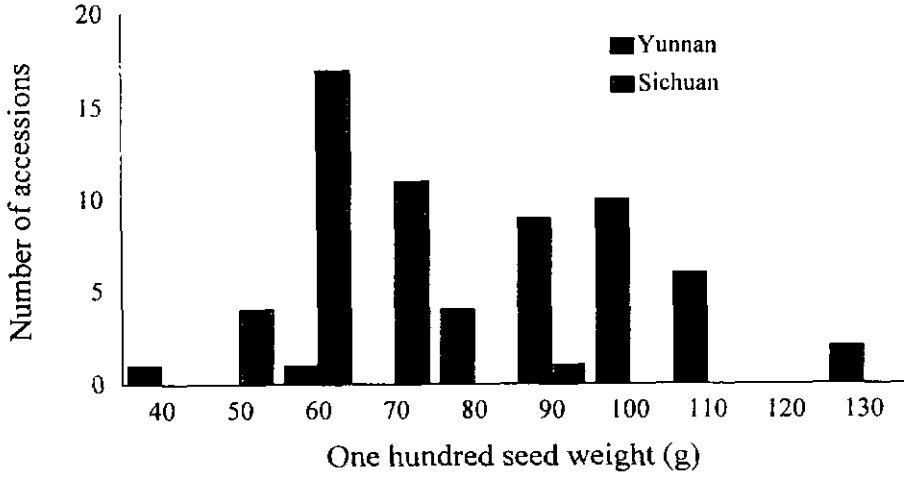

Fig. 16. Distribution of 100-seed weight(g) in faba bean accs. collected in China

In all, 34 faba bean landraces were collected from Yunnan province and 34 landraces were collected from Sichuan. These faba bean accs. showed a large variation for 100-seed weight (Fig. 16). The accs. from Yunnan were with a larger 100-seed weight than those from Sichuan. All accs. were with equina seeds, except one from Yunnan which was of the major type. All accs. from Sichuan were with black hilum, 7 from Yunnan had white hilums with the rest black. The ground color of testa was mostly light brown for both Yunnan and Sichuan, though Yunnan had one light green and Sichuan had five light green and one dark green testa colored accs. There were also three red testa color accs. from Yunnan. The green testa color has a preference for the export market to Japan.

Seed of ecotypes collected was divided into equal halves. One half was left in China and the other sent to ICARDA for multiplication and germplasm conservation after fulfilling quarantine regulations. This germplasm has been added to ICARDA's holdings maintained under the auspices of the FAO. Passport data has been computerized and put into the ICARDA germplasm collection database. Results of screening this germplasm for resistance to chocolate spot and *Ascochyta* blight is reported in Section 1.4.13 and 1.4.14., respectively, of this report.

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1.3. Germplasm characterization, evaluation and utilization

1.3.1. Characterization of bread wheat landraces

Bread wheat (*Triticum aestivum*) ranks first among the cereals grown in WANA region. Bread wheat has its primary center in Transcaucasia and adjacent areas and is by far the most important commercial crop that this region has given the world. Natural cross-fertilization still takes place between wild and cultivated *Triticum* spp. and many authors believe that bread wheat is still evolving. It is said to have arisen as a result of a cross between *T. dicoccum* (emmer wheat) and *Ae. tauschii*. This cross must have taken place much time after emmer evolved from its wild progenitor, *T. dicoccoides* in the area south of the Caspian Sea. In comparison with durum wheat which is tetraploid ($2n=4x=28$), bread wheat is hexaploid ($2n=6x=42$). The additional D genome give this wheat its excellent loaf bread-making qualities, unlike durum wheat whose dough cannot make loaf bread.

A total of 2,049 accs. of bread wheat landraces (Table 16) were planted for characterization and evaluation during the 1995-96 season in the post-quarantine area at Tel Hadya. Three standard ICARDA checks (Cham 4, Mexipak and Sonalika) were systematically included in the study in non-replicated two-rows plots. The plots were 1m long with row and plot distance of 0.45m and 0.9m, respectively. The checks were repeated every 20 plots.

The following characters were recorded: Growth habit, awnedness, tillering capacity, plant height(cm), spike density, number of days to heading, number of days to maturity, plant waxiness, spike length(cm), spike density, 1000-kernel weight (g), kernels per spike, spikelets per spike, lodging resistance, effect of cold, and reaction to naturally occurring yellow rust (*Puccinia striiformis* West f.sp. *tritici*) races at Tel Hadya. There were 24 accs., predominantly from Ethiopia, which were completely resistant to yellow rust (Table 17). Some results of the evaluation on quantitative traits are shown in Table 18. The mean plant height(cm) and days to maturity by country of origin is given in Fig. 17 and Fig. 18.

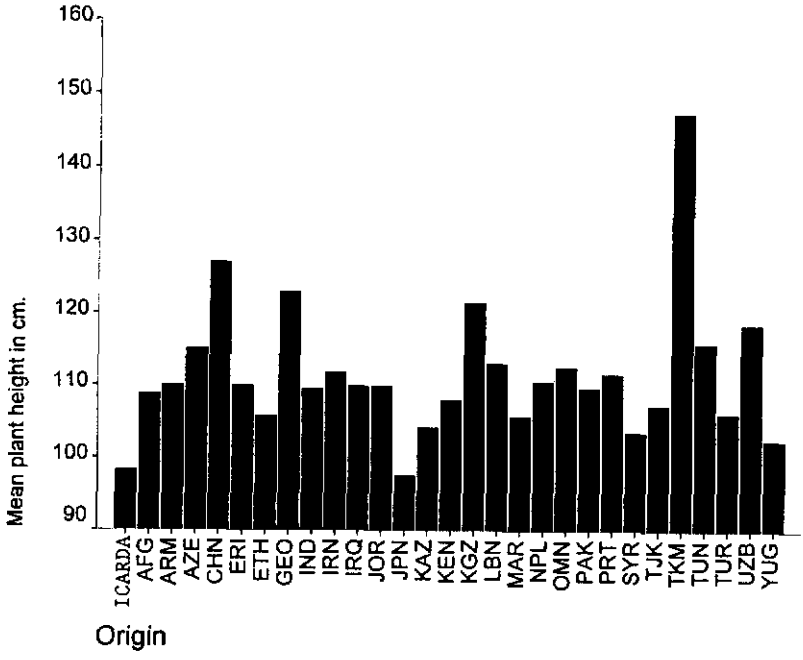

Fig. 17. Means of plant height(cm) by country for 2,049 accs. of bread wheat characterized in 1995-96

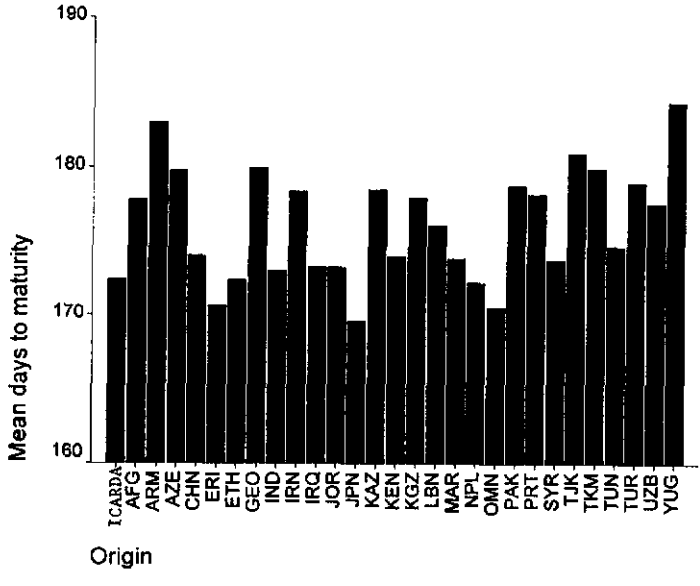

Fig. 18. Means of days to maturity by country for 2,049 accs. of bread wheat characterized in 1995-96

Table 16. Country of origin for 2,049 bread wheat landraces at Tel Hadya during the 1995-96 season

Country	No. of accs.	Country	No of accs.
Afghanistan	5	Kyrgystan	2
Armenia	6	Morocco	205
Azerbaijan	20	Nepal	10
China	3	Oman	57
Eretria	3	Pakistan	194
Ethiopia	283	Portugal	17
Georgia	1	Syria	84
India	56	Tadjikistan	4
Iran	96	Turkmenistan	2
Iraq	108	Tunisia	194
Jordan	18	Turkey	200
Japan	168	Uzbekistan	11
Kazakhstan	25	Yugoslavia	16
Kenya	1	ICARDA	260

Table 17. List of 24 bread wheat accs. completely resistant to yellow rust at Tel Hadya during the 1995-96 season

Crop No.	ORI	Crop No.	ORI
200020	ICARDA	203109	ETH
200050	ICARDA	203117	ETH
200356	ICARDA	203124	ETH
200398	ICARDA	203185	ETH
202297	TUR	203259	ETH
202408	ETH	203312	ETH
202488	ETH	203427	ETH
202537	ETH	203473	ETH
202829	ETH	203784	ETH
202931	ETH	203790	ETH
202953	ETH	203795	ETH
203079	ETH	203798	ETH

Table 18. Simple statistics for 2,049 bread wheat landraces at Tel Hadya during the 1995-96 season

ORI	Plant height(cm)				Days to heading				Days to maturity			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
AFG	98	70	135	11	136	122	156	6	172	166	188	4
ARM	109	95	118	9	147	142	158	7	178	174	185	4
AZE	115	38	150	25	146	138	160	5	180	174	203	6
CHN	127	113	140	14	137	129	148	10	174	171	180	5
ERI	110	100	125	13	137	135	138	2	171	168	174	3
ETH	106	65	153	13	140	127	158	5	172	166	185	4
GEO	123	-	-	-	146	-	-	-	180	-	-	-
IND	110	85	148	14	135	124	154	8	173	166	182	4
IRN	112	70	138	13	144	133	156	5	178	170	188	4
IRQ	110	68	135	12	137	127	150	5	173	168	182	3
JOR	110	85	133	15	139	133	142	3	173	168	180	3
JPN	98	65	128	11	132	118	156	8	170	162	188	5
KAZ	104	80	135	16	146	135	156	5	179	174	188	4
KEN	108	-	-	-	136	-	-	-	174	-	-	-
KGZ	122	118	125	5	146	144	148	3	178	177	179	0

Table 18 (Cont'd)

ORI	Plant height(cm)				Days to heading				Days to maturity			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
LBN	113	90	135	12	142	129	148	5	176	174	180	2
MAR	106	75	143	14	138	126	156	5	174	165	185	4
NPL	111	93	128	11	133	127	142	5	172	168	174	2
OMN	113	78	133	12	133	125	158	5	171	163	187	3
PAK	110	70	138	13	145	127	160	8	179	168	190	5
PRT	112	93	133	13	146	135	152	5	178	171	187	4
SYR	104	70	143	14	140	133	150	4	174	168	182	4
TJK	107	98	128	14	149	144	152	3	181	178	182	2
TKM	148	145	150	4	149	146	152	4	180	178	182	3
TUN	116	80	143	15	140	129	148	5	175	168	182	4
TUR	106	73	148	14	146	126	160	6	179	168	189	3
UZB	119	98	148	16	144	133	150	6	178	171	182	4
YUG	103	75	115	10	154	140	161	5	184	174	188	4
Cham 4	88	70	98	5	138	135	142	2	174	170	180	1
Sonalika	105	75	18	7	127	122	150	3	169	166	179	2
Mexipak	95	75	110	7	138	124	140	3	171	168	176	2

A second set of 2,162 bread wheat landraces, received as a donation or collected by GRU from several countries, was characterized at Tel Hadya during 1996-97 (Table 19). These were planted in the same manner as in 1995-96 with three checks (Cham 6, Mexipak, and Sonalika). The checks were repeated every 20 plots. The following characters were recorded: Growth habit, number of days to heading, cold effect, plant height(cm), days to maturity, tillering capacity, waxiness, spike density, awnedness, stem solidness, spike length(cm), number of kernels per spike, number of spikelets per spike, lodging resistance, grain yield per plot, and yellow rust reaction. There were 23 accs. (mostly from Europe) which were completely resistant to yellow rust races at Tel Hadya (Table 20). Some of the results of the evaluation of quantitative traits are shown in Table 21. The mean plant height(cm), days to heading and days to maturity by country of origin is given in Fig. 19, Fig. 20, and Fig. 21, respectively.

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Table 19. Country of origin for 2,162 bread wheat landraces evaluated at Tel Hadya during 1996-97 season.

Country	No. of accs.	Country	No of accs.
Austria	18	Pakistan	549
Czech Republic	39	Russia	100
Germany	21	Turkmenistan	1
Algeria	458	Turkey	784
Egypt	60	Ukraine	44
Ethiopia	1	USA	19
France	12	Yemen	29
Unknown	27	**Total**	**2162**
Checks			
Cham 6	37	Sonalika	35
Mexipak	37		

Table 20. List of 23 bread wheat accs. completely resistant to yellow rust at Tel Hadya during 1996-97 season

Acc. No.	ORI	Acc. No.	ORI
206974	CSK	205043	DZA
206975	CSK	201781	EGY
206979	CSK	205481	TUR
206977	CSK	205594	TUR
206978	CSK	204404	UKR
207114	CSK	204409	UKR
207123	CSK	207574	AUT
207124	CSK	207582	AUT
207126	CSK	207583	AUT
207132	CSK	206231	DEU
207408	CSK	206135	FRA
204971	DZA		

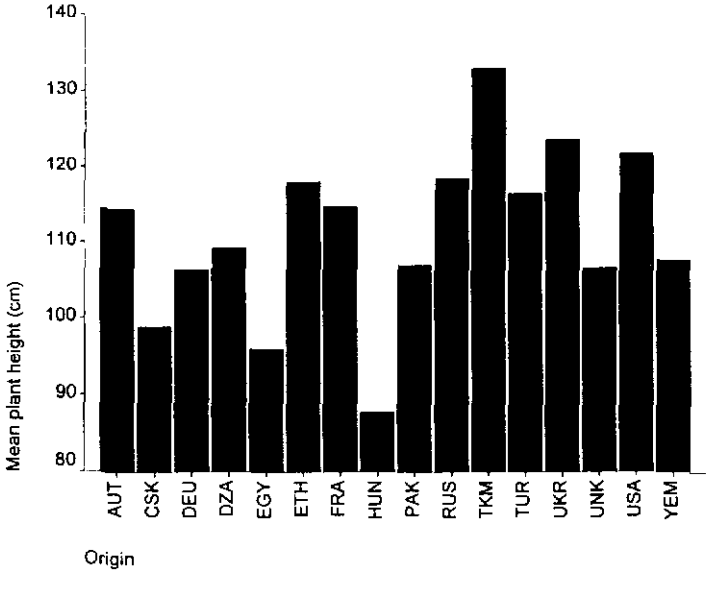

Fig. 19. Means of plant height(cm) by country for 2,162 accs. of bread wheat in 1996-97

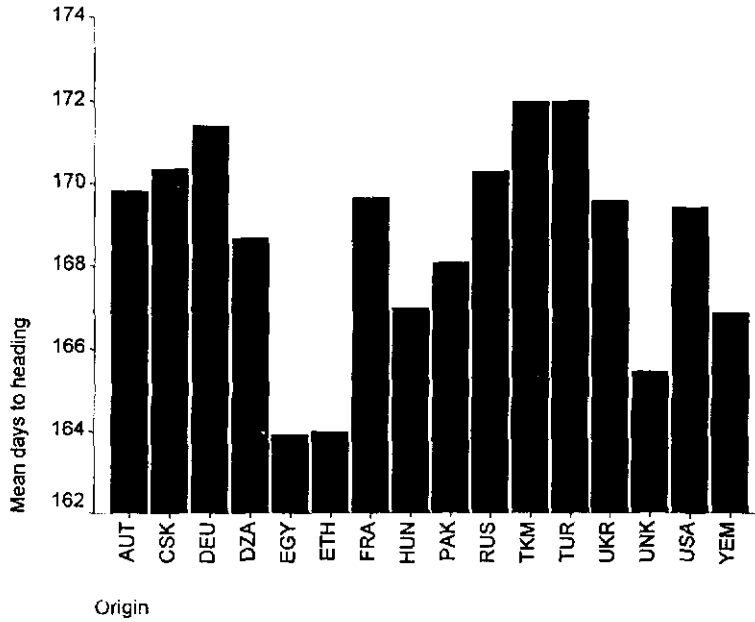

Fig. 20. Days to heading by country for 2,162 accs. of bread wheat in 1996-97

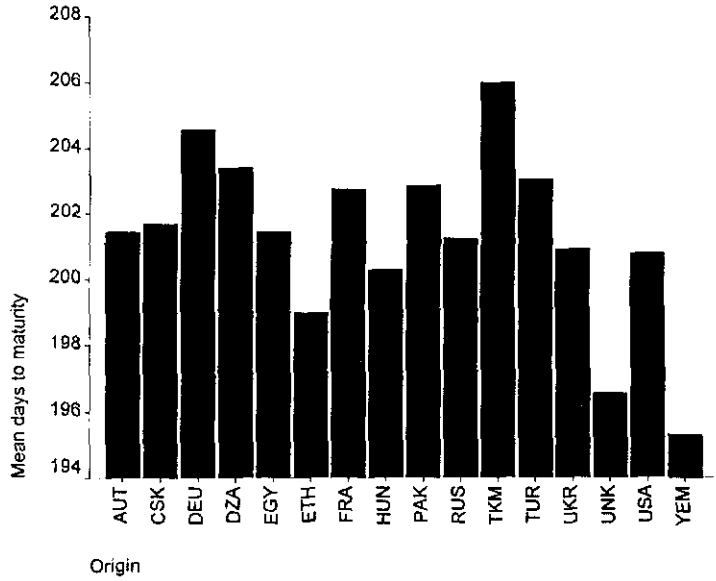

Fig. 21. Days to maturity by country for 2,162 accs. of bread wheat in 1996-97

Table 21. Simple statistics for 2,162 bread wheat landraces at Tel Hadya during the 1996-97 season

ORI	Plant height(cm)				Days to heading				Days to maturity			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
AUT	114	83	130	13	170	160	179	5	201	194	209	4
CSK	99	83	125	10	170	160	174	4	202	194	206	3
DEU	106	84	120	10	171	160	179	4	205	194	209	3
DZA	109	63	138	12	169	160	174	5	203	194	213	4
EGY	96	73	138	14	164	160	172	3	201	194	209	3
ETH	118	-	-	-	164	-	-	-	199	-	-	-
FRA	115	88	133	13	170	164	172	3	203	199	209	4
HUN	88	68	133	12	167	160	172	4	200	199	206	2
PAK	107	58	133	12	168	159	186	7	203	194	213	6
RUS	118	73	148	14	170	159	180	5	201	195	213	4
TKM	133	-	-	-	172	-	-	-	206	-	-	-
TUR	116	63	143	9	172	159	180	3	203	195	213	4
UKR	124	103	153	15	170	160	174	4	201	195	209	4
USA	122	98	143	12	169	160	180	5	201	195	206	4
YEM	107	83	123	8	167	161	172	3	197	195	202	1
UNK	107	73	133	11	165	161	180	4	197	195	209	4
Cham 6	83	73	93	5	160	159	161	1	202	197	206	2
Sonalika	89	73	103	6	161	160	169	2	199	195	202	2
Mexipak	83	73	93	5	161	160	164	2	200	195	209	2

1.3.2. Characterization of wild *Triticum* spp. from Jordan and Turkey

Triticum dicoccoides is the wild progenitor of all modern cultivated wheats. Complete crossing compatibility with durum wheat means that positive attributes (such as, disease resistance, abiotic stress tolerance, etc.) from the wild progenitor can be successfully transferred to the cultivated species. Einkorn wheat was domesticated in the Near East arc from one of its wild progenitor, *T. baeoticum*. Wild einkorn has been previously reported growing in wild stands in the province of Diyarbakir in Turkey.

A large set of wheat wild relatives consisting of 1,266 entries collected from Jordan and Turkey (population samples and single-plant progenies) were planted during the 1995-1996 growing season in the post-quarantine area at Tel Hadya as follows: *T. dicoccoides* (Jordan = 111, Turkey = 254, Total = 365 entries) *T. urartu* (Jordan = 78, Turkey = 271, Total = 349 entries), *T. baeoticum* (Turkey = 502 entries), and *T. araraticum* (Turkey = 50 entries). The main objective of this study was to characterize the germplasm under the eco-geographical conditions of northern Syria. The germplasm was planted in non-replicated plots of single 1m meter rows with a distance of 1.35 m between rows. Two cultivated durum wheat checks (Cham 1 and Hourani) were systematically included in this study and repeated 36 and 38 times, respectively. A set of qualitative and quantitative descriptors were evaluated on a plot basis as follows: Growth habit, number of days to heading, growth class, waxiness of the plant, flag leaf attitude, leaf attitude, tillering capacity, leaf shape and size, spike and awn length, spike length, number of spikelets/spike, plant height, yellow rust reaction, number of days to maturity, glume hairiness, spike density, glume color and awn color. The simple statistics for plant height, days to heading, and spike length(cm) is given in Table 22. Out of 1,266 accs. 647 (or 51%) were observed to be unaffected by the locally occurring races of yellow rust. Only one acc. was completely susceptible. The means of plant height(cm) and days to heading, for all four *Triticum* spp., is given in Fig. 22. The means for spike length(cm) and spikelets/spike are given in Fig. 23 for comparison.

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Table 22. Simple statistics for 1,266 wild wheats evaluated at Tel Hadya during the 1995-96 season

ORI	Plant height(cm)				Days to heading				Spike length(cm)			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
JORDAN												
dicoccoides	109	68	148	18	169	160	177	4	13.6	9.0	17.3	1.4
urartu	133	110	155	9	162	153	173	5	14.6	12.0	17.3	1.0
TURKEY												
dicoccoides	87	50	123	14	178	167	188	4	12.8	9.0	17.3	1.4
urartu	120	60	153	14	180	173	192	3	18.7	12.0	24.3	1.9
araraticum	90	63	103	10	182	173	190	3	14.6	10.0	18.0	1.7
baeoticum	110	50	153	16	182	167	194	5	18.0	8.3	26.0	2.7
Checks												
Cham 1	98	78	123	9	156	153	164	2	10.5	8.7	14.7	1.0
Haurani	122	83	153	15	159	153	164	4	7.3	5.7	11.7	0.9

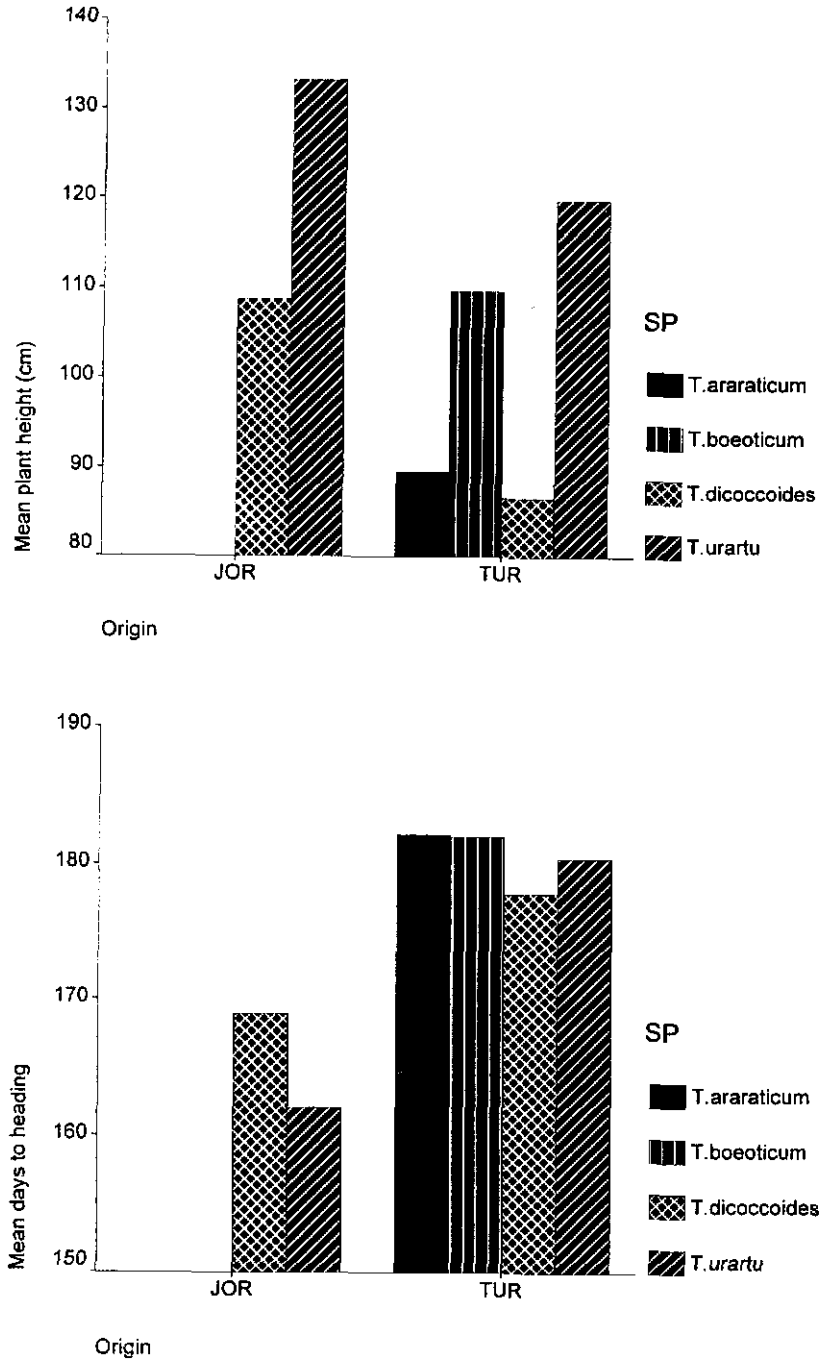

Fig 22. Means of plant height(cm) and days to heading for wild wheat accs. from Jordan and Turkey in 1995-96

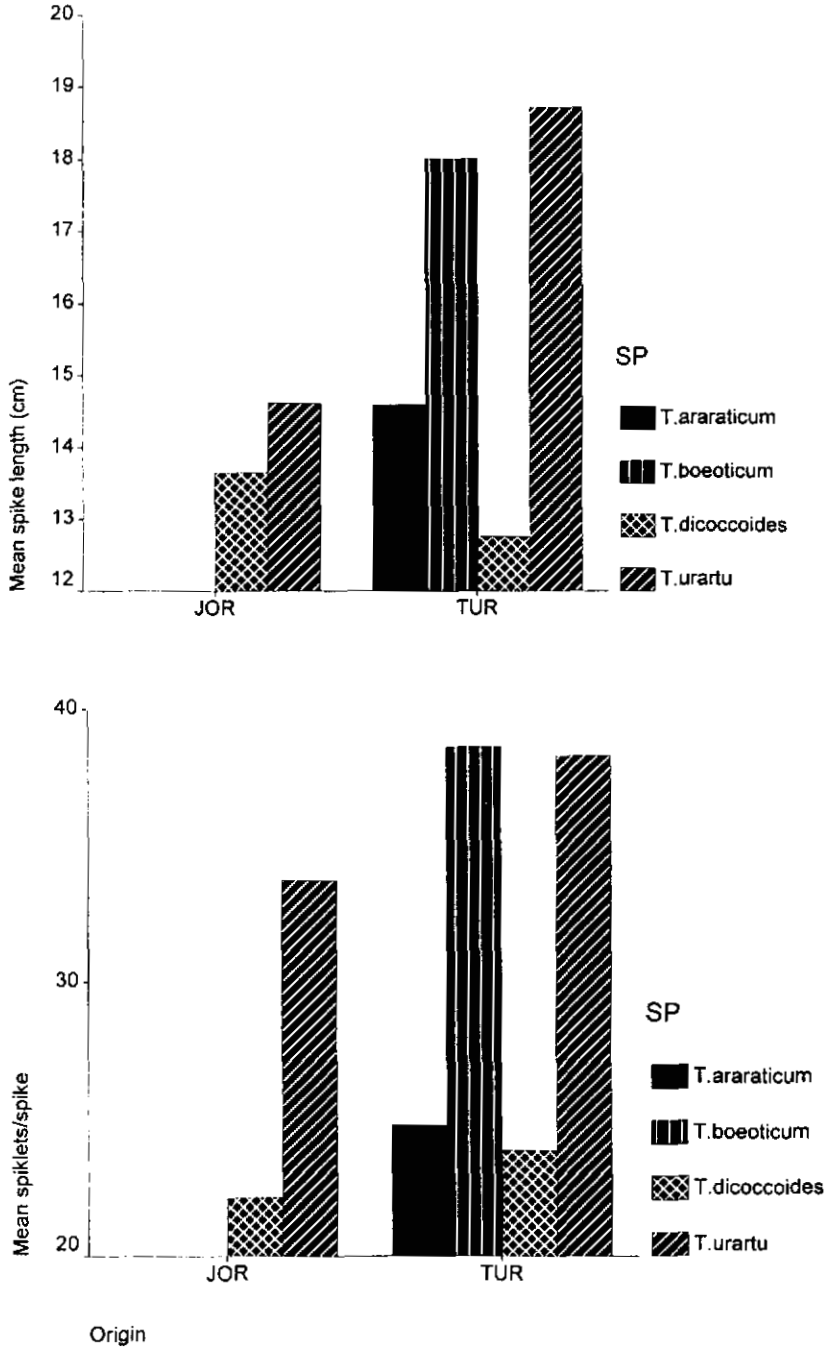

Fig 23. Means of spike length(cm) and spikelets/spike for wild wheat accs. from Jordan and Turkey in 1995-96

1.3.3. Characterization of wild barley

Wild barley, *Hordeum spontaneum* L., is the progenitor of all cultivated barleys. It crosses without any compatibility problems with cultivated barley and hence is a source for several useful genes or gene combinations required for barley improvement in WANA. This species is found in the eastern Mediterranean, West Asia, and as far as Turkmenistan and Afghanistan. Barley was domesticated around 9000 BP in the Near East arc. It later spread in several directions and is now widely grown throughout the world for animal feed, brewing, and for human food as well.

A set of 167 accs. of wild barley (*H. spontaneum*) was planted at Tel Hadya during the 1995-96 season as follows: Jordan (46 entries), Palestine (89) and Turkey (32). The principal objective of this study was to characterize wild barley germplasm under environmental conditions of northern Syria. The germplasm was planted in non-replicated plots of single 1m meter rows with a distance of 1.35 m between rows. Three standard cultivated barley checks (Tadmor, Harmal and Roho) and two wild barley checks (ICWB 181541, 181542) were included in the experiment (repeated 2 times).

The following descriptors were recorded on plot basis: Growth habit, number of days to heading, awn roughness, hoodedness/awnedness, leaf color, flag leaf width, number of days to maturity, powdery mildew reaction, scald reaction, yellow rust reaction, growth class, plant height(cm), peduncle length, spike length, awn length, and peduncle extrusion.

The simple statistics on plant height, days to heading and spike length(cm) together with data on the checks are given in Table 23. The following accs. were completely resistant to powdery mildew (from Jordan: ICWB 181660, 181661, 181665, and from Turkey: IC 181677, 181682, 181686, 181702, 181704).

The following accs. were completely resistant to naturally occurring races of yellow rust at Tel Hadya (from Palestine: ICWB 180470, 180471, 180472, 180475, 180481, 180514, 180515, 180525, and from Turkey: IC 181703, 181704, 181705). All the resistant accs. will be re-tested in disease nurseries, in cooperation with GP program, in the next season.

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Table 23. Simple statistics for 167 wild barley (*H. spontaneum*) evaluated at Tel Hadya during the 1995-96 season

ORI	Plant height(cm)				Days to heading				Spike length(cm)			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
H.spontaneum												
Jordan	118	95	146	11	146	138	160	5	12.84	6.30	17.0	2.18
Palestine	130	94	169	17	154	144	173	7	13.48	7.00	25.0	2.61
Checks(wild)												
181541	135	133	137	3	145	143	147	3	10.5	10.0	11.0	0.7
181542	139	135	143	6	148	143	152	6	11.0	11.0	11.0	0.0
Checks(cult.)												
Harmal	106	102	110	6	138	138	138	0	10.1	10.0	10.3	0.21
Roho	95	89	101	8	140	138	141	2	10.1	9.7	10.6	0.64
Tadmor	100	99	100	1	143	143	143	0	10.0	9.3	10.7	0.99

1.3.4. Characterization of *Aegilops* spp. from the Near East arc

A number of *Aegilops* spp. or goat grass are native to West Asia and the Near East. *Aegilops* was known to the ancient Greeks, and the name is related to its supposed healing properties of an eye disease from which goats suffer. *Ae. columnaris* is spread from Turkey through Iraq, Iran and Caucasia. It is a common weed found in and on the borders of fields. *Ae. crassa* is also found in Turkey, Syria, Palestine, Iraq, Iran, and Afghanistan. *Ae. cylindrica* is found in the Balkan peninsula, Crete, Turkey, Caucasia, Armenia, Azerbaijan, Iran, Iraq and Afghanistan. It is a weed in fallow fields and along slopes of hillsides. *Ae. kotschyi* is found from North Africa across Palestine, Iraq, Iran, Afghanistan and Caucasia. *Ae. laurentii* has a wider distribution i.e., from southern Europe, former USSR, Turkey, Palestine, Iraq and Iran. *Ae. mutica* is restricted somewhat to Armenia and Anatolia in Turkey and *Ae. ovata* is just the opposite being found all over the Mediterranean, Palestine, Syria, Lebanon, Turkey, Iraq, Iran and Afghanistan. A weed of cultivated wheat fields, it has a male-sterilization action on the nucleus of *Triticum aestivum* and *T. turgidum*. *Ae. speltoides* has its primary center in southern Turkey and northern Syria and Iraq. It is less common in places bordering the above. It is often found growing with wild wheat *T. baeoticum* in southern Turkey and northern Syria. *Ae. triaristata* is found in the Mediterranean, West Asia, Iraq, Iran and southern parts of the former USSR. *Ae. triuncialis* is all over the Mediterranean area, Turkey, Palestine, Syria, Lebanon, Iraq, Iran, Turkmenistan, and Afghanistan. It has been suggested that it is a hybrid between female *Ae. caudata* X a male *Ae. umbellulata* that originated in West Asia. *Ae. umbellulata*, on the other hand, occurs on moist steppe, dry slopes of hills, and is a weed in cultivated fields in the Greek islands, Turkey, northern Syria, Iraq, northwestern Iran, and Transcaucasia. It is resistant to leaf rust and hence used often in wheat breeding. Some *Aegilops* spp. are cross readily with others, e.g., *Ae. sharonensis*, whereas others are cross pollinators which readily produce hybrids. *Aegilops* spp. which occur on the borders of cultivated *Triticum* fields often exchange genes although the hybrids are mostly sterile.

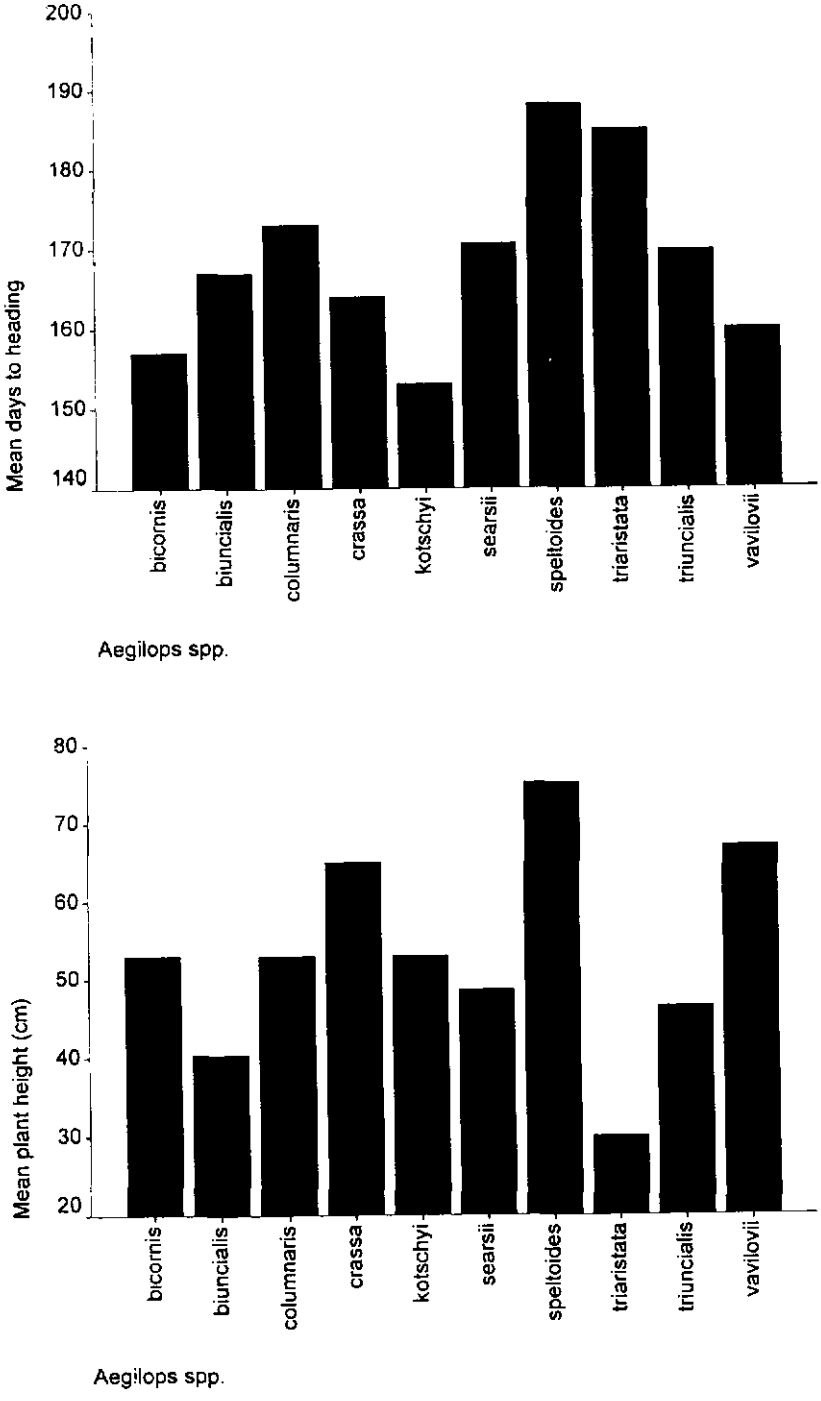

Fig. 24. Mean days to heading and plant height(cm) for 118 accs. of *Aegilops* spp. from Jordan, Syria and Turkey in 1995-96

A set of 118 accs. of *Aegilops* spp. from Jordan (73), Syria (4), and Turkey (41) was characterized at Tel Hadya during 1995-96. The germplasm was planted in non-replicated plots of two rows of 1m length and sown 0.45m apart. A distance of 1.35m was maintained between plots. The following characters were recorded: Growth habit, growth class, number of days to heading, waxiness, flag-leaf attitude, tillering capacity, leaf shape, plant height(cm), number of days to maturity and yellow rust reaction. Fig. 24. gives the mean days to heading and plant height(cm) for the 118 accs. of *Aegilops* spp.

There were 18 accs. resistant to naturally occurring races of yellow rust at Tel Hadya. These 18 accs. were among those collected by ICARDA in cooperation with AARI, in Gaziantep province, Turkey during 1995 (see GRU Annual Report 1994 and 1995 for details). The reaction of the entire set of *Aegilops* spp. to yellow rust at Tel Hadya is shown in Fig. 25. Only 18 accs., all from Turkey, were resistant (Table 24), whereas all the accs. from Jordan and Syria showed varying degree of susceptibility to yellow rust.

Table 24. List of 18 *Aegilops* accs. resistant to naturally occurring yellow rust races at Tel Hadya during 1995-96 season

ICAG No.	Species	ORI	ICAG No.	Species	ORI
402989	*biuncialis*	TUR	402990	*columnaris*	TUR
402991	*speltoides*	TUR	402992	*speltoides*	TUR
402993	*speltoides*	TUR	402994	*speltoides*	TUR
402995	*speltoides*	TUR	402996	*speltoides*	TUR
402998	*speltoides*	TUR	403003	*speltoides*	TUR
403004	*speltoides*	TUR	403009	*speltoides*	TUR
403010	*speltoides*	TUR	403011	*speltoides*	TUR
403014	*speltoides*	TUR	403023	*speltoides*	TUR
403024	*speltoides*	TUR	403025	*triaristata*	TUR

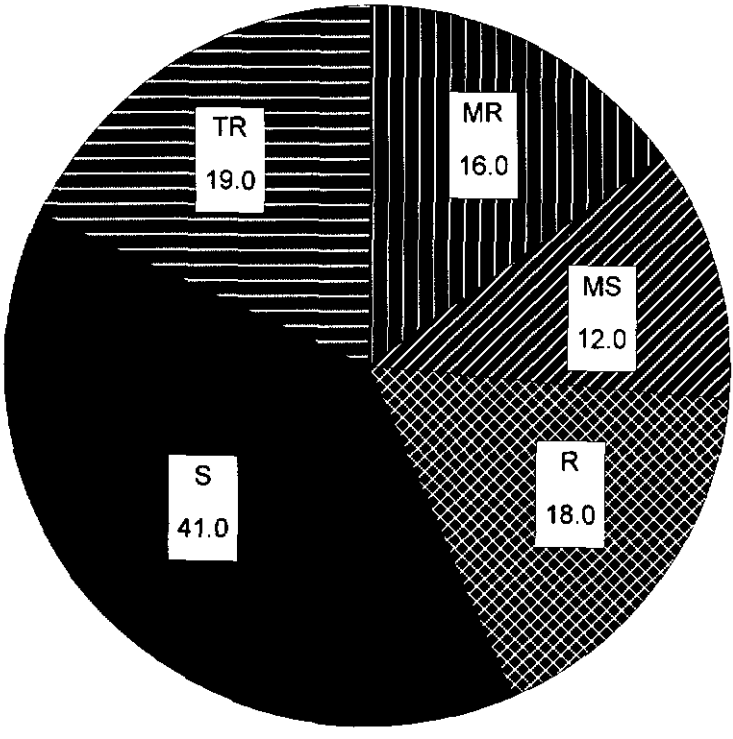

Fig. 25. Pie-chart showing reaction of *Aegilops* spp. to naturally occurring yellow rust races at Tel Hadya. (R=resistant; TR=trace resistance; MR=moderately resistant; MS=moderately susceptible and S=susceptible)

A second set of 453 accs. of *Aegilops* spp. and 2 accs. of *Amblyopyrum mutica* from 15 countries was evaluated at Tel Hadya during the 1996-97 season (Table 25 and Table 26). Three *Aegilops* checks, viz. *Ae. vavilovii*, *Ae. triuncialis*, and *Ae. biuncialis* were also systematically planted in the experiment and repeated 15 times. The same characters were once again recorded as in the 1995-96 season. There were 115 accs. (from Greece, Iran, Iraq, Jordan, Lebanon, Pakistan, Portugal, Syria and Turkey) resistant to naturally occurring races of yellow rust. These are not reported here. The simple statistics for plant height(cm), days to heading and number of productive tillers are given in Table 27. The bar-charts for means of productive tillers and spike length(cm) is given in Fig. 26.

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Table 25. Country of origins of 455 *Aegilops* and *Amblyopyrum* spp. planted at Tel Hadya during the 1996-97 season

Country	No. of accs.	Country	No of accs.
Afghanistan	1	Morocco	1
Armenia	1	Pakistan	9
Cyprus	1	Palestine	7
Greece	235	Portugal	11
Iran	68	Russia	7
Iraq	8	Syria	42
Jordan	30	Turkey	26
Japan	1	Unknown	7
Total	**455**		

Table 26. *Aegilops* and *Amblyopyrum* spp. for 455 accs. planted at Tel Hadya during the 1996-97 season

Species	No. of accs.	Species	No. of accs.
Ae. biuncialis	87	*Ae. neglecta*	33
Ae. caudata	29	*Ae. peregrina*	30
Ae. columnaris	3	*Ae. searsii*	4
Ae. comosa	30	*Ae. speltoides*	10
Ae. crassa	11	*Ae. tauschii*	35
Ae. cylindrica	20	*Ae. triuncialis*	100
Ae. geniculata	38	*Ae. umbellulata*	8
Ae. kotschyi	8	*Ae. vavilovii*	5
Ae. longissima	1	*Ae. ventricosa*	1
Ap. mutica	2	**Total**	**455**

Table 27. Simple statistics for 473 *Aegilops* spp. evaluated at Tel Hadya during the 1996-97 season

Species	Plant height(cm)				Days to heading				No. of productive tillers			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
biuncialis	42.3	26.0	72.5	7.12	169	154	188	6	197	44	573	85.3
caudata	52.6	32.0	64.0	8.53	178	172	188	4	253	99	675	149.5
columnaris	40.8	36.5	43.5	3.79	164	159	175	9	158	96	245	77.7
comosa	40.8	25.0	54.5	6.76	176	166	195	6	245	53	470	110.1
crassa	64.8	51.5	75.5	7.77	162	154	168	5	71	44	117	22.3
cylindrica	57.6	42.0	67.5	7.65	172	166	184	4	215	46	348	79.1
geniculata	41.9	33.5	63.0	6.17	163	147	172	6	156	53	292	65.6
kotschyi	36.4	28.0	51	6.77	158	151	168	6	133	55	332	97.6
longissima	70.0	70.0	70.0	-	172	172	172	-	81	81	81	-
mutica	73.7	67.5	80.0	8.84	179	179	179	-	85	73	98	17.3
neglecta	52.1	39.0	82.0	8.33	175	168	179	3	239	99	456	97.7
peregrina	51.0	30.0	66.0	7.63	157	147	175	7	110	52	266	51.9
searsii	50.8	36.5	66.5	12.75	169	166	172	3	103	63	140	37.1
speltoides	70.8	57.0	82.5	9.78	175	160	188	9	201	85	409	96.4
tauschii	59.5	36.0	82.0	10.66	167	158	179	7	102	30	187	38.3
triuncialis	53.1	30.0	77.0	7.47	173	154	184	5	268	57	611	120.2
umbellulata	36.9	30.0	44.0	4.56	169	154	179	9	208	57	611	87.4
vavilovii	64.3	53.0	78.5	9.34	158	154	166	5	107	49	207	61.4
ventricosa	64.0	64.0	64.0	-	168	168	168	-	51	51	51	-

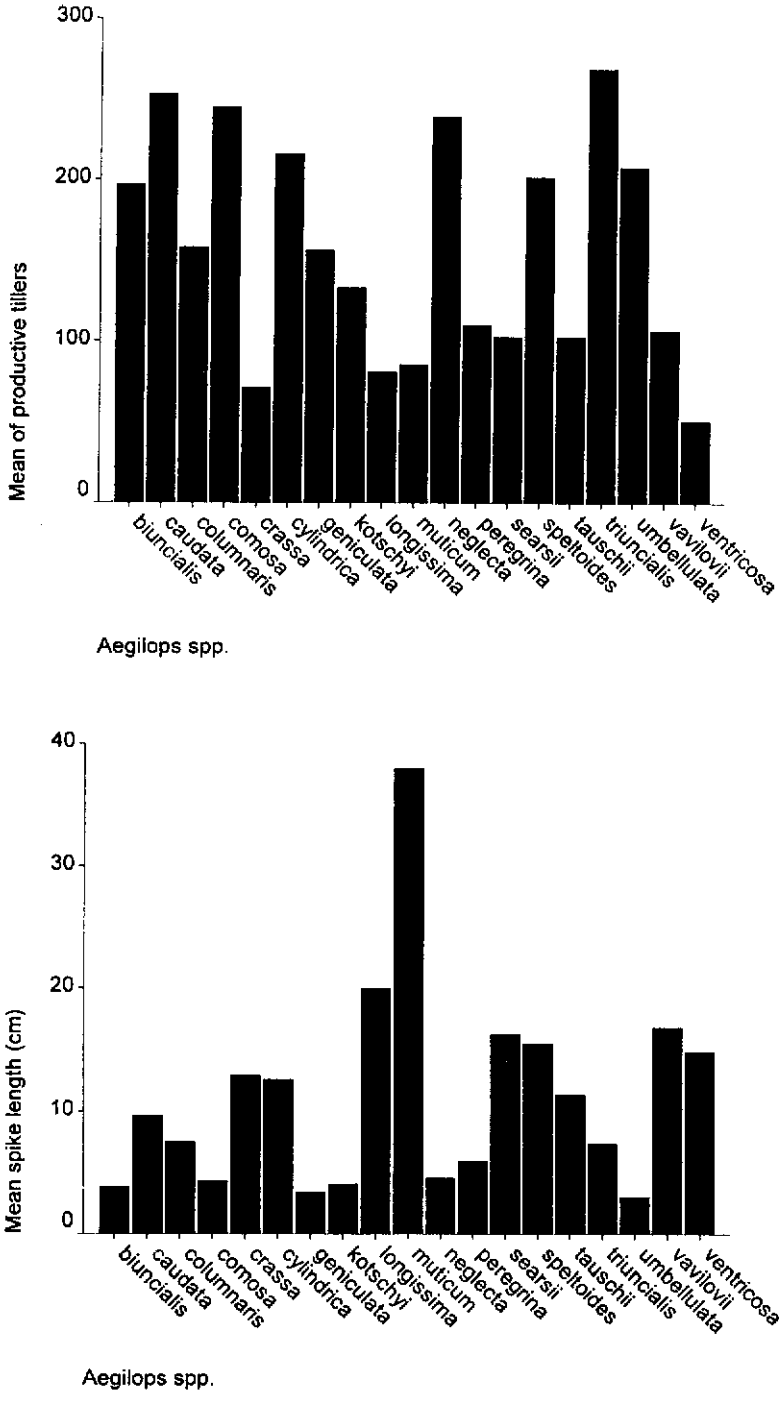

Fig. 26. Means of productive tillers and spike length(cm) for *Aegilops* and *Amblyopyrum* spp. by species in 1996-97

1.3.5. *Evaluation of lentil landraces*

During the 1996-97 season, a total of 2,295 lentil landraces and ICARDA breeding lines were evaluated in an unreplicated augmented design with one systematic (ILL 4000) and two random (ILL 4401 and ILL 5582) checks, with a block size of 23 plots. The plot size was 4 rows, 37.5cm between rows, 5m long ($7.5m^2$). The seeding rate was 1200 seeds per plot. Only 4 m length ($3m^2$) of the center two rows were used for yield determinations.

There were 25 descriptors observed: days to 50% flowering (DFLR), days to 90% maturity (DMAT), biomass in kg/ha (BYLD), seed yield in kg/ha (SYLD), straw yield in kg/ha (STYLD), harvest index in % (HI), 100 seed weight in g (HSW), plant height in cm (PTHT), height to first pod in cm (HLP), number of pods per plant (PPP), seeds per plant (SPP), seeds per pod (SPD), pod shedding (PSS), pod dehiscence (PDH), lodging susceptibility (LOD), testa ground color (TCO), testa pattern (TPA), cotyledon color (COC), testa pattern color (TPC), leaflet size (LFS), tendril length (TL), leaf pubescence (LFP), and pod pigmentation (PDP), seedling stem pigmentation (SPF), flower ground color (FGC).

There was no variation for seedling stem pigmentation, with all accessions with a value of absent seedling stem pigmentation. There was little variation for LFS, LFP, FGC, with 71.9% of accessions with medium LFS, 79.6% with slight LFP, and 92.8% of accessions with violet FGC, respectively (Table 28). TL was equally divided between rudimentary and prominent. Greater than 61% of LOD was considered medium or lower. PDH was mostly none or low (63.4%) and PSS was mostly low or medium (75.9 %). COC was mostly orange (61.1%) followed by yellow (35.1%) and only 0.1% was green. The TCO was mostly brown (59.4%). 43.1% of the accessions had no testa pattern and 32.6% had a dotted testa pattern. Those accessions that had a testa pattern had mostly a gray color for the testa pattern.

Summary statistics (Table 29) reveal that the largest variation for quantitatively scored descriptors was for both SPP and PPP with CVs over 60%. This was followed by the yield descriptors SYLD, BYLD, STYLD, HI and HSW, all with CVs over 40%. The means

Table 28. Frequency distributions for 2,295 lentil germplasm accs. evaluated at Tel Hadya, Syria, during the 1996-97 season

Descriptor/Score[a]		Freq. (%)
LFS	Small	22.3
	Medium	71.9
	Large	5.8
LFP	Absent	4.9
	Slight	79.6
	Dense	15.5
TL	Rudimentary	45.7
	Prominent	54.3
SPF	Absent	100.0
FGC	White	7.1
	Violet	92.8
LOD	None	10.8
	Low	15.8
	Medium	34.5
	High	38.9
PDH	None	15.2
	Low	48.2
	Medium	36.5
	High	.0
PSS	None	.0
	Low	32.2
	Medium	43.6
	High	24.1
TCO	Green	8.4
	Grey	19.4
	Brown	59.4
	Black	1.0
	Mixed	11.8
TPA	Absent	43.1
	Dotted	32.6
	Spotted	9.1
	Marbled	.0
	Mixed	15.2
PCO	Absent	43.1
	Olive	2.0
	Grey	34.8
	Brown	.0
	Black	6.1
	Mixed	14.0
COC	Yellow	35.1
	Orange	61.1
	Mixed	2.7

Table 29. Summary statistics for 2,295 lentil germplasm accs. evaluated at Tel Hadya, Syria during the 1996-97 season

	Check mean[a]	Min.	Max.	Mean	CV(%)
DFLR[b] (days)	118.5	109	139	119.1	3.6
DMAT (days)	155.0	146	179	154.6	4.5
HLP (cm)	14.9	1	35	14.0	31.7
PTHT (cm)	28.9	8	55	26.9	21.2
PPP	28.2	.0	130.3	25.4	63.7
SPP	30.0	0	170	31.9	66.6
SPD	1.04	.4	2.1	1.25	20.6
SYLD (kg/ha)	873.4	23	2409	28.8	55.3
STYLD (kg/ha)	3142.8	140	6227	515.2	44.4
BYLD (kg/ha)	4014.5	278	8136	241.9	41.5
HI (%)	21.06	1.0	90.1	23.22	43.4
HSW (g)	3.79	.89	7.93	3.03	40.6

a: ILL 4400, 4401 and 5582
b: Descriptor abbreviations as per text

of the accs. for SYLD and STYLD were respectively, 16.6 % and 20.0%, lower than the three checks. For other quantitative traits, the means were similar to the three check means.

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1.3.6. Evaluation of *Medicago* germplasm collections

The *Medicago* collection comprising of entire *Medicago lacinata* (196 accs.) and *M. littoralis* (246 accs.) was tested in the 1995-96 season. The entire *M. orbicularis* (649 accs.) and *M. scutellata* (127 accs.) germplasm collections were tested in the 1996-97 season. All trials were evaluated in augmented nurseries using one systematic check (IFMA 7858 *M. polymorpha* var. *vulgaris*), and two random checks (IFMA 811, *M. rigidula* and IFMA 2600, *M. rotata*). Most *M. lacinata* accs. were from the western Mediterranean area (64 from Morocco, 43 from Spain and 27 from Tunisia).

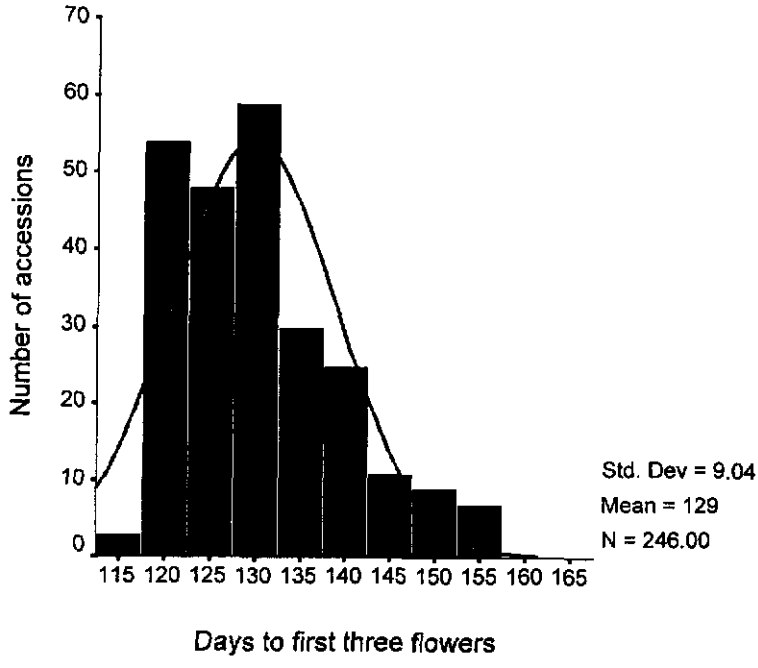

Fig. 27. Distribution of days to first 3 flowers in *M. lacinata* evaluated at Tel Hadya during the 1995-96 season

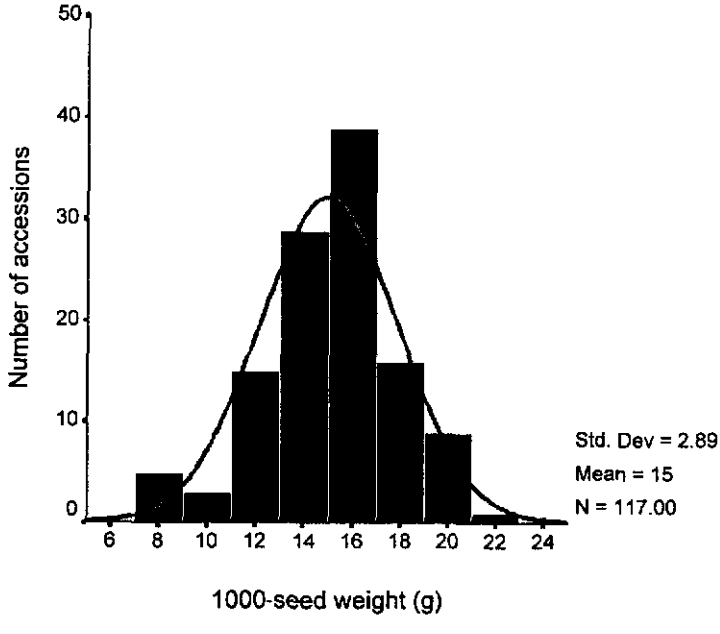

Fig. 28. Distribution of 1000-seed weight(g) for *M. scutellata* evaluated at Tel Hadya during the 1996-97 season

It should be noted that the entire *Medicago rigidula* (933 accs.) and *M. radiata* (135 accs.) were evaluated in previous years (see GRU Annual Report 1994 and 1995, page 102). Most *M. littoralis* accs. were also from the western Mediterranean area (47 from Libya, 40 from Morocco, 40 from Tunisia and 23 from Algeria). From west Asia the largest number of *M. littoralis* accs. were from Cyprus (25) and Turkey (18). The largest numbers of M. orbicularis accs. were from west Asia (177 from Syria, 90 from Jordan and 84 from Turkey). In addition, there were also large number of *M. orbicularis* accs. from Algeria (89), Spain (37), Italy (36), and Tunisia (23). The largest number of *M. scutellata* accs. were from Syria (25), Jordan (24), Italy (15), Turkey (11), and Cyprus (10).

The 12 descriptors observed were: Growth habit (GRH), vigor (VIG), frost susceptibility (FROST), days to first 3 flowers (DFLR), days to 100% maturity (DMAT), days to first 3 pods (DPOD), plant height in cm (PTHT), canopy width in cm (CANOPY), 1000-seed weight in g (S1000), seed yield in kg/ha (SYLD), biomass in kg/ha (BYLD), and harvest index in % (HI).

The majority of both *M. lacinata* and *M. littoralis* accs. were with prostrate GRH (79.9% and 84.6%, respectively). The remainder were with almost entirely semi-erect GRH. This was not measured in the other two species. VIG was high for all species except *M. orbicularis*. *M. orbicularis* showed high FROST tolerance with greater than 99% of accs. with low susceptibility. *M scutellata* showed 73% of accs. with intermediate or high FROST susceptibility. This was not measured in the other two species.

The mean phenology of the tested medics was slightly later than the checks (Table 30), which is to be expected since the checks are of different species than the tested accs. However, there was a significant number of accs. of the tested medic species that flowered earlier than the checks (Fig. 27 for *M. lacinata*). The mean biomass productions of the tested species accs. were much lower than the check means. Mean S1000 of the tested species were normal for the species tested. The highest S1000 was for *M. scutellata*, a large seeded medic species (Fig. 28).

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Table 30. Summary statistics for *M. lacinata* (195 accs.) and *M. littoralis* (246 accs.) evaluated in 1995-96 and *M. scutellata* (117 accs.) and *M. orbicularis* (647 accs.) evaluated in 1996-97

Species/ Decrip.	Check means	Min.	Max.	Mean	CV(%)
M. lacinata					
DFLR	132.2	121	158	136.30	4.7
DPOD	142.6	132	169	146.54	4.9
DMAT	188.5	186	195	190.76	1.1
HGT	37.3	2	34	12.77	38.8
CANOPY	139.7	5	152	84.90	34.4
BYLD	8235.2	55.3	8879.2	1643.6	76.8
S1000	4.6	.76	4.11	1.84	26.4
M. littoralis					
DFLR	126.5	114	154	129.30	7.0
DPOD	141.2	122	166	144.32	5.2
DMAT	186.5	183	198	190.15	1.8
HGT	34.2	5	55	14.10	48.1
CANOPY	135.6	10	163	94.80	30.2
BYLD	10052.5	126.7	17440.0	2774.2	90.7
S1000	4.70	1.39	12.71	2.63	45.7
M. scutellata					
DFLR	127.8	123	163	137.6	5.8
DPOD	139.0	135	170	145.7	4.7
DMAT	167.0	165	196	178.0	3.6
HGT	34.3	3	53	19.9	49.5
CANOPY	131.4	4	189	81.0	50.0
BYLD	8466.2	50.7	14353.5	2988.0	93.4
S1000W	4.74	7.12	21.19	15.00	19.2
M. orbicularis					
DFLR	127.2	121	163	133.7	5.0
DPOD	137.0	132	170	142.0	4.1
DMAT	171.9	163	195	174.1	4.1
HGT	35.9	2	44	18.0	34.0
CANOPY	139.9	12	157	108.6	19.9
BYLD	8452.6	136.8	9115.5	2962.6	54.5
S1000W	4.95	1.39	6.32	4.19	16.4

1.3.7. Evaluation of *Vicia* species in 1996

During the 1995-96 season, 700 accs. of five *Vicia* species were evaluated as follows: *V. hybrida* (142 accs.), *V. lutea* (81 accs.), *V. monantha* (110 accs.), *V. palaestina* (95 accs.) and *V. villosa* (272 accs.). Most *V. hybrida* accs. were from Syria (73) and Turkey (43), most *V. lutea* accs. were from Italy (25) and Turkey (20), most *V. monantha* accs. were from Algeria (48) and Syria (30), most *V. palaestina* accs. were from Syria (71) and most *V. villosa* accs. were Turkey (62), Hungary (47), Italy (37) and Morocco (22).

Table 31. Distribution of discretely scored descriptors for *Vicia* spp. evaluated at Tel Hadya during 1995-96

		Vicia spp.				
Descrip.[a] Score		***hybrida***	***lutea***	***monantha***	***palaestina***	***villosa***
GRH	Prostrate	0.0	0.0	0.9	0.0	0.0
	Semi-prostrate	0.0	0.0	0.0	0.0	0.7
	Semi-erect	14.1	64.2	93.6	76.8	16.5
	Erect	85.9	35.8	5.5	23.2	82.7
VIG	Very poor	2.1	8.6	11.8	21.1	3.3
	Poor	9.2	21.0	20.9	13.7	19.5
	Medium	57.7	56.8	43.6	51.6	52.9
	Good	29.6	11.1	20.9	13.7	23.5
	Very good	1.4	2.5	2.7	0.0	0.7
ANT	Very weak	48.6	40.7	46.4	41.1	28.7
	Medium	42.3	45.7	42.7	41.1	48.5
	Strong	9.2	13.6	10.9	14.7	21.7

[a]: Descriptor abbreviations as per text

The 24 descriptors observed were: Growth habit (GRH), anthocyanin (ANT), vigor (VIG), leaf shape (LFSH), leaflet shape (LFTSH), days to 50% flowering (DFLR), days to 90% maturity (DMAT), days to 90% podding (DPOD), height to lowest pod in cm (HLP), plant height in cm (PTHT), height to the first flower in cm (HTFF), number of leafs per plant (NOLF), number of leaflets per leaf (LFLF), leaf length in cm (LFL), leaf width in cm (LFW), pods per peduncle (PPPD),

pods per plant (PPP), seeds per plant (SPP), seeds per pod (SPD), 100 seed weight in g (HSW), hay yield (HYLD) in kg/ha dry matter, seed yield in kg/ha (SYLD), straw yield in kg/ha (STYLD), and harvest index in % (HI). Most accs. of *Vicia hybrida*, *V. villosa* were of erect GRH, the others were with mostly erect GRH (Table 31). The VIG of most accs. was intermediate or better. Except for *V. villosa*, the species at approximately 10-15% of accs. with strong ANT with the rest equally divided between very weak and medium ANT. 75% of all accs. were with weak ANTH. *V. villosa* had 49% accs. with medium ANT and 29% with weak ANT.

The accs. of the vetch species were within the ranges of the checks for the phenology descriptors (DFLR, DPOD and DMAT) (Tables 32 and 33), though the earliest tested accs. were significantly earlier than the checks. The yield components SPP, PPP and SDP were lower for the tested accs. The HSW for the tested accs. followed the expectations for the particular species evaluated. The means of the two best checks, IFVI 2541 and IFVI 2627 were significantly higher for than the tested accs. for the yield descriptors, HYLD, SYLD, STYLD and HI. However, this can be attributed to the difference in species of the checks (which were *V. sativa*). Again, there were large variations for these descriptors with the range of the tested accs. showing accs. with potential for use for these descriptors. Some of these accs. have been selected for further testing in the breeding program at ICARDA.

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1.3.8. Evaluation of *Vicia* spp. collected in North Africa

In the 1996-97 season, 700 accs. of six *Vicia* species collected in North Africa were evaluated. The species evaluated were *V. narbonensis* (9 accs.), *V. lutea* (9 accs.), *V. monantha* 15 accs.), *V. sativa* (197 accs.) *V. villosa* (24 accs.) and *V. ervilia* (46 accs.). These accs. were mostly from Morocco and Tunisia. Their collection and characterization was supported through the project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" funded by the Australian Center for International Agricultural Research (ACIAR). The collection of germplasm was in collaboration with CLIMA.

Table 32. Summary statistics for *Vicia* species evaluated in 1995-96 at Tel Hadya

Species	Descriptor[a]	N	Minimum	Maximum	Mean	CV(%)
hybrida	DFLR (days)	142	108	166	137.9	10.3
	DPOD (days)	142	139	172	160.1	4.8
	DMAT (days)	142	180	215	197.5	3.7
	HLP (cm)	142	11	61	26.1	35.2
	PTHT (cm)	142	27	141	78.4	25.3
	PPP	142	20.3	139.3	57.4	32.6
	SPP	142	35.0	275.3	127.8	41.6
	SPD	142	1.2	4.7	2.23	24.7
	HYLD (kg/ha)	142	318	3125	1569.4	33.3
	SYLD (kg/ha)	142	165	2668	1164.34	40.8
	STYLD (kg/ha)	142	2837	8925	5206.3	25.4
	HI (%)	142	3.88	31.7	18.04	30.7
	HSW (g)	142	2.85	10.00	5.26	22.8
lutea	DFLR (days)	81	122	172	149.8	7.7
	DPOD (days)	81	145	179	165.4	3.9
	DMAT (days)	81	186	210	197.5	2.6
	HLP (cm)	81	9	57	28.4	36.7
	PTHT (cm)	81	34	154	83.3	26.5
	PPP	81	15.0	131.3	40.0	56.0
	SPP	81	16.0	373.7	84.2	73.7
	SPD	81	.71	4.87	2.06	31.4
	HYLD (kg/ha)	81	628	4320	1883.0	43.6
	SYLD (kg/ha)	81	57	2960	887.6	59.3
	STYLD (kg/ha)	81	2939	11584	5226.7	31.0
	HI (%)	81	1.9	27.8	14.05	39.1
	HSW (g)	81	2.45	11.75	6.29	25.8
monantha	DFLR (days)	110	124	163	145.79	5.3
	DPOD (days)	110	145	172	162.20	4.0
	DMAT (days)	110	168	208	196.15	2.5
	HLP (cm)	110	8	113	29.9	57.9
	PTHT (cm)	110	28	171	82.7	32.2
	PPP	110	10.7	191.7	51.2	65.9

	SPP	110	43.3	411.0	169.8	53.8
	SPD	110	1.8	5.5	3.53	20.1
	HYLD (kg/ha)	109	248	3987	1409.8	44.4
	SYLD (kg/ha)	110	60	2385	905.9	58.7
	STYLD (kg/ha)	110	1078	8371	4046.2	31.8
	HI (%)	110	1.9	39.9	17.53	43.8
	HSW (g)	110	1.60	8.00	4.46	37.4
palaestina	DFLR (days)	95	117	161	139.4	6.9
	DPOD (days)	95	139	172	158.2	4.8
	DMAT (days)	95	170	200	190.4	3.4
	HLP (cm)	94	8	42	19.8	41.1
	PTHT (cm)	94	30	128	67.0	30.6
	PPP	95	14.7	158.7	59.7	48
	SPP	95	28.0	295.7	117.3	45.7
	SPD	95	1.0	3.9	2.05	26.5
	HYLD (kg/ha)	95	96	3509	969.0	51.2
	SYLD (kg/ha)	95	160	2549	974.9	55.5
	STYLD (kg/ha)	95	1441	8816	4265.0	32.3
	HI (%)	95	2.7	36.2	18.55	43.6
	HSW (g)	95	1.60	4.80	3.05	18.8
villosa	DFLR (days)	272	131	172	158.56	4.8
	DPOD (days)	272	156	179	171.92	2.1
	DMAT (days)	272	180	208	196.65	2.1
	HLP (cm)	272	7	106	43.1	43.8
	PTHT (cm)	272	48.0	165	111.4	19.7
	PPP	271	21.7	234.7	91.5	39.3
	SPP	271	48.0	532.3	219.02	37.9
	SPD	271	1.16	6.89	2.4507	21.9
	HYLD (kg/ha)	267	511	3991	1785.8	32.4
	SYLD (kg/ha)	270	73	2271	614.8	45.5
	STYLD (kg/ha)	270	2322	11188	4699.1	26.3
	HI (%)	270	2.3	29.5	11.46	33.0
	HSW (g)	272	1.60	9.30	3.30	29.5

a: Descriptor abbreviations as per text.

Table 33. Means and S.D. for checks used in *Vicia* evaluation trials during 1995-96

	IFVI 683[b]		IFVI 1416		IFVI 2541		IFVI 2627	
Descriptor[a]	Mean	Std. dev.	Mean	Std. dev.	Mean	Std. dev.	Mean	Std. dev.
DFLR	150.9	3	159.5	3.5	136.7	2.4	136.4	1.9
DPOD	168.4	1.1	168.1	1	161.3	2.3	157.5	3.6
DMAT	191.5	3.7	199.6	7.7	185.5	5.2	188.7	5.3
HLP	38.9	10.3	38.5	12.8	33.8	10.5	21.9	4.6
PTHT	131.4	17.3	88.3	14.8	91.6	11.8	69.3	12.8
PPP	104.4	37.6	36	13.5	54.2	22.3	47.7	16.8
SPP	246.7	100.4	238.2	93	228.3	96.8	226.3	73.7
SPD	2.34	0.28	6.59	0.51	4.2	0.34	4.77	0.3
HYLD	2589.6	594.4	1995.7	713.6	2413.1	461	1955.7	536.2
SYLD	665.1	154.1	872	331.8	2049.9	451.7	2306.7	762.9
STYLD	6012.7	684.3	5639.5	1294.7	6153.6	1623.9	5035.8	1532.8
HI	9.94	2.1	13.45	3.92	25.32	3.73	31.39	4.84
HSW	3.39	0.53	2.31	0.2	4.52	0.33	4.89	0.29

a: Descriptor as per text, units as per Table 2.
b: IFVI 2541, 2627 and 1416 are *Vicia sativa* and IFVI 683 is *V. villosa*.

The 20 descriptors observed were: Growth habit (GRH), anthocyanin (ANT), days to 50% flowering (DFLR), days to 90% maturity (DMAT), days to 90% podding (DPOD), plant height in cm (PTHT), height to the first flower in cm (HTFF), number of leafs per plant (NOLF), number of leaflets per leaf (LFLF), leaf length in cm (LFL), leaf width in cm (LFW), pods per peduncle (PPPD), pods per plant (PPP), seeds per plant (SPP), seeds per pod (SPD), 100-seed weight in g (HSW), hay yield (HYLD) in kg/ha dry matter, seed yield in kg/ha (SYLD), straw yield in kg/ha (STYLD), and harvest index in % (HI).

Results for discretely scored descriptors and quantitative descriptors are given in Table 34 and Table 35, respectively. The accs. of the vetch species were within the ranges of the checks for the phenology descriptors (DFLR, DPOD and DMAT), though the earliest tested accs. were significantly earlier than the checks. The yield components SPP, PPP and SDP were lower for the tested accs. The HSW for the tested accs. followed the expectations for the particular species evaluated.

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Table 34. Discretely scored descriptors for *Vicia* spp. from North Africa evaluated at Tel Hadya in 1996-97

Descriptor[a]	Score	*ervilia*	*lutea*	*monantha*	*narbonensis*	*sativa*	*villosa*
GRH	Prostrate	0.0	33.3	6.3	0.0	2.1	0.0
	Semi-prostrate	100.0	66.7	81.3	11.1	60.5	83.3
	Semi-erect	0.0	0.0	12.5	77.8	33.8	16.7
	Erect	0.0	0.0	0.0	11.1	3.6	0.0
ANT	Low	27.7	77.8	37.5	0.0	1.0	0.0
	Medium	55.3	11.1	18.8	0.0	42.6	25.0
	High	17.0	11.1	43.8	100.0	56.4	75.0

[a] Descriptor abbreviations as per text

Table 35. Summary statistics for *Vicia* spp. from North Africa evaluated at Tel Hadya in 1996-97

Species		N	Minimum	Maximum	Mean	C.V. (%)
ervilia	DFLR (days)	47	143	159	153.2	2.4
	DPOD (days)	47	159	168	163.1	1.3
	DMAT (days)	47	175	184	180.9	1.4
	PTHT (cm)	47	27	78	60	17.8
	SYLD (kg/ha)	47	108	4149	1521.1	56.8
	STYLD (kg/ha	47	3639	8426	6121.4	17.4
	HI (%)	47	2	36.7	18.7	40.2
	HSW (g)	47	3.36	4.7	4.04	7.4
lutea	DFLR (days)	9	133	149	143.4	3.5
	DPOD (days)	9	151	161	157	2.4
	DMAT (days)	9	175	189	178.3	2.5
	PTHT (cm)	9	34	63	47.4	20.8
	SYLD (kg/ha)	9	463	1688	934.7	43.3
	STYLD (kg/ha	9	3570	6417	4747.2	18.8
	HI (%)	9	10	24.5	16.2	31.4
	HSW (g)	9	6.03	11.87	8.64	22.7
monant	DFLR (days)	16	143	149	145.1	1.5
-ha	DPOD (days)	16	154	159	156.8	1
	DMAT (days)	16	175	189	179.6	2.3
	PTHT (cm)	16	33	68	49.8	18.5
	SYLD (kg/ha)	16	71	1358	687.8	61.6
	STYLD (kg/ha	16	1961	5051	3585.5	25.3
	HI (%)	16	3.5	27.3	14.8	47.6
	HSW (g)	16	2.43	6.84	5.49	25.5

narbone	DFLR (days)	9	133	143	139.4	2.7
-nsis	DPOD (days)	9	151	156	153.9	0.8
	DMAT (days)	9	175	177	175.2	0.4
	PTHT (cm)	9	33	87	55.3	34.8
	SYLD (kg/ha)	8	88	2146	465.9	151.8
	STYLD (kg/ha	8	4079	6554	4763.6	16.8
	HI (%)	8	1.9	30.5	7.4	130.7
	HSW (g)	8	7.65	14.9	9.82	22.9
sativa	DFLR (days)	195	139	161	149.2	3.2
	DPOD (days)	195	151	170	160.3	2.4
	DMAT (days)	195	175	200	179.5	2.6
	PTHT (cm)	195	17	91	43.9	34.6
	SYLD (kg/ha)	195	73	2498	940.9	55.1
	STYLD (kg/ha	195	2238	10813	4662.8	28.2
	HI (%)	195	1.6	33.6	16.5	44.9
	HSW (g)	195	1.21	7.9	3.79	37.1
villosa	DFLR (days)	24	139	161	146.9	2.7
	DPOD (days)	24	156	170	161.1	1.4
	DMAT (days)	24	175	189	182.2	2
	PTHT (cm)	24	24	103	58	34.8
	SYLD (kg/ha)	24	198	2187	770.5	57.1
	STYLD (kg/ha	24	1768	10475	4888.3	40.2
	HI (%)	24	7.4	33.6	13.7	42
	HSW (g)	24	3.16	7.09	5.1	23

1.3.9. Evaluation of *Lathyrus* spp. collected in North Africa

In the 1996-97 season, 74 accs. of six *Lathyrus* species collected in North Africa were evaluated. The species evaluated were *L. aphaca* (4 accs.), *L. articulatus* (39 accs.), *L. cicera* (10 accs.), *L. ochrus* (17 accs.) *L. sativus* (2 accs.) and *L. tingitanus* (2 accs.). These accs. were mostly from Morocco and Tunisia and their collection and characterization was supported through the project "Development and Conservation of Plant Genetic Resources for the Western Mediterranean Region" funded by the (CLIMA) and supported by ACIAR.

Table 36. Discretely scored descriptors for *Lathyrus* from North Africa evaluated at Tel Hadya during 1996-97

Descriptor[a]	Score	*aphaca*	*articulatus*	*cicera*	*ochrus*	*sativus*	*tingitanus*
GRH	Prostrate	0.0	0.0	0.0	0.0	0.0	0.0
	Semi-prostrate	50.0	100.0	100.0	100.0	100.0	100.0
	Semi-erect	50.0	0.0	0.0	0.0	0.0	0.0
	Erect	0.0	0.0	0.0	0.0	0.0	0.0
ANT	Low	100.0	41.0	40.0	100.0	0.0	100.0
	Medium	0.0	53.8	50.0	0.0	100.0	0.0
	High	0.0	5.1	10.0	0.0	0.0	0.0

[a]: descriptor abbreviations as per text.

The 20 descriptors observed were: Growth habit (GRH), anthocyanin (ANT), days to 50% flowering (DFLR), days to 90% maturity (DMAT), days to 100% podding (DPOD), plant height in cm (PTHT), height to the first flower in cm (HTFF), number of leafs per plant (NOLF), number of leaflets per leaf (LFLF), leaf length in cm (LFL), leaf width in cm (LFW), pods per peduncle (PPPD), pods per plant (PPP), seeds per plant (SPP), seeds per pod (SPD), 100 seed weight in g (HSW), hay yield (HYLD) in kg/ha dry matter, seed yield in kg/ha (SYLD), straw yield in kg/ha (STYLD), and harvest index in % (HI).

Results for discretely scored descriptors and quantitative descriptors are given in Table 36 and Table 37, respectively. The accs. of the *Lathyrus* species were within the ranges of the checks for the phenology descriptors (DFLR, DPOD and DMAT), though the earliest

tested accs. were significantly earlier than the checks. The yield components SPP, PPP and SDP were lower for the tested accs. The HSW for the tested accs. followed the expectations for the particular species evaluated.

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Table 37. Summary statistics for *Lathyrus* from in North Africa evaluated at Tel Hadya in 1996-97

Species	Descriptor[a]	N	Minimum	Maximum	Mean	C.V. (%)
aphaca	DFLR (days)	4	143	151	146.5	2.8
	DPOD (days)	4	156	161	158	1.6
	DMAT (days)	4	177	191	181.5	3.5
	PTHT (cm)	4	32	33	32.4	2.1
	PPP	4	49.7	59.7	53.3	8.7
	SPP	4	209.7	254	232.6	9
	SDPD	4	4.2	5.1	4.4	10
	SYLD (kg/ha)	4	168	448	323.6	36
	STYLD (kg/ha)	4	2909	3929	3632.3	13.4
	HI (%)	4	4.1	10.8	8.27	36.7
	HSW (g)	4	0.95	2.21	1.66	35.4
articulatus	DFLR (days)	39	136	159	155.3	2.9
	DPOD (days)	39	156	168	164.9	1.8
	DMAT (days)	39	175	200	188.6	3
	PTHT (cm)	39	30	82	57.3	20.5
	PPP	39	4.7	37	17.7	33.8
	SPP	39	13.3	106.7	48.1	37.4
	SDPD	39	1.9	3.7	2.75	16.8
	SYLD (kg/ha)	39	50	2192	394	87
	STYLD (kg/ha)	39	2536	7060	3997.6	25.3
	HI (%)	39	1.7	26.7	8.39	53.2
	HSW (g)	39	5.84	9.24	6.85	10.4
cicera	DFLR (days)	10	143	149	144.8	1.7
	DPOD (days)	10	154	161	156.3	1.6
	DMAT (days)	10	175	179	175.4	0.7
	PTHT (cm)	10	28	47	37.1	14.9
	PPP	10	8	17.7	12.9	25.5
	SPP	10	17.3	49.7	35.5	30.2
	SDPD	10	2.2	3.8	2.7	18.5
	SYLD (kg/ha)	10	77	499	269.2	51.2
	STYLD (kg/ha)	10	1957	7871	3995.8	47.5
	HI (%)	10	2.6	13.6	6.78	51.8
	HSW (g)	10	6.24	9.7	8.21	13.1

ochrus	DFLR (days)	17	147	151	148.5	1
	DPOD (days)	17	156	161	158.8	1
	DMAT (days)	17	175	179	178.7	0.6
	PTHT (cm)	17	21	49	31.1	25.2
	PPP	17	3	12.7	7.6	38
	SPP	17	10	60	30.4	45.3
	SDPD	17	3	4.8	4.06	12.7
	SYLD (kg/ha)	17	31	1173	443.5	78.4
	STYLD (kg/ha)	17	1145	9835	3839.3	49.8
	HI (%)	17	1.2	19	9.52	54.3
	HSW (g)	17	8.42	12.35	10.76	11.9
sativus	DFLR (days)	2	147	151	149	1.9
	DPOD (days)	2	156	161	158.5	2.2
	DMAT (days)	2	191	191	191	0
	PTHT (cm)	2	54	67	60.2	15.3
	PPP	2	19.3	29.3	24.3	29.1
	SPP	2	44	68.7	56.3	31
	SDPD	2	2.3	2.4	2.36	5
	SYLD (kg/ha)	2	1270	2056	1663.1	33.4
	STYLD (kg/ha)	2	4711	6195	5452.9	19.2
	HI (%)	2	21.2	24.9	23.08	11.3
	HSW (g)	2	14.01	14.81	14.41	3.9
tingitanus	DFLR (days)	2	147	156	151.5	4.2
	DPOD (days)	2	159	168	163.5	3.9
	DMAT (days)	2	191	191	191	0
	PTHT (cm)	2	34	73	53.5	50.7
	PPP	2	8.7	45.3	27	96
	SPP	2	18.7	129	73.8	105.7
	SDPD	2	2.2	2.9	2.52	19.6
	SYLD (kg/ha)	2	290	469	379.3	33.4
	STYLD (kg/ha)	2	2944	6777	4860.7	55.8
	HI (%)	2	4.1	13.7	8.92	76.4
	HSW (g)	2	2.99	6.8	4.9	55

a: Descriptor abbreviations as per text.

1.4. GENETIC RESOURCES SUPPORT RESEARCH

1.4.1. Molecular characterization of genetic diversity in diploid wheat: *Triticum urartu* using AFLP fingerprinting

The size of a germplasm sample to be collected in the field, and conserved in a gene bank for each species' natural population, has vital importance for its optimal utilization. This size must be determined on the basis of the magnitude of genetic variation in the population. Amplified fragment length polymorphisms (AFLP), detected in both the nuclear and organellar DNAs, can be used as the selectively neutral markers of genetic variations. The recently developed molecular marker systems based on amplification have facilitated and enhanced fundamental and applied biological studies. Although, DNA amplified-derived techniques are in general more advantageous than classical markers. All have their limitations and specific applications.

Among the most important factors, they possess the multiplex ratio and the information content of a marker technique. The choice of a particular method depends on the specific application. If the objective is to assess genetic diversity, the method with a high multiplex ratio such as AFLP is appropriate. Nucleotide diversity, estimated from the genetic distances between different accs., has been adopted as a parameter of the genetic variability of a population or a taxon. AFLP is a powerful DNA fingerprinting technique, which is especially suitable to investigating or natural populations. AFLP was already adopted to characterize plant natural populations. It has been found to be a very fast and reliable technique avoiding the obstacles of previously used markers, such as RFLPs and RAPDs. For a crop improvement program, plant breeders require a marker technology which is technically simple, cost- and time-effective, and which generates a high level of polymorphism. AFLPs offer an opportunity to perform detailed genetic studies in a large number of organisms. The polymorphism detected per reaction is much higher than the one revealed by RFLPs or RAPDs because of the number of loci sampled in a single assay. In the present study, we have applied AFLPs to study genetic variation between and within populations of wild wheat (*Triticum* spp.).

Materials and methods

Plant material

The plant material (*Triticum urartu* Tum ex Gand.) used consists of 18 genotypes of six accs. (three samples per acc.) collected from different parts of Syria by GRU scientists.

DNA extraction

DNA was extracted from leaf tissue of three-week-old seedlings, and frozen in liquid nitrogen, according to the modified CTAB protocol for this procedure.

Digestion of DNA

The AFLP procedure was performed using the protocol described by N.V. Keygene, with some minor modifications. Five hundred nanograms of DNA from each sample were double digested with 5 U MseI and 10 U PstI; the One-Phor-All buffer (10x, Pharmacia), in a final volume of 40 µl, was used.

Ligation of the adapters

Dynal beads procedure

The DNA fragments were then ligated with PstI adapters, viz., 5'biotinylated and MseI. DNA fragments containing the biotin-labeled PstI adapters were separated from the reaction using streptavidin beads (supplied by DYNAL Inc., New Hyde Park. N.Y.). They decreased the complexity of the DNA by removing the more abundant MseI-MseI. Adaptor ligation was achieved by adding 50 pmol MseI-adapter, 5 pmol PstI-adapter, 1µl 10 mM ATP, and T4-DNA ligase. 1µl of One-Phor-Buffer (10x) and sterile distilled water were added to the double-digested DNA sample (50 µl final volume) and incubated further at 37°C.

Biotinylated restriction fragments in each ligation mixture were used as template for polymerase chain reaction amplifications. Sixteen different primer combinations were used. For every amplification, only MseI-directed primer was radio-labeled with [γ^{33}P] ATP (Amersham redivue AH 9968), and all primers carried either two or selective nucleotides at the 3' end. Polymorphic amplification products were visualized by autoradiography and scored manually as described by Vos (1995). All AFLP polymorphisms were scored as dominant markers (presence or absence of a band).

Selective-amplification

For selective PCR, PstI were end-labeled with [γ^{33}P] ATP (Amersham) using a T4 polynucleotide kinase reaction (New England Biolabs). Selective amplification was performed using two AFLP primers specific for Pst and Mse I adapters. Each primer contained two or three selective nucleotides at the 3'end. AFLP fingerprintswere generated in selective amplification in the 20 µl of PCR mix composed by 5 µl of the diluted 5.10x pre-selective amplification, 5mM dNTPs, 0.5 U of Taq polymerase, 30 ng each of two primers in PCR buffer.

Data analysis

Assigning a number to each band visually scored the fingerprinting profiles. Only full intensity bands were scored. Polymorphism was scored as either present (1) or absent (0) across all genotypes. Calculation of the distance matrix and cluster were carried out using the statistical package NTSYS Version 2.00 (1997). Data from the four primer combinations were mixed and the pairwise similarities calculated between samples using the Jaccard coefficient. The resultant similarity matrix was input into the unweighted pair group method (UPGMA) cluster analysis and a principal coordinate analysis. Analysis of molecular variance (AMOVA) has been used to determine the percentage of variation among and between the populations and the region to the amalysis using GENSTAT statistical package 5.0.

Results

AFLPs were performed on 18 T. urartu genotypes and gave highly informative banding patterns. When AFLP analysis was performed on a *T. urartu*, 50 to 100 DNA bands were separated on a sequencing gel when two to three selective nucleotides were used. An average of 50 bands was obtained by genotype, ranging from 50 to 300 bp. The total number of bands scored across the 18 genotypes was 176 for the four primer combinations studied. Among sixteen primer combinations, four gave interesting and informative results. The restriction enzymes coupled with selected primers produced multiple polymorphic bands in all the wild *T. urartu* plants used in this study. For the genetic diversity studies 176 bands were included for statistical analysis. Two most informative primer combinations were Pst+AA/Mse+CCG and Pst+ CC/Mse+ACC (Fig. 29 and Fig. 30).

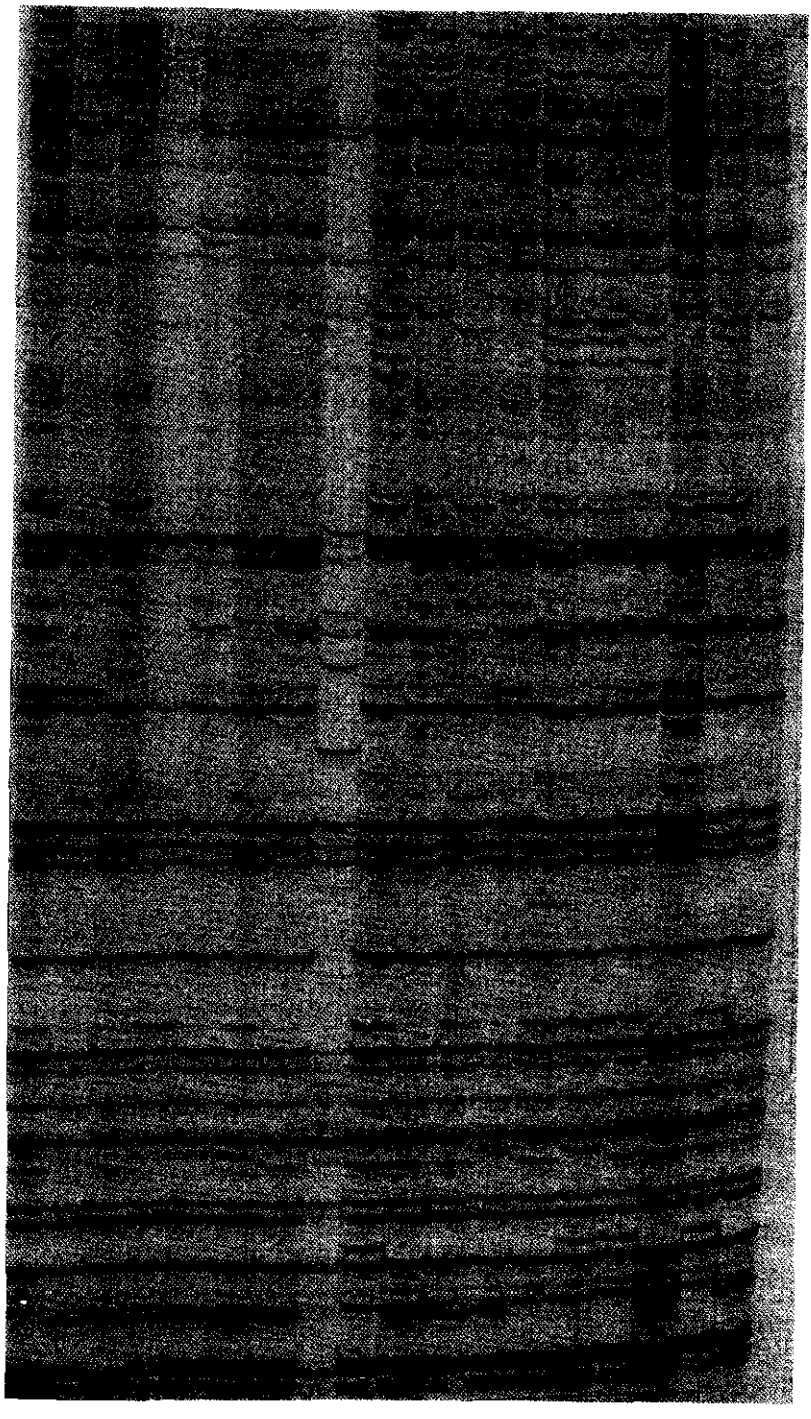

Fig. 29. AFLP pattern obtained by primer combination Pst+AA/Mse+CCG

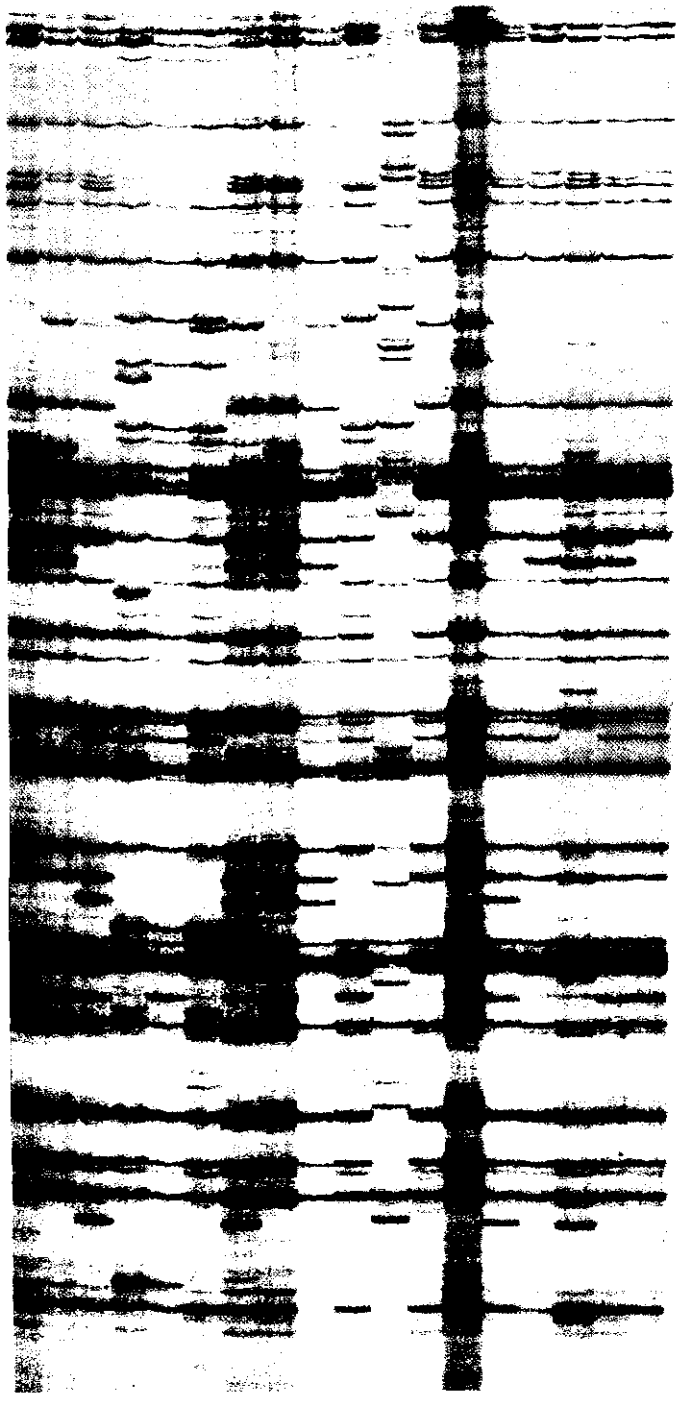

Fig. 30. AFLP pattern obtained by primer combination Pst+CC/Mse+ACC

Statistical analysis

Cluster analysis

When NTSYS analysis was performed with each primer combination individually, the major groups obtained were similar to those with four primer combination together using a similarity matrix produced by Genstat. The dendrograms based on the neighbor-joining (NJOIN) method for cluster analysis using Jaccard Similarity Coefficients are showed in the Fig. 31. The *T. urartu* pool is arranged in two geographic groups, from Aleppo (North Syria) and Sweida (South Syria) respectively. Both populations from Aleppo region were more diverse that the Southern populations. However, the accs. from the South showed a high diversity between them. The high correlation between pair of combination of primers suggests that each combination provided different but complementary information.

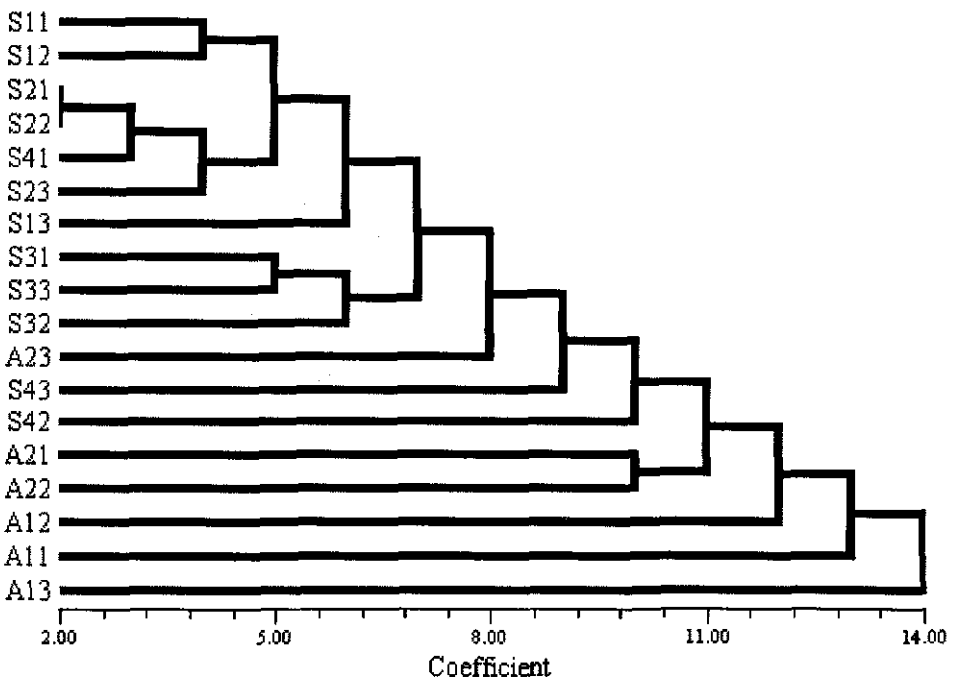

Fig. 31. Midpoint-rooted NJOIN tree for 18 *T. urartu* single-plants (S=from Sweida and A=from Aleppo regions)

Principal coordinate analysis

The principal coordinate analysis demonstrated the structure of the genetic diversity. The first and second principal coordinates accounted for 32% and 22% of the total variation in the AFLP data, respectively. The results suggest that the first principal coordinate clearly separates the two regions. The second principal coordinate shows a distinct separation between the Aleppo accs.

AMOVA

The variation estimates within and between regions were calculated. The lowest variance within a region was obtained from northern Syria, which was different from the southern region. Accs. from southern Syria were more diverse than those of the northern part. This result could be due to the different mutations or recombinations whicg may have occurred during evolution over a period of time. Also, it is possible that populations have a high proportion of heterozygotes. The variation within populations and regions was 67.8% and 78.7%, respectively.

The genetic variability of the 18 genotypes of *T. urartu* derived from natural populations as revealed by AFLP technique showed highly informative banding patterns that were polymorphic both at plant and population level.Using AFLPs all the 18 plants and six populations were easily distinguished.

The four primer combinations gave some putative specific bands as Pst+CC/Mse+CCG where a high polymorphism has been obtained. Genstat 5.0 statistical package was used to determine which primer couple would be best retained among the four pairs of combinations for the screening of *Triticum urartu.* The difference among them was, however, very small.

Each combination of primers could be used to distinguish the geographic origin, such as Pst+CC/Mse+CCG or Pst+AA/Mse+CCG. These should be used for fingerprinting. The *T.urartu* both from the north and south of Syria clustered differently in the PCO plot shown. This corroborates the previous results obtained with multivariate statistical analysis of agro-morphological quantitative data (see GRU Annual Report 1993).

The southern groups were more dispersed on the PCO plot, which is a reflection of their wider genetic variation. AFLP appears to

represent an additional molecular polymorphism assay, which can be applied to analysis of genetic diversity and population genetics in wild wheat. The AFLP technique is expected to yield more reproducible results because the polymorphism is based on the presence or absence of band reflecting dominant mutations on the DNA level. Repeatability of AFLP banding patterns was very high; thus showing credibility to the conclusions derived from the analysis. AFLP displayed a high rate of polymorphism compared to that obtained with RAPD (see Chabane and Valkoun 1997).

The number of accs. studied permit preliminary conclusions about genetic structure of wild wheat *T. urartu* populations and to answer various questions such as which and/or how many markers must be used for their genetical study. The high frequency of identifiable AFLP polymorphism's make AFLP DNA analysis an attractive technique for identifying polymorphism in plant germplasm characterization.

An AFLP data analysis of natural populations of wild *Triticum* species with AMOVA may be a useful tool for the optimization of a strategy for the collection and *in situ* conservation of this important component of the wheat gene pool.

K. Chabane and J. Valkoun (GRU-ICARDA), A. Karp and J. Baker (University of Bristol, UK)

1.4.2. Standardization of RAPD marker techniques to determine the diversity of diploid wild wheat, *Triticum urartu*

Characterization and quantification of genetic diversity has long been a major objective in evolutionary biology and plant breeding. DNA-based polymorphisms allowed direct comparisons of variation in nucleotide sequences, and proved to be a powerful tool in different genetic analysis.

The first DNA polymorphic marker method used by several workers for genetic mapping was RFLP. However, it was found to be time consuming and expensive. Later, the successful development of various PCR-based polymorphic marker techniques rendered fingerprinting of plant genomes a routine laboratory work.

Among the recently-developed techniques, RAPD analysis is a rapid tool for this purpose, and PCR easily produces these markers. This

method is based on the amplification of genomic DNA fragments with a single short primer of an arbitrary nucleotide sequence. The use of RAPD as a genetic system in wheat was evaluated. DNA with selected primers rigorously optimized reaction conditions.

These short primers have been used to reproducibly amplify segments of genomic DNA in a wide variety of species. The RAPD technique is preferred to overcome limitations of RFLP analysis. The objective of this study was to evaluate the use of RAPD as a source of genetic markers in *Triticum urartu*.

Materials and methods

Plant material

Accs. *Triticum urartu*, obtained from GRU-ICARDA collections representing diversity and variation of three natural populations, based on previously obtained data of gliadin analysis with electrophoretic technique, were used. In the present study, seeds were sown in "jiffy seven pots" containing compost under plastic house conditions. Leaves were harvested from three-week-old seedlings from each acc. and later pooled to provide a total of 100 to 200 mg of material for DNA extraction.

DNA isolation

The young leaves were ground to a powder in 2 ml Eppendorf tubes under liquid nitrogen. The powder was then mixed with 1 ml CTAB extraction buffer. The homogenate was incubated at 65°C for one hour before adding 900 µl chloroform/isoamylalcohol (24:1, v/v). The whole mixture was shaken and the aqueous phase recovered after centrifugation at 12,000g for 10 min. The chloroform/isoamylalcohol treatment was repeated and the DNA precipitated by 660 µl of ice-cold isopropanol. The DNA was washed with 1000 µl of 76% ethanol, then dried under vacuum and dissolved in 100 µl sterilized TE. DNA concentration was checked by subjecting samples to 1% agarose gel electrophoresis in TAE 1X buffer. Band intensities were visually compared with lambda DNA standards. The results were obtained by dosage with a spectrophotometer.

PCR amplification

The amplification conditions were tested in optimization experiments. Experiments were carried out with the aim of establishing standard conditions for RAPD analysis in wheat. Twenty decanucleotides of

arbitrary sequence obtained from Operon Technologies were used. The PCR conditions were carried out in a volume of 25 µl. DNA amplification was performed in a Perkin Elmer Cetus DNA Thermal 9600 Cycler programmed for 40 cycles of 30 s at 94°C, 1 min at 36°C, 1 min at 72°C, using the fasting available temperature transition. The procedures established above were used for the following experimentation. The PCR volume was 25 µl and contained 15 pmoles of primer, 100 µM each of dATP, dCTP, dGTP and dTTP, 50 ng template DNA and 1.5 U of Taq DNA polymerase in 1X PCR buffer. Amplification products were analyzed by electrophoresis in 1.4% agarose gels, visualized by ethidium bromide staining and photographed under UV light with RFLP scan (Stratagene). Molecular weights were estimated using DNA cleaved with EcoRI and Hind III (Boehringer).

Data analysis

For each individual primer, the PCR products were designated. Data were scored for computer analysis on the basis of the presence or absence of the amplified products. If a product was present in a genotype it was scored as "1", if absent, it was designated as "0". Pair-wise comparisons of genotypes, based on the presence or absence of unique and shared polymorphic products, were used to generate Jaccard's similarity coefficients. The similarity coefficients were then used to construct a dendrogram by UPGMA, using the computer program Numerical Taxonomy and Multivariate Analysis System (NTSYS) for personal computers.

Results

The sensitivity of RAPD PCR technology to changes in experimental parameters is well known. Therefore, several experiments were carried out to establish a protocol yielding results which could be reproduced. We have optimized the DNA concentration ranging from 25, 50 and 100 ng/µl.

All reactions were replicated three times to examine the possible influence of DNA concentration on the fidelity of the amplification. The results showed that the concentration 50 ng/µl yielded reproducible patterns with a primer concentration of 15 pmoles.

The influence of the Taq DNA polymerase was also tested. Different concentrations were used (0.5, 1 and 1.5 U). The concentration of

1.5U of the Taq polymerase gave a higher number of bands and more reliable banding patterns than the lower concentrations. The primer performances were tested to generate RAPD patterns with 20 primers. The optimal template concentration were not identical for all primers. Furthermore, not all primers performed equally well.

Three concentrations of primers were tested (5, 10 and 15 pmoles). Some, presumably becausae of the lack of suitable priming sites in the wheat genomic DNA, gave poorly amplified banding patterns, while others created clear bands. For the choice of RAPD primers, we considered only unambiguous and qualitative (present or absent) fragments that gave repeatable patterns when tested twice with the same acc. From these option, we chose the primers that also gave two band patterns. These primers are given in (Table 38).

Table 38. Sequences and codes of random primers analysis (RAPDs)

Primer	Sequence 5' to 3'	Mol. Wt.
OPA-11	CAATCGCCGT	2979
OPA-17	GACCGCTTGT	3010
OPB-08	GTCCACACGG	3004
OPB-18	CCACAAGCAGT	2988
OPG-08	TCACGTCCAC	2939
OPK-16	GAGCGTCGAA	3068

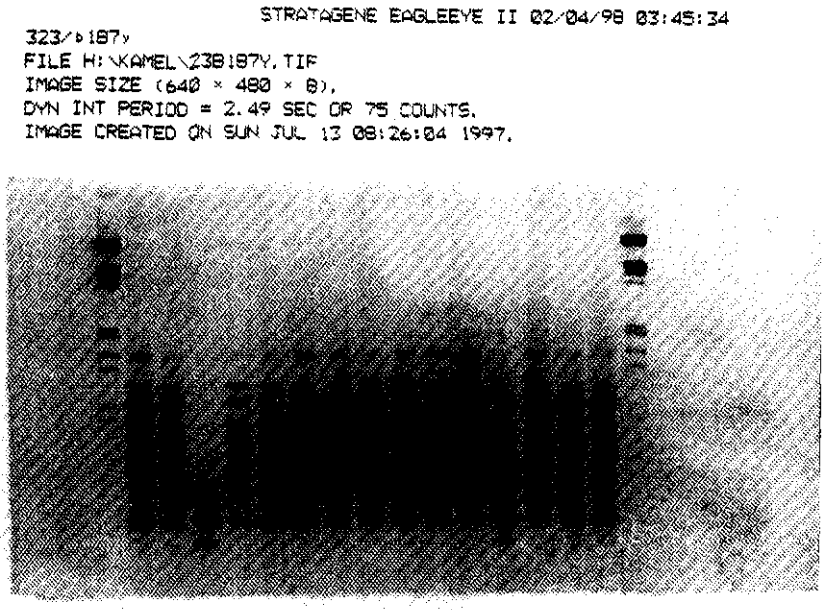

Fig. 32. Example of patterns obtained by OPB18 primer in *T. urartu*

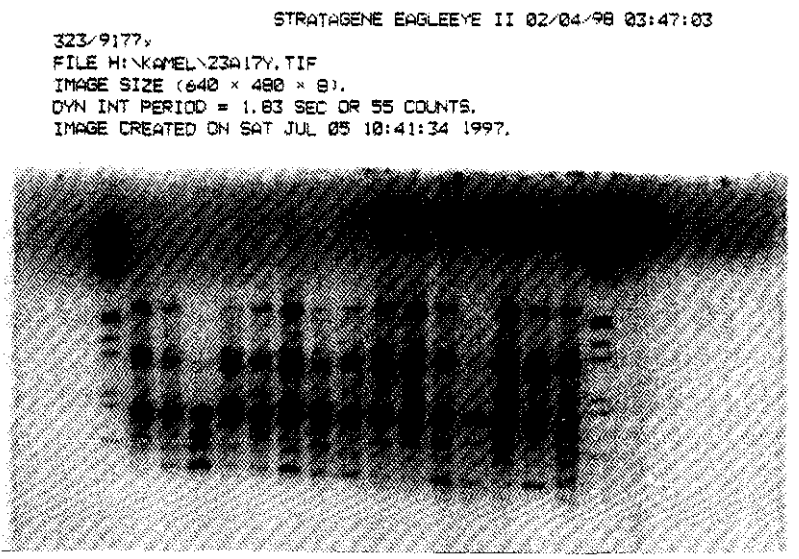

Fig. 33. Example of patterns obtained by OPA17 primer in *T. urartu*

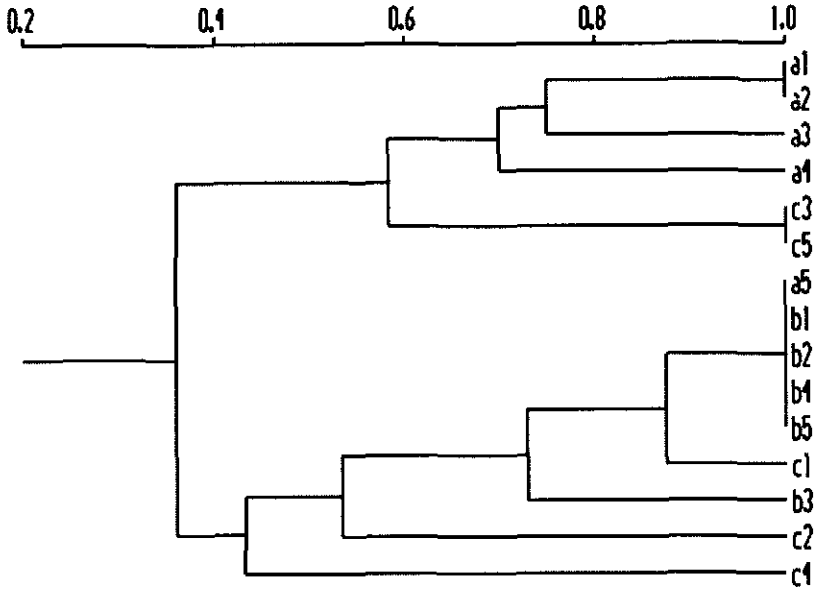

Fig. 34. Dendrogram clusters generated by using UPGMA analysis with OPA17 primer

Variation within and between populations

The use of all six primers led to amplification products; results of only three primers are presented below. The primers OPB-18, OPA-17 and OPG-08 gave patterns showing reproducibility for a large number of bands. For all three of the primers, clear reproducible patterns were obtained when the primer concentration was increased from 10 to 15 pmoles and the Taq polymerase from 1U to 1.5U. The number of polymorphic bands varied between one and nine per primer. An example of RAPD variation using primers OPB-18 and OPA-17 and DNA of fifteen single plant-progenies is shown in Fig. 32 and 33, respectively. The amplification products obtained from these three primers were easy to score.

The RAPD marker technology can be standardized to provide repeatable and reliable polymorphism of the amplification products with different genotypes of the diploid wild wheat, *T. urartu*. The selected six primers generated sufficient polymorphism to estimate both among-and within-population diversity. Results of the genetic similarity analysis (Fig. 34) did not indicate a clear geographical pattern of the DNA polymorphism.

However, it must be pointed out that the number of single-plant progenies per population was low, as was the number of populations of different geographical origins. This preliminary study demonstrated that RAPD marker technology can be an additional and effective tool for the assessment of genetic diversity within and among natural populations of wild wheat, *T. urartu*. The high within-population polymorphism of the amplification products indicate that this technique may also be suitable for molecular fingerprinting of accs. in a gene bank's *ex situ* collections.

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1.4.3. The use of DNA markers in study of diversity in barley

Plant germplasm collections of global crops like barley have grown fairly large in size over the years. Developing procedures for reducing the size of a collection to a manageable and accessible level is becoming one of the important issues in the management and utilization of plant germplasm collections. Genetic resources collections must contain as much as possible of the available genetic diversity required for research and breeding programs. The core collection (derived from an existing germplasm collection) should represent the genetic spectrum in the whole collection and include as much as possible of its genetic diversity in avoiding the duplicates.

The conservation of genetic diversity must be concerned not only with establishing adequate procedures to conserve the natural diversity of species and genes, but also with identifying and making available potentially useful genetic characteristics. Various criteria have been used to analyze genetic diversity in crop plants, including morphological, agronomic, ecogeographic and molecular traits or markers. Molecular markers reflect direct changes at the DNA sequence level, their major advantage is the presumed selective

neutrality.

From a purely management point of view, there are distinct advantages in trying to identify duplicate accs. and, thereby, only conserving unique genetic materials in the collection. Until now the identification of duplicate has had to rely on a comparison of morphological characters. Some of which are subject to routine use of molecular markers based directly upon genomic DNA for the identification of duplicate accs. of seed propagated species.

In this study DNA markers were employed to: (i) detect genetic polymorphism between different accs. of barley, (ii) include those possessing passport data and genetic diversity, and (iii) evaluate the WANA barley core collection.

Materials and Methods

Three hundred and fifteen cultivated barley accs. provided by GRU were used in this study (Table 39). They represent a barley core collection covering the WANA regions. Leaves of individual 15 day-old seedlings were collected for DNA extraction. Total genomic DNA was isolated from fresh leaf material using the method of Benito et al. (1993). One plant per acc. was analyzed. Three Operon primers were used (OPG-08, OPK-16 and OPS-09) for DNA amplification. Agarose 1.2% gel was used to separate the products of amplification. RAPD was observed as the presence versus absence of amplified fragments of the same size.

The Shannon-Weaver Information Index was used for the measurement and comparisons of phenotypic diversity. The index was calculated as:

$$Hs = \sum i \, [Pi \; Ln \; (Pi)],$$

Where *Pi* is the proportion of the total number accs. in the category. Relative indices *H*sr was calculated according to the method of Andrivon and de Vallavieille-Pope (1995). Each *H*s value was divided by its maximum value (1n/*N*), where *N* is the maximum number of the character categories. The overall countries diversity *H*sr was calculated as the arithmetic mean of the character *H*sr values.

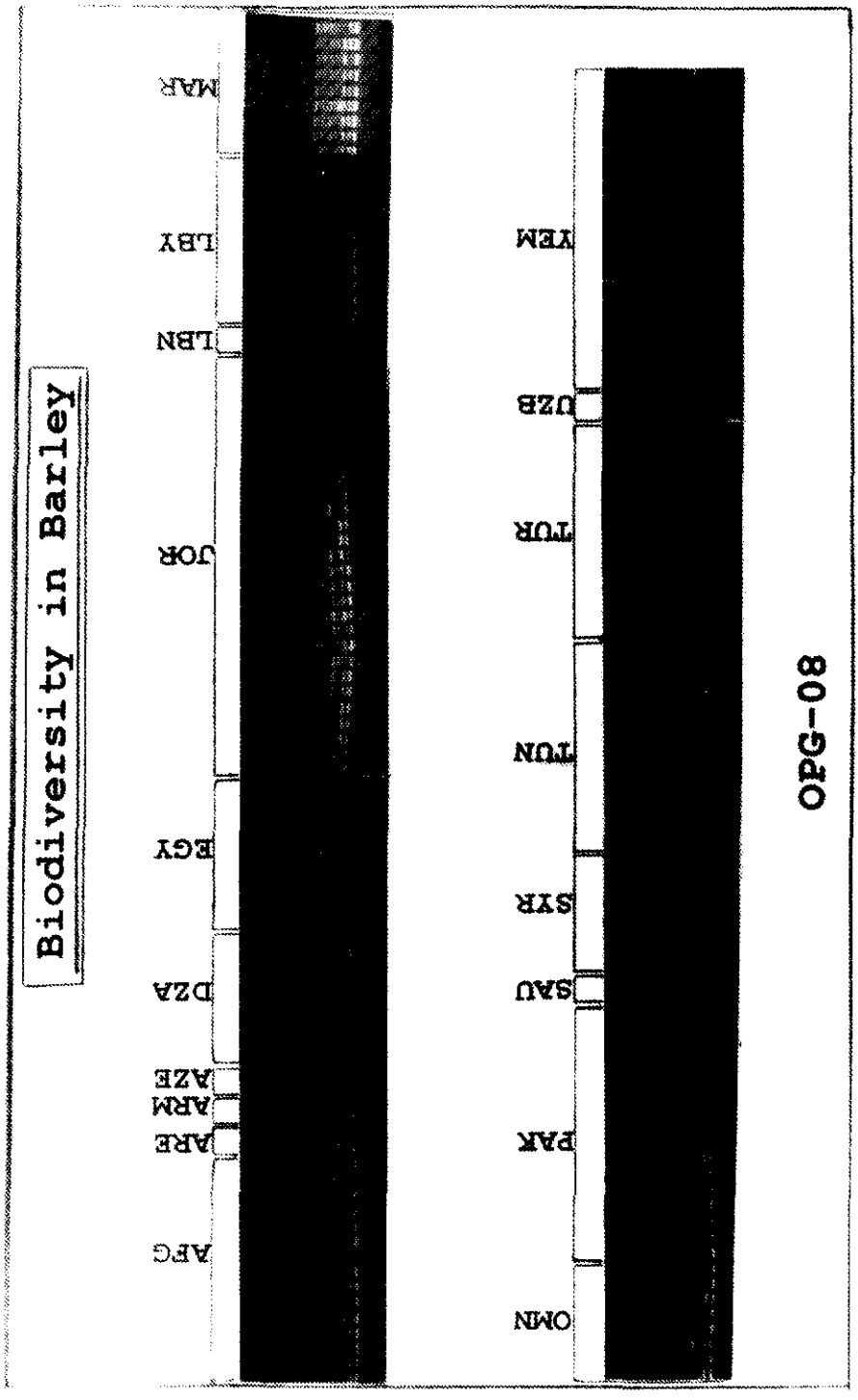

Fig. 35. DNA of 315 accs. from the barley core collection amplified with Operon primer OPG-08

Table 39. Origin, no. of accs. analyzed, and patterns detected and their frequencies (No. before the parenthesis indicates the pattern and that between them represents the frequency of this pattern)

Countries	Number of accessions	Number of patterns	Frequency of patterns
AFG	36	18	1(1)-2(11)-3(1)-14(1)-15(3)-17(1)-21(1)-22(1)-35(5)-47(2)-54(1)-58(2)-66(1)-80(1)-81(1)-85(1)-89(1)-94(1)
ARE	2	2	3(1)-39(1)
ARM	2	2	2(1)-59(1)
AZE	4	3	5(2)-18(1)-44(1)
CYP	5	4	3(2)-5(1)-47(1)-76(1)
DZA	20	12	3(1)-5(1)-22(7)-23(1)-36(1)-49(1)-52(1)-68(1)-70(3)-75(1)-88(1)-95(1)
EGY	10	6	2(1)-15(1)-17(1)-21(4)-22(1)-41(1)-85(1)
IRN	23	15	14(2)-15(3)-17(1)-21(1)-34(1)-35(1)-36(3)-37(1)-38(3)42(1)-48(1)-52(2)-60(1)-66(1)-76(1)
IRQ	13	9	19(1)-21(1)-29(2)-35(2)-36(2)-37(1)-42(1)-66(2)-69(1)
JOR	14	9	4(1)-19(3)-35(2)-36(2)-48(2)-49(1)-54(1)-56(1)-80(1)
LEB	2	1	72(2)
LBY	14	12	7(1)-21(1)-22(1)-28(1)-63(1)-69(1)-71(1)-73(1)-77(2)-85(2)-90(1)-96(1)
MOR	17	13	6(1)-7(1)-8(1)-9(3)-10(1)-11(2)-12(1)-13(1)-15(1)-28(2)-64(1)-65(1)-78(1)
OMN	8	6	28(1)-40(1)-45(1)-61(1)-91(3)-92(1)
PAK	23	11	3(1)-15(4)-17(2)-19(1)-30(6)-33(1)-45(1)-46(1)-57(1)-85(1)-86(4)
SAU	2	2	53(1)-64(1)
SYR	20	13	10(5)-38(1)-42(1)-43(1)-44(1)-54(2)-55(1)62(1)-64(1)-72(3)-79(1)-93(1)-97(1)
TJK	3	3	5(1)-76(1)-86(1)
TKM	8	8	16(1)-19(1)-20(1)-24(1)-25(1)-27(1)-50(1)-59(1)
TUN	12	8	5(4)-7(1)-26(1)-38(1)-61(2)-74(1)-77(1)-87(1)
TUR	46	21	5(6)-20(1)-22(4)-31(1)-32(1)-35(2)-37(2)-38(1)-47(1)-49(7)-51(1)-52(2)-58(1)-59(1)-61(2)-67(3)-70(1)-82(1)-83(6)-84(1)-88(1)-
UZB	2	2	17(1)-67(1)
YEM	29	11	3(1)-21(2)-28(1)-36(3)-37(6)-38(10)-44(2)-48(1)-58(1)-60(1)-88(1)

Results

The DNA samples of 315 accs. were assayed for RAPD-PCR using three primers. Every primer produced several amplified fragments reflected by different number of patterns (12 patterns for OPS-09, 14 for OPK-16 and 17 for OPG-08). The accumulated results with the three primers gave ninety-seven different profiles or patterns (Table 39).

The different profiles represent a genetic diversity between the accs. analyzed and permit the identification of most accs. (Fig. 35). The distribution of this diversity across and within the countries provides information on the level of diversity present in these countries. Two kinds of profiles were detected. The first one is considered as a `frequent' profile. It was present in many countries with high number of accs. For example, profile number 5 is present in 15 accs. dispersed over 6 countries (2 in Azerbaijan, 1 in Cyprus, 1 in Algeria, 1 in Tadjikistan, 4 in Tunisia, 6 in Turkey).

The second kind of profile is considered as a `characteristic' one. It was only present in one country. For example, profile number 1 is present only in Afghanistan, profiles 6 and 8 are present only in the Moroccan accs., etc. The frequency of each profile across the countries shows the distribution of the diversity between the countries. In some case the same profile is frequent in the same country. For example: profile 2 is present in 11 accs. in Afghanistan. This high frequency can be interpreted to signify the following:

* A dominant profile in the country.
* A low level of diversity within the country.
* A non-random strategy employed in the collection of the samples.
* The presence of replicates in the core collection tested.

On the contrary, the higher the number of patterns detected in a country the higher the level of its genetic diversity, and hence a good selection for the core collection. This was observed in the case of Libya, where 12 profiles were identified in 14 accs., and in Morocco, where 13 profiles were detected in 17 accs. Hence, the level of diversity in Morocco is higher than that in Pakistan where only 11 profiles were detected for 23 accs. analyzed.

Another situation arose in some countries where the number of accs. tested was small (8 accs. for Turkmenistan, etc.). However, every acc.

has a specific pattern. This means that even if the level of diversity is not very high in these countries their selection for the core collection was warranted since no duplicates were detected in the study.

The comparison between the value of diversity estimated for the whole collection of the WANA region (using 12 agro-morphological characters) and the core collection derived from it (using RAPD markers) showed similar results. In both cases, Turkey had the highest level of diversity (0.57 and 0.60, respectively) followed by Iran then Afghanistan (Table 40). The similarity between both levels of diversity indicates that the core collection tested has retained the same level of diversity present in the whole collection. It represents the collection of the WANA regions very well.

Table 40. Comparison of diversity in WANA barley core collection and all accs. (*=maximum number of accs.)

Countries	WANA core coll.		WANA all accs.	
	No. of accs.	Hrs-RAPD	No. of accs.*	Hrs-categ.data
Turkey	46	0.60	1373	0.57
Iran	23	0.56	425	0.55
Afghanistan	36	0.54	279	0.55
Morocco	17	0.54	643	0.50
Libya	14	0.53	--	--
Syria	19	0.51	285	0.56
Iraq	13	0.47	--	--
Algeria	20	0.47	--	--
Pakistan	20	0.46	238	0.40
Jordan	14	0.45	128	0.45
Turkmenistan	8	0.45	--	--
Yemen	29	0.41	--	--
Tunisia	11	0.41	591	0.34
Egypt	10	0.38	--	--
Oman	8	0.36	--	--

To conclude, we can say that the RAPD assay is a useful tool for germplasm characterization and for assessing the genetic diversity. The level of genetic diversity in the core collection tested is high.

This finding, in turn, also reflects the genetic diversity existing in the country of origin.

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1.4.4. Development of synthetic hexaploid wheat

In a pre-breeding project, which started in the 1994-1995 season, a number of triploid hybrids between durum wheat cvs. Haurani and Cham 5 and wild *Triticum* spp., as well as *Aegilops speltoides* and *Ae. tauschii*, were produced. Seventy eight seeds were obtained in Haurani x *Ae. tauschii* hybrids after colchicine treatment and chromosome doubling, and twelve seeds were produced in two untreated hybrid plants. The well-developed and fully viable seeds gave rise to vigorous plants, which had the same genomic constitution AABBDD as bread wheat. The A- and B-genome chromosomes of the synthetic hexaploid wheats originate from durum wheat Haurani, well adapted to semi-arid regions of Syria, whereas the D-genome chromosomes were received from *Ae. tauschii* parents, which were collected from heat-affected and low-rainfall sites (150-250mm per year) in northern and central Syria. The synthetic hexaploid wheats can be crossed with bread wheat and their chromosomes are fully homologous. Because of this, they may be a valuable source of heat and drought tolerance genes in bread wheat breeding for rainfed and semi-arid areas of WANA and for other regions affected by abiotic stresses, such as drought and heat.

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1.4.5. Diversity in barley germplasm collection at ICARDA

The world barley collection held at ICARDA was initiated in 1977. During the early years of ICARDA, barley germplasm was maintained at the Cereal Improvement Program (CIP) as a working collection. In 1983, when the GRU was established, the barley genetic resources were transferred to the active collection and maintained under medium-term storage conditions at 5°C. The base collection has been developed since 1989, when the long-term store facility became available with the financial and technical assistance from the Government of Italy.

Table. 41. Barley germplasm collected by GRU-ICARDA

Country	No. of accessions	
	Cult. barley (ssp. *vulgare*)	Wild barley (ssp. *spontaneum*)
Morocco	459	-
Syria	220	113
Egypt	151	1
Jordan	107	139
Pakistan	102	2
Algeria	95	-
Ecuador	56	-
Iran	46	8
Lebanon	12	25
Turkmenistan	5	8
Tadjikistan	5	1
Tunisia	3	-
Uzbekistan	1	2
Turkey	-	36
Iraq	-	8
Libya	-	7
Cyprus	-	3
Russia	-	2
Total	**1271**	**352**

The present composition and high genetic diversity of the barley collection is a result of ICARDA's acquisition and collection strategy. From the outset the focus was on acquiring germplasm indigenous to the West Asia and North Africa (WANA) region. However, landraces from other parts of the world were also acquired, mostly through donations from other centers rather than collection. There were two main reasons for this strategy: i) indigenous germplasm, i.e., the barley wild progenitor, *Hordeum vulgare* ssp. *spontaneum,* and cultivated barley landraces are subjected to genetic erosion in WANA,

and ii) they are a valuable source of genes for adaptation to stress tolerance in breeding barley for low-input and less-favorable environments in semi-arid regions of developing countries. With the total number of 24,500 accs., ICARDA holds the third largest barley collection in the world. More than a half of this total (14,489 accs.) were received from the United States Department of Agriculture (USDA)'s Small Grain Collection located then at Beltsville, Maryland. 2,049 were obtained from the Germplasm Resources Institute, CAAS, Beijing, China, and 1068 from the Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany. Twenty other institutions also contributed to GRU-ICARDA's collection with smaller donations. The Cereal Improvement Program (now merged part of the Germplasm Program) provided 2,336 accs., mostly breeding lines and named cultivars.

GRU-ICARDA, in collaboration with NARS collected accs. to fill gaps in the collection These are listed in Table 41. Other major gaps were filled through germplasm acquisition from IBPGR/IPGRI-supported missions to Bhutan, Libya, Morocco, Oman, Saudi Arabia and Yemen (399 accs.), and by donations from national programs of Tunisia (490 accs.), Nepal (317 accs.), Morocco (258 accs.), Syria (209 accs.), Iraq (108 accs.) and Iran (100 accs.).

Cultivated barley germplasm held at ICARDA was characterized and evaluated for a number of descriptors. The characterization and preliminary evaluation data, for more than 12,000 accs., were published in two catalogs (in 1986 and 1988). The third catalog with data on about 9500 accs. was published in 1998.

Summary data for 16 characters are shown in Table 42. The major part of the ICARDA genebank holdings is spring barley (11,270 accs.), followed by facultative types (5,607 accs.) and winter barley (4,141 accs.). Six-rowed barley with 14,545 (70 %) accs. is morefrequent than two-rowed barley (6,312 accs., i.e. 30%, including the types with rudimentary sterile florets). Barley with covered (hulled) kernels prevails (17,978 accs.); naked barley is less frequent (2,274 accs.).

Table 42. Frequency distribution of categories in 16 characters of barley germplasm collection

Category Code	No. of accs.	Description
GCL	4141	winter
	5607	facultative
	11270	spring
RNO	14545	six-row
	6312	two-row
KCV	2274	naked (hulless)
	17978	covered (hulled)
ARG	1180	smooth
	19468	rough
SDE	2074	lax (rachis internode >4 mm)
	16964	intermediate
	1918	dense
GHA	2548	erect
	11235	intermediate
	5333	prostrate
H_A	168	sessile hoods
	213	elevated hoods
	129	awnless or awnleted (<2 cm)
	20366	awned, on all six rows
	147	awned on central rows for six rows
LCO	14343	white/brown
	3257	purple or black
	1931	other
ACO	4390	white
	8371	yellow
	2904	brown
	738	reddish/brown
	465	black
GCO	3531	white
	6175	yellow

Table 42 (Cont'd).

Category Code	No. of accs.	Description
	1165	brown
	1061	black
	794	other
KCO	1491	white
	3149	blue
	1030	black
	6949	other
RHL	7181	short
	5731	long
SCO	607	green
	187	purple
	12156	other
FRD	675	1 total damage (1-9 scale)
	399	3 very poor
	1292	5 fair
	3070	7 good
	173	9 no damage
LOD	1920	1 excellent (1-9 scale)
	11454	3 good
	2125	5 fair
	1775	7 poor
	1151	9 very poor
PM	14	1 resistant (1-9 scale)
	1862	3 moderate resistant
	2030	5 moderate
	1003	7 moderate susceptible
	174	9 very susceptible

Key: GCL=Growth class; RNO=Kernel row no.; KCV=Kernel cover; ARG=Awn roughness; SDE=Spike density; GHA=Growth habit; H_A=Hoodedness/Awnedness; LCO= Lemna color; ACO= Awn color; GCO=Glume color; KCO=Grain color; RHL=Rachilla hair length; SCO=Stem color; FRD=Frost damage; LOD=Lodging resistance; and PM=Powdery mildew incidence.

The characterization data were used for estimating phenotypic diversity for individual characters in 21 countries well-represented in the collection. The relative Shannon-Weaver information index (H_{SR}) standardized, according to Adrivon and de Vallavieille-Pope (1995), was used for the measurement and comparison of phenotypic diversity. The overall country diversity H_{SR} was calculated as the arithmetic mean of the character H_{SR} values. World collection diversity was estimated from pooling over countries. The diversity estimates by character and country and the mean country diversity are shown in Table 43. The highest diversity in the world estimates was for rachilla hair (1.00), growth class (0.92) and growth habit (0.87), while the lowest diversity was in hoodedness/awnedness (0.17) and stem color (0.26). The mean diversity in the collection (0.65) was higher than in any individual country and in the USDA barley collection (0.57) when calculated by the same method from the data provided by Tolbert *et al.* (1979).

The diversity estimates obtained from ICARDA's characterization data were substantially higher than those from the USDA barley collection for all developing countries, except Pakistan. For example, Turkey (0.57 vs 0.43), Syria (0.56 vs 0.43), Ethiopia (0.55 vs 0.48), Iran (0.55 vs 0.46), Afghanistan (0.55 vs 0.46), China (0.55 vs 0.36), India (0.53 vs 0.43), Morocco (0.50 vs 0.28), Jordan (0.45 vs 0.31) and Tunisia (0.34 vs 0.13). ICARDA's data indicate that barley germplasm from countries of the primary and secondary centers of diversity such as Turkey, Syria, Iran, Afghanistan, Ethiopia, China, India and Morocco possesses high phenotypic diversity, as those from developed countries which utilized exotic germplasm extensively in their breeding programs (i.e., USA, Japan, Russia and Germany). The above results indicate that ICARDA's systematic focus on the germplasm collection and acquisition in the WANA region and other developing countries resulted in high genetic diversity being conserved *ex situ* for all users.

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Table 43. Estimates of H_{SR} for 21 countries and 12 characters and mean diversity H_{SR} over all characters in barley

Origin	$N^1_{(MAX)}$	ACO[2]	ARG	GCL	GCO	GHA	H/A	KCO	KCV	LCO	RHL	RNO	SCO	Mean
U.S.A.	2168	0.66 0.73	0.93	0.71	0.88		0.30	0.83	0.23	0.17	0.92	0.50	0.06	**0.58**
Turkey	1373	0.67 0.47	0.99	0.63	0.92		0.02	0.74	0.03	0.64	1.00	0.63	0.07	**0.57**
Syria	285	0.70 0.99	0.41	0.70	0.59		0.01	0.87	0.06	0.58	0.56	0.38	0.89	**0.56**
Ethiopia	2640	0.92 0.05	0.48	0.88	0.80		0.00	0.84	0.29	0.56	0.84	0.85	0.10	**0.55**
Iran	425	0.57 0.29	0.83	0.61	0.93		0.00	0.79	0.26	0.97	0.77	0.62	0.00	**0.55**
Afgh'tan	279	0.65 0.23	0.84	0.61	0.96		0.03	0.66	0.43	0.71	0.97	0.42	0.03	**0.55**
China	2892	0.35 0.10	0.72	0.67	0.68		0.14	0.64	0.94	0.86	1.00	0.35	0.11	**0.55**
Japan	258	0.71 0.04	0.98	0.71	0.95		0.11	0.70	0.87	0.47	0.71	0.38	0.00	**0.55**
Russia	277	0.77 0.21	0.88	0.69	0.80		0.06	0.81	0.14	0.43	1.00	0.54	0.04	**0.53**
India	424	0.60 0.13	0.59	0.68	0.95		0.14	0.68	0.73	0.66	0.85	0.21	0.09	**0.53**
Germany	486	0.66 0.30	0.87	0.57	0.65		0.04	0.63	0.21	0.55	0.95	0.62	0.16	**0.52**
Morocco	643	0.69 0.10	0.58	0.54	0.63		0.30	0.53	0.13	0.33	0.94	0.53	0.75	**0.50**
France	70	0.69 0.26	0.94	0.55	0.86		0.00	0.62	0.19	0.00	0.97	0.62	0.07	**0.48**
Y'slavia	423	0.68 0.15	0.81	0.63	0.83		0.00	0.69	0.02	0.60	0.79	0.50	0.04	**0.48**
Hungary	62	0.60 0.12	0.97	0.55	0.66		0.00	0.68	0.00	0.61	0.97	0.59	0.00	**0.48**
Jordan	128	0.59 0.20	0.29	0.76	0.42		0.00	0.65	0.00	0.62	0.84	0.53	0.52	**0.45**
Spain	229	0.38 0.28	0.84	0.51	0.53		0.00	0.76	0.00	0.49	0.84	0.41	0.00	**0.42**
Greece	339	0.50 0.11	0.89	0.42	0.80		0.00	0.53	0.05	0.81	0.55	0.26	0.03	**0.41**
Pakistan	238	0.40 0.00	0.56	0.18	0.83		0.00	0.37	0.91	0.16	0.70	0.04	0.58	**0.40**
Switz'nd	669	0.67 0.04	0.62	0.42	0.69		0.03	0.36	0.25	0.02	0.96	0.37	0.04	**0.37**
Tunisia	591	0.39 0.10	0.69	0.39	0.45		0.00	0.32	0.00	0.44	0.50	0.12	0.65	**0.34**
World	**18995**	**0.77 0.30**	**0.92**	**0.81**	**0.87**		**0.17**	**0.82**	**0.49**	**0.73**	**1.00**	**0.65**	**0.26**	**0.65**

1 - maximum number of accs. evaluated

2 - for character codes see Table 42

1.4.6. *In situ* conservation of wild *Triticum* spp.

In situ conservation is the preservation of threatened populations of plants in their natural habitats. This is usually achieved through control of the disturbance factors. In 1994, experiments with self-regenerating populations of wheat wild progenitors were established at Yahmoul ARC Research Station in Aleppo Province, northern Syria, and in 1995, at two other research stations in the south of the country in cooperation with the Agricultural Research Center (ARC) Douma. The main objectives of these experiments were: i) to explore the possibility of restoring lost natural populations of wheat wild progenitors using seed from accs. which were collected from the natural populations and conserved *ex situ* in the gene bank; ii) to establish self-regenerating local populations of wild *Triticum* spp. and their mixtures with other cereal wild relatives and wild legume species. The aim is to study population dynamics under conditions similar to *in situ* conservation; iii) to have reference populations for *in situ* management studies to develop appropriate *in situ* conservation methodology for cereal wild relatives; and iv) to restore semi-natural plant eco-systems similar to those which had existed in the region before the land was cultivated. The experiments, at each station, consist of 16 plots of 100 m^2 (10 x 10 m). Population dynamics is monitored in five 1 m^2 quadrates in each plot. There are eight treatments, which include genotype and species mixtures of different complexity, with two replications. The initial planting density was 30-50 spikelets/m^2 in single-species treatments.

Results of the Yahmoul station experiments show that during the first three years (three vegetation seasons) the wild *Triticum* spp. competed very successfully with the autochthonous vegetation (mostly field weedy species). Therefore, the number of plants per m^2 increased in diploid species, *T. baeoticum* and *T. urartu* from approximately 25 in the first season to 150 in the third one, and to 70 in tetraploid *T. dicoccoides*. This plant density and plant height of the target species is similar to that in natural populations. Consequently, a plot of 100m^2 can be sufficient to conserve populations of 6,000 to 15,000 individuals.

J. Valkoun, B. Humeid (GRU-ICARDA) and Kh. Obari (ARC, Douma, Syria)

1.4.7. Effect of *Pyrenophora graminea* on barley yield and its components in Northern Syria.

The object of the study was to assess the effect of infection of *P. graminea* on barley yield and its components for the two barley cultivars, Roumi and Faiz. Seeds with five different infection levels were planted with three seed-rates (100, 150 and 200 kg/ha) in randomized complete block design (RCBD, with three replicates). Percentage of infection, yield (kg/ha), 1000-kernel weight (g) and yield components for healthy and infected plant were recorded. ANOVA showed significant differences between healthy and infected plants in terms of number of tillers/plant, spikes/plant, seeds/spike and seed weight/spike. Significant interaction was also recorded between seeding rate and yield. The level of seed infection has significantly affected the 1000-kernel weight, where the highest infection level gives the lowest weight. ANOVA revealed that *P. graminea* can reduce significantly the yield of barley grown in northern Syria. There the average percentage of yield loss for the two varieties was 11, 24, 34 and 48%, when the average percentage of infection was 15, 19, 22 and 32, respectively. However, 24.54% of losses could be attributed to reduction in 1000-kernel weight, 41.36% to seed number/spike, and 34.10% to number of spikes/plant.

A. El-Ahmed and S. Asaad.

1.4.8. Production of antiserum to *Pseudomonas syringae* pv. *pisi*.

During the 1996-97 season, the seed health laboratory, in cooperation with the Virology laboratory (GP), produced a polyclonal antiserum for virulent Syrian isolates of *Pseudomonas syringae* pv. *pisi*, the casual agent of bacterial blight of pea. The antiserum, prepared by the SHL is made available to the seed health laboratories of the national programs in WANA countries for their own use.

A. El-Ahmed (GRU-ICARDA), Kh. Makkouk (GP-ICARDA), A. Hamouieh (University of Aleppo) and S. Asaad (GRU-ICARDA)

1.4.9. Screening for pea blight (*Pseudomonas syringae* pv. *pisi*) resistance.

In 1997, two hundred and one accs. of pea, collected from 17 countries and preserved in ICARDA's gene bank, were screened under

artificial inoculation for resistance to a mixture of four virulent Syrian isolates of *Pseudomonas syringae* pv. *pisi*. Twenty accs. of *Pisum sativum* and nine of *P. fulvum* were found to be resistant. These small-leaf-type accs. were collected from Syria (20), southern Turkey (7) and Jordan (2).

A. El-Ahmed (GRU-ICARDA), A. Hamouieh (University of Aleppo), S. Asaad (GRU-ICARDA).

1.4.10. Enhancing wheat productivity in stress environments utilizing wild progenitors and primitive forms

The special project, between ICARDA and the University of Tuscia, Viterbo, Italy on "Enhancing wheat productivity in stress environments utilizing wild progenitors and primitive forms" continued its research work on the use of wild wheat relatives and progenitors for durum wheat improvement. This research is being conducted since 1995 by Elena Iacono, under the overall supervision of professor Enrico Porceddu. During 1995-96 the following activities were undertaken on experimental materials consisting of germplasm accs. of cultivated wheat and *Triticum urartu*:

1. Germination and growing of wheat plants;
2. DNA extraction and purification;
3. DNA digestion by restriction enzymes, electrophoretic separation of the fragments on agarose gels and southern blotting on nylon membranes;
4. non-radioactive labelling of RFLP probes by digoxigenin through PCR amplification;
5. Southern hybridization and detection of the signal using digoxigenin labelled probes.

The following plant material was analyzed using the above-named advanced techniques.

Evaluation of durum wheat germplasm from Ethiopia

Ethiopia is considered to be a center of diversity of tetraploid wheats and has been sampled for wheat genetic resources since the early 1970s by Porceddu and others. Durum wheat (*Triticum durum*) accs. from three environmentally diverse Ethiopian regions were analyzed by means of RFLP markers. Three populations were sampled for each of the regions in order to assess the level and distribution of genetic

variation within and between the three regions. For each of these nine populations 20-30 genotypes of durum wheat were analyzed and a total of 241 genotypes were screened.

The digested DNAs were hybridized with 14 RFLP probes, each of them located on a different chromosome arm, in order to probe the whole genome. Eleven of the probes used had been previously cloned and located on the chromosome arms at the University of Tuscia, Viterbo, Italy. The statistical analysis of the data gathered by these experiments is in progress. During 1996-977 the hybridization was completed and the data entered in the database for statistical analysis.

RFLP analysis of accs. of *Triticum urartu* from Jordan and Syria

Fourteen probes located on different chromosomes are being used for assessing the genetic variation in germplasm collections of *T. urartu* supplied by GRU. These accs. originate in Jordan and Syria. A number of genotypes ranging between 20 and 30 have been sampled for each of 10 populations from Jordan and Syria in order to evaluate the genetic variation within and between populations. Most of the 177 genotypes analyzed through RFLP have already been screened in the field, and the data is being analyzed using statistically.

RFLP analysis of the parental genotypes of three crosses of tetraploid wheat

Segregant populations from three intra- and interspecific crosses were made at ICARDA, viz., a) Cham 1 x *T. dicoccum*, b) Cham 1 x *T. dicoccoides* and c) Cham 1 x Jennah Khetifa. These populations were used for comparison of genetic maps obtained using different mapping populations. The first step was to screen the available markers by southern hybridization with the parental genotypes for identifying those showing genetic polymorphism, which will be used for genetic analysis. The DNA of the four parentals has been digested with five restriction enzymes (Hindili, EcoRi, BamHi, EcoRV and Psti) and hybridized with 57 RFLP probes. The following number of polymorphic probes were identified between the parentals of the crosses:

a) Cham 1 x *T. dicoccum*	40	probes
b) Cham 1 x *T. dicoccoides*	46	probes
c) Cham 1 x J. Khetifa	34	probes

Four probes did not detect any polymorphism among the parentals of the crosses. During 1996-97, the following number of polymorphic probes were identified between the parentals of the crosses:

a) Cham 1 x *T. dicoccum*	62	probes
b) Cham 1 x *T. dicoccoides*	49	probes
c) Cham 1 x J. Khetifa	48	probes

Recombinant inbred lines (RIL) from the cross Cham 1 x Jennah Khetifa

Recombinant inbred lines from the cross Cham 1 x J. Khetifa were received from ICARDA. The 113 available RILs were grown at Viterbo and the extraction of the DNA which will be digested is now in progress. The fragments were separated by electrophoresis on agarose gel and will be hybridized with digoxigennin labelled RFLP probes. These probes were previously chosen on the basis of their ability to detect genetic polymorphism between the parental genotypes of the cross.

The segregation data will be used to construct a genetic map. During 1997, about 100 hybridizations were carried out. As soon as the four hybridizations for each probe were completed (all the RILs have been hybridized with digoxigennin labelled RFLP probe) the data was entered in a database.

When completed, the results from the above-listed experiments will be submitted to refereed journals to be published.

E. Porceddu and E. Iacono (University of Tuscia, Viterbo, Italy), M. Nachit (GP-ICARDA) and J. Valkoun (GRU-ICARDA)

1.4.11. Contrasting genetic variation amongst lentil landraces from different geographical origins

The domestication of lentil was associated with the Neolithic agricultural revolution which is thought to have taken place in the Eastern Mediterranean around 7000 BC. Lentil cultivation spread rapidly to the Nile Valley, Europe and Central Asia. It was part of the Harappan crop assemblage in Pakistan and northwest India between 2250 and 1750 BC. After 1500 AD, the Spanish introduced lentil to South America via Chile. More recently it was introduced to Mexico,

Canada, the USA and Australia. Today, almost half of the world's area (48.2%) of lentil is grown in South Asia.

Lentil landraces from South Asia exhibit a low diversity and discordance with landraces from other regions, according to a combination of qualitative morphological characters. For example, short or rudimentary tendrils and marked pubescence, and for quantitative agro-morphological characters, such as, early maturity and low biological yield. This low diversity and discordance indicates a possible bottleneck (a temporary reduction in population size) when lentils were first introduced into South Asia *ca.* 2000 BC.

The specific adaptation of this germplasm (resulting in early flowering and maturity), precludes the direct use of alien germplasm in breeding programs in South Asia. This has limited the progress of plant breeding efforts in the region. An understanding of the genetic relationships and diversity of South Asian lentil landraces, in relation to landraces from other countries, is important in attempting to widen the genetic base of germplasm in the region.

Barulina studied the morphological variation in lentil landraces throughout their geographic range, and broadly classified them into *macrosperma* and *microsperma* types, according to seed size and an array of associated characters generally insensitive to the environment. *Microsperma* types are characteristic of the Indian subcontinent, parts of the Near East, and the lower latitudes of the Old World, including Ethiopia and Yemen. More recently, however, seed size and other morphological characters have been found to form a continuum between *macrosperma* and *microsperma* types. As results of random amplified polymorphic DNA (RAPD) analysis showed, the division was purely arbitrary.

Barulina further classified *microsperma* types into six regional groups or grex, according to geographical origin and morphological characters. Landraces from South Asia belonged exclusively to the grex *pilosae*. Later, Erskine *et al.*, on the basis of quantitative morphological characters, classified the germplasm into three groups which largely supported those of Barulina. Besides, they found similarities between accs. from India and Ethiopia, and grouped them together.

Although the distinctness of South Asian germplasm is evident at

the morphological and phenological levels, it has not been studied in the genome as a whole. Rates and modes of evolutionary divergence may differ greatly between different regions of the genome. For example, they differ between coding and non-coding regions, because of the differential operation of natural or artificial selection. It is thus important to make inferences about population genetic structure, from information derived from different regions of the genome.

The objectives of this study were: (i) to investigate the genetic relationships between lentil landraces from three South Asian countries and those from 13 other countries, and (ii) to estimate their relative genetic diversities, at both, the protein level using isozyme electrophoresis, and at the DNA level using random amplified polymorphic DNA (RAPD).

Ten lentil landrace accs. from each of India (IND), Pakistan (PAK) and Nepal (NPL) were used to represent South Asian germplasm. Ten accs. each from 13 other countries were included for comparison. These were, Afghanistan (AFG), Bulgaria (BGR), Chile (CHL), Egypt (EGY), Ethiopia (ETH), Iran (IRN), Jordan (JOR), Lebanon (LBN), Morocco (MAR), Spain (ESP), Syria (SYR), Turkey (TUR), and Yemen (YEM). This germplasm was acquired from the ICARDA genebank.

Lentil accs. within each country were selected from passport data to represent broad ecological and geographical distributions. A single plant was analyzed per acc. The number of *microsperma* types per country, defined as a 100-seed weight of less than 4.5g, is given in Table 44. The lentil cultivar ILL 5582 was used as a control in all isozyme analyses in order to facilitate the comparison of banding patterns between gels.

Starch gel electrophoresis was used to resolve isozymes from 11 enzyme systems: aspartate aminotransferase (Aat), phosphoglucose isomerase (Pgi), malic enzyme (Me), shikimic acid dehydrogenase (Skdh), acid phosphatase (Aps), leucine aminopeptidase (Lap) and glucose 6-phosphate dehydrogenase (Pgd), peroxidase (Prx), diaphorase (Dia), aldolase (Aldo), and isocitrate dehydrogenase (Idh).

Twenty primers, comprising the Operon F kit (Operon Technologies Inc., Alameda, California), were screened on a small number of lentil accs. to identify those revealing repeatable polymorphic amplification

products. Three primers, OPF1, 4 and 14 and also OPS14, which was recommended for lentil, were selected to screen all accs. in the study. Each sample/primer combination was repeated and only those amplification products which were unambiguous and repeatable were scored as present (1) or absent (0). No account of band intensity was taken.

Phenetic relationships were calculated according to Nei's genetic distance using NTSYS-pc. Cluster analysis was performed by UPGMA using NTSYS-pc. To estimate the congruence between isozyme and RAPD data sets, the correlation between the distance matrices was calculated with the nonparametric permutation test of Mantel using NTSYS-pc.

An arbitrary genetic distance of 0.1 to define groups of similar countries was used, from the phenograms. Canonical discriminant analysis of SPSS was used to reveal a 2-dimensional view of the relationships between countries by representing the multivariate data on orthogonal axes such that maximum discrimination was obtained between groups, when tested against variation within groups. Characters for inclusion were selected, stepwise, to minimize Wilk's lambda between groups.

Shannon's Information Index (H_s) was used for the analysis of isozyme and RAPD data. It was used to calculate genetic diversity in each country for both data sets, based on allozyme frequencies and RAPD product frequencies. Concordance between the diversity indices for RAPD and isozyme data was tested by the Kendall (tau) coefficient of rank correlation using SPSS. In addition, the isozyme data were described by the percentage of polymorphic loci and the mean number of allozymes per locus for each country.

The 12 enzyme-staining systems revealed 18 scorable loci. Seven loci, Lap-1, Aat-p, Me-1, Me-2, Pgd-p, Skdh-1 and Prx-2, were polymorphic. The monomorphic loci were Pgi-1, Pgi-2, Aat-c, Pgd-2, Aps-1, Aldo, Amy, Dia-1, Dia-2, Dia-3, and Idh-1. Only 1.25% of plants were found to be heterozygous at one or more isozyme loci. One acc. from BGR and another from NPL were heterozygous at Aat-p and Pgd-p, respectively. The four primers used in RAPD analysis,

Table 44. Percentage of accs. of *microsperma* type from 10 accs. per country used in this study

Country	% of *microsperma* accs.	Country	% of *microsperma* accs.
AFG	100	JOR	70
BGR	90	LBN	40
CHL	10	MAR	70
EGY	90	NPL	100
ESP	30	PAK	100
ETH	100	SYR	60
IND	90	TUR	10
IRN	70	YEM	100

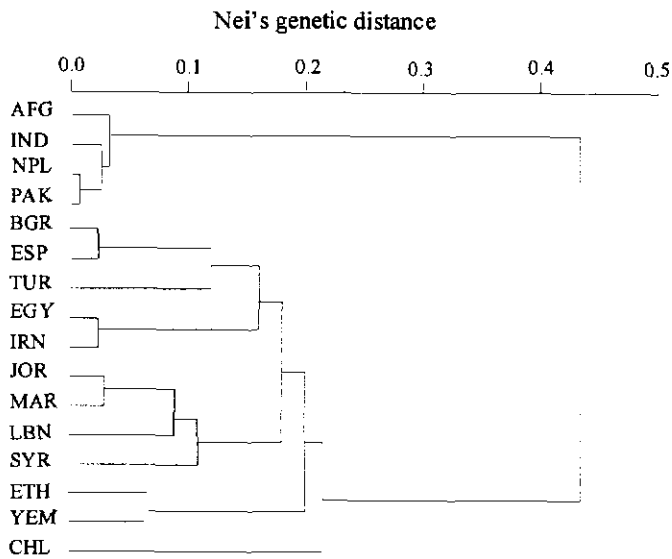

Fig. 36. Dendrogram of relationship of lentil landraces from 16 countries based on RAPD variation

Table 45. Mean genetic distance (Nei 1972) between countries based on isozyme (above diagonal) and RAPD (below diagonal) analysis.

	Isozyme data															
RAPD	AFG	BGR	CHL	EGY	ESP	ETH	IND	IRN	JOR	LBN	MAR	NPL	PAK	SYR	TUR	YEM
AFG	-	0.522	0.429	0.112	0.766	0.356	0.046	0.210	0.338	0.401	0.666	0.022	0.007	0.405	0.339	0.654
BGR	0.506	-	0.056	0.213	0.049	0.141	0.278	0.109	0.053	0.029	0.082	0.416	0.555	0.037	0.211	0.210
CHL	0.624	0.170	-	0.208	0.136	0.123	0.268	0.140	0.130	0.111	0.178	0.373	0.490	0.066	0.256	0.172
EGY	0.284	0.168	0.269	-	0.311	0.114	0.099	0.045	0.169	0.172	0.242	0.139	0.139	0.141	0.058	0.327
ESP	0.448	0.021	0.157	0.138	-	0.279	0.476	0.191	0.158	0.111	0.054	0.658	0.812	0.141	0.225	0.246
ETH	0.634	0.310	0.212	0.236	0.271	-	0.266	0.126	0.189	0.167	0.275	0.357	0.418	0.067	0.127	0.338
IND	0.031	0.313	0.459	0.158	0.276	0.478	-	0.117	0.134	0.178	0.423	0.012	0.039	0.222	0.304	0.459
IRN	0.273	0.175	0.227	0.022	0.138	0.227	0.155	-	0.063	0.065	0.102	0.199	0.235	0.056	0.107	0.151
JOR	0.482	0.135	0.163	0.224	0093	0.189	0.325	0.252	-	0.005	0.125	0.236	0.335	0.051	0.249	0.214
LBN	0.430	0.199	0.327	0.184	0.125	0.245	0.306	0.223	0.068	-	0.092	0.296	0.404	0.038	0.212	0.204
MAR	0.541	0.085	0.148	0.222	0.065	0.155	0.377	0.238	0.028	0.082	-	0.610	0.712	0.111	0.185	0.113
NPL	0.027	0.451	0.652	0.269	0.418	0.741	0.028	0.263	0.525	0.478	0.584	-	0.012	0.347	0.387	0.634
PAK	0.034	0.425	0.627	0.246	0.393	0.712	0.028	0.250	0.492	0.443	0.553	0.003	-	0.449	0.383	0.724
SYR	0.366	0.197	0.165	0.119	0.107	0.229	0.250	0.132	0.092	0.093	0.122	0.419	0.400	-	0.174	0.161
TUR	0.449	0.122	0.249	0.112	0.106	0.233	0.243	0.129	0.192	0.212	0.188	0.384	0.354	0.171	-	0.371
YEM	0.558	0.232	0.220	0.205	0.176	0.060	0.392	0.192	0.139	0.177	0.123	0.629	0.590	0.180	0.134	-

revealed a total of 22 polymorphic repeatable bands which could be scored unambiguously. Primer OPF4 was used to detect 9 of these bands; OPS14 revealed a single polymorphic band.

The mean genetic distances between countries, based on isozyme and RAPD analyses, are given in Table 45. The associated dendrogram is given in Fig. 36. The Mantel statistic (Z) is monotonically related to the ordinary product-moment correlation coefficient, r, which gave a matrix correlation between isozyme and RAPD distance matrices of r = 0.94581.

Two major groups of germplasm were evident from both the isozyme and RAPD analysis. One group consisted of closely related germplasm from South Asia (PAK, IND, NPL) and AFG. These were strikingly different from the germplasm from all other countries. Both analyses also showed the close relationship of EGY and IRN, and SYR, JOR and LBN (this group included BGR as a result of isozyme analysis and MAR as a result of RAPD analysis). CHL germplasm was isolated according to RAPD data, but showed some affinity towards SYR/JOR/LBN/BGR germplasm from isozyme data. The CHL germplasm was most closely related to that of ESP (0.157) and MAR (0.148), as a result of RAPD analysis.

Two major disparities occurred from the results obtained from RAPD and isozyme analysis. With RAPDs, ETH and YEM appeared closely related (0.06) (Fig. 36), whereas with isozymes they were fairly distantly related (0.338). ESP and MAR were closely related according to isozyme data, but relatively distantly related according to RAPDs. ESP had a close affinity with BGR (0.021), and MAR had a similar affinity with JOR (0.028).

An arbitrary genetic distance of 0.1 was used to divide countries into 6 groups, on the basis of isozyme data, and 7 groups, on the basis of RAPD data. Countries and group centroids derived from canonical discriminant analysis for isozymes and RAPD are shown in Fig. 37 and Fig. 38, respectively. The first two canonical variates accounted for 89 % of the variation in isozyme data and 99 % of the variation in RAPD data. The isozyme study showed Group 1, consisting of the South Asian countries and AFG and group 4, consisting of EGY, IRN and TUR as being fairly closely related.

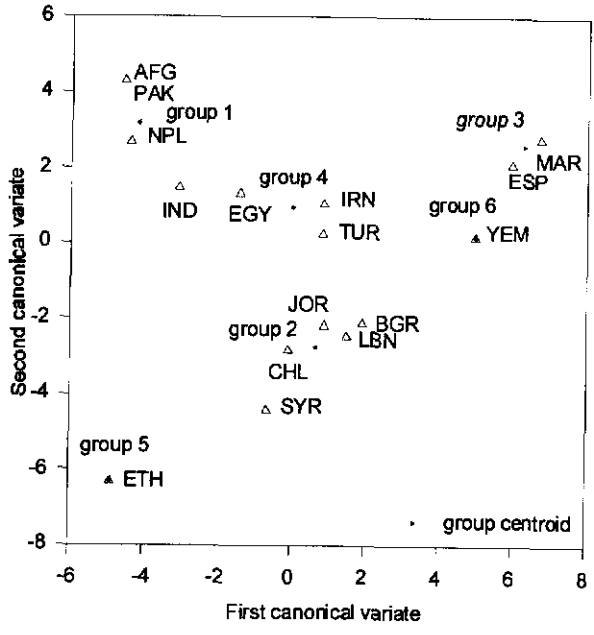

Fig. 37. First two canonical variate mean values for country means and group centroids (Nei's genetic distance of isozyme data)

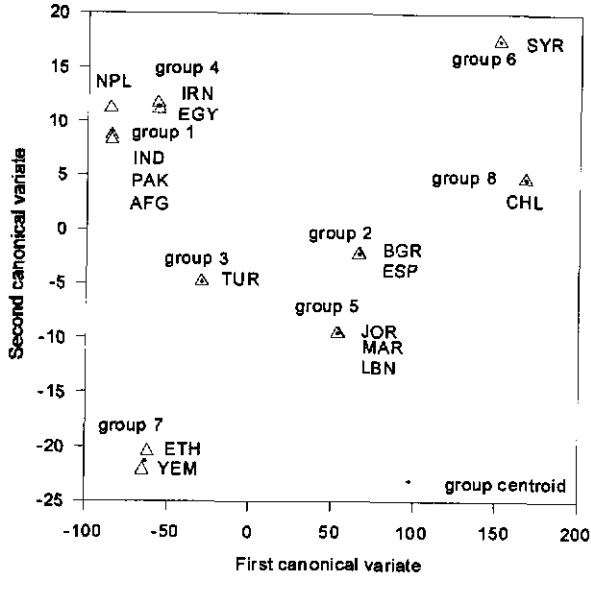

Fig. 38. First two canonical variate of mean values and group centroids (Nei's genetic distance based on RAPD)

Table 46. Genetic diversity parameters (Shannon's Information Index, mean number of allozymes per polymorphic locus and % polymorphic loci) for isozyme and RAPD data

Country *of origin*	Shannon's Information Index based on *isozyme data*		Shannon's Information Index based on RAPD data		Mean no. allozymes per polymorphic locus		% polymorphic isozyme loci (over 18 loci)	
	Value	Rank	Value	Rank	Value	Rank	Value	Rank
AFG	1.33	12	1.59	15	1.429	9-13	16.7	9-12
BGR	1.85	9	4.59	7	1.429	9-13	16.7	9-12
CHL	2.85	2	5.53	4	2.000	1	33.3	1
EGY	2.84	3	4.48	9	1.714	2-4	27.8	2-4
ESP	2.19	5	5.18	6	1.571	5-8	22.2	5-8
ETH	1.03	14	4.34	10	1.286	14	5.6	14-16
IND	2.11	7	5.31	5	1.571	5-8	22.2	5-8
IRN	2.98	1	4.53	8	1.714	2-4	27.8	2-4
JOR	2.26	4	8.48	1	1.714	2-4	27.8	2-4
LBN	2.17	6	2.55	12	1.571	5-8	22.2	5-8
MAR	1.84	10	6.21	3	1.571	5-8	22.2	5-8
NPL	1.21	13	1.63	14	1.429	9-13	16.7	9-13
PAK	0.50	16	1.15	16	1.143	15,16	5.6	14-16
SYR	1.61	11	6.79	2	1.429	9-13	16.7	9-13
TUR	1.89	8	3.46	13	1.429	9-13	16.7	9-13
YEM	0.67	15	3.93	11	1.143	15,16	5.6	14-16

This is accentuated in the results of the RAPD analysis, although TUR appears in a group of its own.

Shannon's Information Index, per country for isozyme and RAPD data, are shown in Table 46. The lowest diversity for isozymes was found in PAK, followed by YEM and ETH, and for RAPD in the South Asian countries of PAK, AFG and NPL. The greatest diversity was found in IRN, followed by CHL and EGY, from isozyme data, and in JOR, followed by SYR and MAR, from RAPD data. Kendall's (tau) gave a correlation coefficient between the diversity measures based on isozyme and RAPD data of 0.333, ($P = 0.072$). CHL had the highest mean number of allozymes per locus, and the highest percentage of polymorphic loci, while PAK and YEM had the lowest mean number of allozymes per locus, and ETH, YEM and PAK had the lowest percentage of polymorphic loci.

Both isozyme and RAPD data reveal the close relationship of lentil landraces from South Asian countries (IND, PAK and NPL) with those of AFG, and the striking difference of this germplasm to lentil landraces from all other countries. This South Asian group coincides, to a large extent, with Barulina's grex *pilosae*. Although, according to her study of morphological characters, AFG appears to have different forms (grex *asiaticae* and *intermediae*, more common in the Middle East region) and was actually suggested by her as a center of origin. Germplasm from PAK was of the *pilosae* group for qualitative characters but intermediate between Afghan and Indian material for quantitative characters. The close relationship between South Asian germplasm and that from AFG supports the argument that lentils were introduced to IND via Central Asia and AFG from a Near East origin. This is contrary to the theory that lentils were introduced via Ethiopia as implied by quantitative morphological similarities.

The remaining germplasm from outside the South Asian group can be divided into four secondary groups. Although discrepancies between RAPDs and isozymes, the overall relative similarity of the germplasm and the relatively small sample size, make these groups less definitive.

1. An Aethiopica group, according to RAPD analysis, is that of ETH and YEM. This agrees with Barulina's grex *aethiopica* which she found exclusively in these countries. Discrepancy in the relationship

between ETH and YEM, revealed by RAPD and isozyme data, particularly evident from the discriminant analysis, may in part be due to the small number of isozyme variants studied which tends to amplify the effect of possible unusual occurrences, such as the fact that Me-2b was found only in YEM and CHL germplasm at a frequency of 0.6 and 0.4, respectively. Alternatively, the discrepancy may reflect selection acting on isozyme loci. Although the germplasm from both YEM and ETH was of the *microsperma* type, the 1000-seed weights, a trait affected by human preference and of low adaptive value (Bejiga *et al.* 1995), were significantly different with means of 31.8g and 27.2g respectively.

2. A Levantine group, which coincides with that of Erskine *et al.* (1989) and consists of SYR, JOR and LBN. EGY is included in this group by Erskine *et al.* (1989), but excluded by the present study. RAPD analysis also shows MAR as being included, but not in the case of isozyme analysis.

3. A European group, according to RAPD data, consists of BGR and ESP. Isozyme results, however, reveal a similarity between MAR and ESP germplasm. Barulina (1930) found similarities between ESP and MAR germplasm. *Macrosperma* types, plus grex *europeae* and *asiaticae* were found in both countries. This discrepancy may reflect the adaptive nature of isozymes.

4. A group which consists of IRN and EGY. According to isozyme data, TUR also belongs to this group. However, in the case of RAPD, it takes an intermediary position between this group and the European one. This group reflects the northern group found by Erskine *et al.* in 1989 as a result of quantitative trait measurements, although they exclude EGY. In addition they found that germplasm from the former USSR and Greece (GRC) were closely related. Both canonical discriminant analyses reveal the relatively close relationship of the South Asia group to EGY, IRN and TUR. Historical evidence suggests that lentils spread to these areas at an early stage of domestication. The Nile delta was probably reached very early on because it was a cultural unity with the Near East. The grex *aethiopicae* exhibits very primitive characters.

The relatively close affinity of CHL germplasm to ESP and MAR according to RAPD data (Table 45) suggests that the germplasm was

introduced to CHL from this region. This agrees with the supposed introduction of lentil to Chile in the post-Columbine period.

Relationships between countries do not coincide with the division into *macrosperma* and *microsperma* types. Although AFG, NPL, and PAK all have 100% *microsperma* types, so do ETH and YEM. In addition, IND has 90% *microsperma* types as BGR and EGY do. These results suggest that variation in seed size has little relation to between-country genetic similarities.

The low diversity in South Asian countries, (PAK and NPL) and AFG, revealed by RAPD analysis suggests a genetic bottleneck in this region. Inbreeding, which tends to promote inherently low levels of DNA variation within populations together with the natural accumulation of multilocus associations and the occurrence of a founder effect when lentil was first introduced to South Asia around 2000 BC, may have contributed to the restricted genetic base of lentil in this region. The genetic diversity in IND, found in both analyses, was surprisingly high. This may reflect the vast area under lentil cultivation.

The Levantine group (JOR and SYR), according to RAPD data, is a center of diversity. This region forms part of the Fertile Crescent, where first lentil is thought to have been domesticated, and where introgression with the wild progenitor of the lentil, *L. culinaris* subsp. *orientalis* (Boiss.) Ponert, is still possible. The comparatively low diversity in LBN may be due to the country's small area. The high diversity in IRN, CHL, and EGY, based on isozyme variation, may reflect a diversity of environment and /or the relatively large area over which lentil is grown. Although gross differences between countries in relative genetic diversity will be clear from this study, the limited sample size restricts the resolution possible in the comparison.

Discrepancies in the results obtained from isozyme and RAPD analysis may be due to several factors. The over-riding factor is likely to be the greater number of polymorphic variants which could be sampled through RAPD analysis (22 loci from RAPD analysis versus 7 loci and 16 alleles from isozyme analysis). This gives greater stability and, thus, statistical reliability to the RAPD results. In addition, it has been suggested that RAPD loci may, in certain instances, be more selectively neutral with respect to natural selection

than isozyme loci. This could lead to discrepancies between results derived from the two techniques. The influence of the dominance of RAPDs as opposed to the co-dominance of isozymes is likely to be minimal in a highly inbreeding species where heterozygotes are few. The effect of the attributes described above may be accentuated in this study by the relatively small sample size, particularly when genetic similarities are large.

This study shows that germplasm from South Asia and AFG is distinctly different from that of all other countries included here. In addition the germplasm exhibits a low genetic diversity, supporting evidence at the morphological level of a genetic bottleneck. The division of germplasm into *macrosperma* and *microsperma* types does not reflect overall country relationships.

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1.4.12. Population genetic structure in *Lens* taxa revealed by isozyme and RAPD analysis

Optimum collection, conservation and utilization strategies of plant genetic resources require an understanding of the genetic structure of populations. In the past, germplasm conservation of crop landraces and their wild relatives has focused primarily on *ex situ* methods, that is, the conservation of components of biological diversity outside their natural habitats. More recently, however, holistic approaches have been adopted involving the use of complementary conservation strategies. In particular the benefits of *in situ* conservation, that is, the conservation of species in their natural habitats, have been recognized. *In situ* conservation allows the evolutionary processes, which create and mould genetic diversity, to continue in relation to changing selection pressures, processes which to a large extent are halted under *ex situ* conditions. In addition, in certain highly diverse populations, it is argued that a greater amount of genetic diversity can be conserved *in situ* as opposed to *ex situ*.

The genus *Lens* comprises the cultivated lentil, *L. culinaris* subsp. *culinaris*, its wild progenitor *L. culinaris* subsp. *orientalis* (Boiss.) Ponert, *L. odemensis* Ladiz., *L. ervoides* (Brign.) Grande, *L. nigricans* (Bieb.) Godr., a recently recognized species *L. lamottei* Czev. and a

newly described taxon *L. tomentosus* Ladiz. All taxa are annual diploids ($2n$=14). An outcrossing rate of less than 1% has been reported in *L. culinaris* subsp. *culinaris* and heterozygosity levels have been found to be low in all taxa. Wild *Lens* are distributed predominantly in the Mediterranean basin and the Middle East, although *L. culinaris* subsp. *orientalis* stretches across into Central Asia and isolated populations of *L. ervoides* have been reported in Ethiopia and Uganda. Populations are generally found in primary undisturbed habitats, although *L. lamottei* and some *L. nigricans* populations are found in secondary habitats or habitats resulting from human intervention. Populations are sporadic in distribution and usually contain small numbers of plants.

The prime determinant of population genetic structure is generally the breeding system. Inbreeding populations tend to exhibit small clusters or patches of related, largely homozygous individuals, often of identical genotype, whereas populations of outbreeders tend to be more heterogeneous, with greater levels of heterozygosity and a larger proportion of diversity within the population. Despite these general trends, variation in population genetic structure has been reported between closely related species and even among different populations of the same species. Besides breeding system, other factors such as evolutionary history, the movement of genes through seed dispersal and natural selection play roles of varying influence.

The objectives of this study are a) to determine the distribution of genetic variation within and between populations in *L. culinaris* subsp. *orientalis*, *L. odemensis*, *L. ervoides*, *L. nigricans* and *L. lamottei* b) to determine whether isozymes and RAPDs indicate similar partitioning of variation within and between populations of each taxon, and c) to provide information relevant to the design of optimal collection and *in situ* conservation strategies.

Collection missions were undertaken in south west Turkey for *L. culinaris* subsp. *orientalis*, *L. odemensis*, *L. ervoides* and *L. nigricans*, Sweida Province, southern Syria for *L. culinaris* subsp. *orientalis* and *L. odemensis* and in Andalucia, Spain for *L. lamottei*. A specific objective of these missions was to collect seed from at least 20 individual plants from populations of each of the wild taxa. Seed was collected from across the distribution area of each population. Table

47 gives relevant passport data of populations.

Twenty plants from each of five populations per taxon (except *L. lamottei* in which fewer plants were used due to small populations) were screened for genetic variation using isozyme electrophoresis and RAPD. Seven isozyme stains were used for all analyses. These were: aspartate aminotransferase (Aat), phosphoglucose isomerase (Pgi), malic enzyme (Me), shikimic acid dehydrogenase (Skdh), acid phosphatase (Aps), leucine aminopeptidase (Lap) and glucose-6-phosphate dehydrogenase (Pgd). RAPD analysis was carried out using three Operon primers (OPF1, OPF4 and OPF14) which had previously been found to reveal high levels of diversity in *Lens*. Each sample/primer combination was repeated once and only those amplification products which were unambiguous and repeatable were scored as present (1) or absent (1).

The multilocus structure of populations revealed by each of the two techniques is described by the number of haplotypes per population and their frequency and a multilocus genotypic diversity index

$$H_j = 1-\Sigma g_i^2$$

in which g_i is the frequency of the *i*th 11-locus genotype in the *j*th population. In addition, an unbiased estimate of Nei's mean gene diversity index over k loci was calculated as follows

$$\overline{H}_e = (1-\Sigma p_{ij}^2) / k,$$

where p is the frequency of the *i*th allele in the *j*th population. The indices of Garcia et al. and Nei are essentially the same, except that of Garcia's index expresses diversity in terms of genotypes as opposed to alleles as in the case of Nei's index.

For comparison of the genetic variation within population of different species, the number of polymorphic loci per population and the mean proportion of polymorphic loci in the average population (L(pop'n)) were calculated. In addition, the mean proportion of loci polymorphic in the species (L(species)) and the mean number of alleles at polymorphic loci (A) (for isozyme data only) were calculated.

The partitioning of variation within and between populations for each taxon was estimated with AMOVA, computed using Arlequin.

The data type was set for "RFLP" in the case of RAPD data and "standard" for isozyme data. For *L. culinaris* subsp. *orientalis* and *L. odemensis*, the partitioning of variation between two regions, southern Syria and south western Turkey, was also assessed using the same methodology. This analysis is based on the conversion of a distance matrix, formulated according to the Euclidean metric of Excoffier et al., into a partition of molecular variation within and among populations. The Euclidean metric is essentially the same as the distance metric of Nei and Li, differing only in the denominator that is used. On the basis of RAPD data, the two measures have been found to be virtually interchangeable. Fixation indices (called ϕ-statistics) which are the molecular equivalent of Weir and Cockerham's F-statistics were also generated. The three calculated AMOVA ϕ-statistics are as follows:

ϕ-ST: the correlation of haplotypes within a population, relative to a random sample from the species as a whole

ϕ-CT: the correlation of haplotypes within a group of populations, relative to a random sample from the species as a whole

ϕ-SC: the correlation of haplotypes within a population, relative to a random sample from a defined group of populations, where

$\phi\text{-}_{ST} = \sigma_a^2 + \sigma_b^2$

where σ_a^2, σ_b^2 and σ_c^2 are the variance components (expected squared deviations) of the effects of groups (*a*), populations (*b*) and individuals within populations (*c*).

The significance of ϕ-statistics was tested using a non-parametric permutation test (1000 replicates).

Variation was scored at eleven isozyme loci, three of which were monomorphic in all populations, namely Pgi-1, Pgi-2 and ACP. No heterozygotes were found. Polymorphism was detected in three populations of *L. culinaris* subsp. *orientalis*, two populations of *L. odemensis* and *L. nigricans*, and a single population of *L. ervoides* and *L. lamottei*. Each was polymorphic at one locus for two alleles except for one population of *L. culinaris* subsp. *orientalis* (ILWL 466) which was polymorphic at four loci, each for two alleles. The number of populations polymorphic at each isozyme locus for each taxon is shown in Table 48. Pgd was the most polymorphic enzyme system, having two populations polymorphic at each of two loci scored.

Table 47. Site locations and the number of plants per population used in the study

Taxon	Accession no. (ILWL)	Longitude	Latitude	Altitude (m)	Site location
L. culinaris	444	E30 39	N37 31	780	Bucak, Burdur, Turkey
subsp. *orientalis*	447	E30 18	N37 47	930	Burdur, Burdur, Turkey
	456	E28 54	N37 39	970	Karahisar, Denizli, Turkey
	466	E36 45	N32 48	1626	Egailat, Sweida, Syria
	469	E36 43	N32 28	1425	Anz, Sweida, Syria
L. odemensis	436	E27 16	N37 53	90	Kusadasi, Aydin, Turkey
	457	E28 08	N38 25	710	Manisa, Turkey
	468	E36 43	N32 31	1200	Arman, Sweida, Syria
	470	E36 35	N32 41	1450	Sweida, Sweida, Syria
	471	E36 35	N32 45	1600	Anz, Sweida, Syria
L. ervoides	439	E29 05	N36 45	60	Inlice, Mugla, Turkey
	440	E29 18	N36 27	125	Kuscukurincir, Mugla, Turkey
	441	E29 41	N36 15	260	Kas, Antalya, Turkey
	451	E29 07	N37 45	660	Denizli, Denizli Province, Turkey
	461	E27 17	N38 30	750	Baspinarlar, Izmir, Turkey
L. nigricans	473	E30 20	N37 45	1080	Burdur, Burdur Province, Turkey
	453	E28 55	N38 00	175	near Buldan, Denizli, Turkey
	454	E29 12	N37 38	1060	Kale, Denizli, Turkey
	459	E28 08	N38 23	1000	near Bozdag, Izmir, Turkey
	474	E28 09	N38 24	980	near Bozdag, Manisa, Turkey
L. lamottei	428	W05 43	N36 48	150	near Villamartin , Cadiz, Spain
	429	W05 25	N36 45	800	El Bosque, Cadiz, Spain
	430	W05 15	N37 07	100	Moron de la Frontera, Sevilla, Spain
	431	W04 15	N37 25	550	Lucena, Cordoba
	432	W04 15	N37 25	660	Lucena, Cordoba

Table 48. No. of populations of *Lens* spp. polymorphic at each isozyme (Pgi-1, PGi-2 and ACP were monomorphic)

Locus	Taxon				
	culinaris ssp. *orientalis*	*odemensis*	*ervoides*	*nigricans*	*lamottei*
Aat-2	1				
Aat-4	1				
Lap				1	
Me-1			1		
Me-2	1				1
Pgd-1	2				
PGd-2		2		1	
Skdh	1				

Of the 27 RAPD bands scored in *L. culinaris* subsp. *orientalis*, 19 were polymorphic (70%), 23 of the 26 bands scored in *L. odemensis* were polymorphic (88%) and 9 of the 20 bands scored in *L. lamottei* (45%) were polymorphic. In *L. ervoides* and *L. nigricans* just 4 of the 14 and 15 bands scored were polymorphic, being 28% and 27% respectively. The results obtained from RAPDs and isozymes are very similar except for two populations of *L. lamottei* (ILWL 429 and 430) which are markedly different. If these two populations are removed, the correlation coefficient of Hj (iso) and Hj (rapd) is 0.79 (P=0.001).

L. culinaris subsp. *orientalis* populations harbored the greatest diversity in terms of: (i) the mean number of loci polymorphic in the average population (0.18 for RAPD and 0.11 for isozymes), (ii) Nei's mean genetic diversity (0.035 for isozyme and 0.049 for RAPD), and (iii) the mean multilocus diversity index (0.2 for isozyme and 0.29 for RAPD) (Table 49). *L. lamottei* followed quite closely for all parameters on the basis of RAPD variation (0.143, 0.038 and 0.32), but ranked last in terms of isozyme variation. The low levels of variation revealed in populations of *L. odemensis* and *L. ervoides* is also reflected in these parameters.

Table 49. Genetic variability parameters in five *Lens* taxa. L (pop'n) = mean proportion of loci polymorphic in the average population; L (species) = mean proportion of loci polymorphic in the species; A = mean number of alleles at the polymorphic loci; H= Mean multilocus diversity index

Taxon	Isozymes					RAPD			
	L (pop'n)	L (species)	A	Nei's mean genetic diversity	H_t	L (pop'n)	L (species)	Nei's mean genetic diversity	H_t
L. culinaris subsp. *orientalis*	0.11	0.54	2.3	0.035	0.2	0.180	0.70	0.049	0.29
L. odemensis	0.04	0.45	2.2	0.008	0.08	0.018	0.88	0.005	0.05
L. ervoides	0.02	0.27	2.3	0.008	0.08	0.029	0.28	0.006	0.05
L. nigricans	0.04	0.45	2	0.011	0.13	0.042	0.27	0.018	0.13
L. lamottei	0.02	0.09	2	0.005	0.06	0.143	0.45	0.038	0.32

Within *L. culinaris* subsp. *orientalis* and *L. lamottei*, considerable variation exists between populations. This is evident from the number of haplotypes and their frequencies derived from isozyme and RAPD data (Table 50). The multilocus genotypic diversity indices vary from 0 to 0.81 and 0.74 in *L. culinaris* subsp. *orientalis* according to RAPDs and isozymes respectively, and from 0 to 0.67 in *L. lamottei* according to RAPDs. This is mirrored by Nei's genetic diversity per population which varies from 0 to 0.148 and0.12 in *L. culinaris* subsp.

Table 50. Population genetic structure. ILWL refers to the accession number, n is the sample size, Hj refers to the multilocus genotype diversity index. The upper figure in the haplotype frequencies is a haplotype identity number, the lower number, in italics, being the frequency.

Taxon	ILWL	n	H_j (iso)	Nei's diversity(iso)	H_j (rapd)	Nei's diversity (rapd)	Isozyme haplotype frequencies	RAPD haplotype frequencies
L. culinaris subsp. *orientalis*	444	20	0.18	0.016	0.34	0.022	1 2 *18 2*	1 2 3 *16 3 1*
	447	20	0	0	0	0	3 *20*	4 *20*
	456	20	0.1	0.009	0.1	0.008	4 5 *19 1*	5 6 *19 1*
	466	20	0.74	0.148	0.81	0.200	6 7 8 9 10 *5 5 1 7 2*	7 8 9 10 11 12 13 14 15 16 *1 1 7 4 2 1 1 1 1 1*
	469	20	0	0	0.18	0.015	9 *20*	17 18 *18 2*
L. odemensis	436	20	0	0	0	0	1 *20*	1 *20*
	457	20	0	0	0	0	1 *20*	2 *20*
	468	20	0	0	0	0	2 *20*	3 *20*
	470	20	0.32	0.029	0.26	0.025	2 3 *16 4*	4 5 *17 3*
	471	20	0.1	0.009	0	0	4 5 *19 1*	6 *20*
L. ervoides	439	20	0	0	0.27	0.031	1 *20*	1 2 3 *1 17 2*
	440	20	0	0	0	0	2 *20*	2 *20*
	441	20	0	0	0	0	3 *20*	4 *20*
	451	20	0	0	0	0	4 *20*	5 *20*
	461	20	0.42	0.038	0	0	4 5 *6 14*	5 *20*
L. nigricans	473	20	0	0	0	0	1 *20*	1 *20*
	453	20	0	0	0	0	2 *20*	2 *20*
	454	20	0.55	0.044	0.46	0.068	3 4 *12 8*	3 4 5 *14 4 2*
	459	20	0.1	0.009	0.18	0.020	3 5 *19 1*	6 1 *18 2*
	474	20	0	0	0	0	6 *20*	3 *20*
L. lamottei	428	20	0	0	0	0	1 *20*	1 *20*
	429	16	0	0	0.66	0.055	1 *16*	2 3 4 5 *8 3 2 3*
	430	12	0.28	0.024	0.67	0.089	1 2 *10 2*	6 7 8 9 10 *3 1 1 1 6*
	431	11	0	0	0.17	0.037	1 *11*	11 12 *10 1*
	432	18	0	0	0.10	0.008	1 *18*	12 13 *17 1*

Table 51. Partitioning of RAPD haplotype and isozyme genotype variation within and *among* populations of five wild *Lens* taxa, using AMOVA. Results from isozyme analysis are in parentheses.

Taxon / Source of variation	Variance components	d.f.	% of total variance	ϕ-statistics	P[a]
L. culinaris subsp. *orientalis*					
Between populations	1.97 (0.78)	4 (4)	78.7 (80.3)	ϕ_{ST} = 0.78 (0.80)	<0.001
Within populations	0.53 (0.19)	95 (195)	21.3 (19.7)		
L. odemensis					
Between populations	5.60 (0.81)	4 (4)	99.5 (95)	ϕ_{ST} = 0.995 (0.95)	<0.001
Within populations	0.03 (0.04)	95 (195)	0.5 (5.0)		
L. nigricans					
Between populations	0.55 (0.73)	4 (4)	79.0 (92.5)	ϕ_{ST} = 0.79 (0.92)	<0.001
Within populations	0.15 (0.06)	95 (195)	21.0 (7.5)		
L. ervoides					
Between populations	0.87 (0.82)	4 (4)	95.0 (95.0)	ϕ_{ST} = 0.95 (0.95)	<0.001
Within populations	0.05 (0.04)	95 (195)	5.0 (5.0)		
L. lamottei					
Between populations	1.44 (0.004)	4 (4)	82.0 (14.8)	ϕ_{ST} = 0.82 (0.15)	<0.001
Within populations	0.31 (0.022)	72 (149)	18.0 (85.2)		

[a] P = probability that chance alone will give a more extreme variance component than the observed value
d.f. = degrees of freedom

orientalis according to RAPDs and isozymes respectively and 0 to 0.089 in *L. lamottei* according to RAPDs (Table 50). AMOVA results for the partitioning of variation within and between populations for each species are shown in Table 51. In all taxa, both isozyme and RAPD data showed that between 78% and 99% of the variation was attributable to between population differences, except for isozyme variation in *L. lamottei*.

All results were significant at the 99% level. RAPD and isozymes results were remarkably similar for *L. culinaris* subsp. *orientalis*, *L. odemensis* and *L. ervoides*. Greater disparity was shown for *L. nigricans* in which 79% of variation according to RAPD analysis was distributed between populations as opposed to 92.5% according to isozymes. RAPD results for the percentage of variation found between populations in *L. lamottei* (82%) are similar to the average across other taxa (88%). Isozyme results are, however, dramatically different for this species in which only 14.8% of variation was found to be distributed between populations. All *L. lamottei* populations possessed identical isozyme profiles, apart from a single population (ILWL 430) which was polymorphic at locus Me-2.

When an additional hierarchical level of geographical region was included in the analysis of variance for *L. culinaris* subsp. *orientalis* and *L. odemensis*, 38% and 57.85% of variation, respectively, was found to be distributed between regions on the basis of RAPD analysis and 20.13% and 78.05% respectively, between regions according to isozyme analysis (Table 52). Although the regional differentiation according to RAPDs in *L. odemensis* is significant at the 95% level, other regional differences are not significant.

Table 52. Partitioning of RAPD haplotype and isozyme genotype variation between two regions, Syria and Turkey, and within and among populations of *L. culinaris* subsp. *orientalis* and *L. odemensis*, using AMOVA. Results from isozyme analysis are in parentheses.

Taxon / Source of variation	Variance components	d.f.	% of total variance	ϕ-statistics	P[a]
L. culinaris subsp. *orientalis*					
Between regions	1.12 (0.21)	1 (1)	38.0 (20.13)	ϕ_{CT} = 0.38 (0.20)	n.s.
Between populations within regions	1.30 (0.65)	3 (3)	44.0 (61.77)	ϕ_{SC} = 0.71 (0.77)	<0.001
Within populations	0.53 (0.19)	95 (195)	18.0 (18.09)	ϕ_{ST} = 0.82 (0.82)	<0.001
L. odemensis					
Between regions	4.39 (0.96)	1 (1)	57.85 (78.05)	ϕ_{CT} = 0.58 (0.78)	<0.001 *
Between populations within regions	3.17 (0.23)	3 (3)	41.80 (18.50)	ϕ_{SC} = 0.99 (0.84)	<0.001
Within populations	0.03 (0.04)	95 (195)	0.35 (3.45)	ϕ_{ST} = 1.00 (0.97)	<0.001

n.s. - not significant * RAPD data not significant

Substantial variation is evident in the levels of diversity between populations of the same taxon. Some populations are quitedepauperate in variation, and others are quite variable. It appears that no general rule can be applied to levels of variation within populations of specific taxa. It is thus vital that recommendations for the *in situ* conservation of particular populations are based on an understanding of the extent of variation within those populations.

The substantial range in variation found within populations of the same taxon is consistent with the findings of other researchers. On average, the relatively high rate of polymorphism found within populations of *L. culinaris* subsp. *orientalis,* and the relatively low levels in *L. odemensis* are consistent with the findings of others.

It is interesting to note that the highly polymorphic *L. culinaris* subsp. *orientalis* population (ILWL 466) is found in a known center of diversity for the taxon, Sweida province, Syria, yet a second population, collected from the same area (ILWL 469) was monomorphic at isozyme loci and consisted of just two haplotypes according to RAPD analysis, with H_j (rapd) = 0.18. In addition, the same area is known as a center of diversity for *L. odemensis*, yet within population variation was limited. South west Turkey is a center of diversity for *L. nigricans* where all the populations of *L. nigricans* used in this study originated. It would be interesting to determine whether within population variation in so called 'centers of diversity' is significantly greater than in populations from other areas. This would also have important implications for the targeting of sites for *in situ* conservation.

The low incidence of heterozygotes (none were observed) in isozyme data is consistent with highly inbred species. This implies that the effect caused by dominance in RAPD markers is negligible and thus phenotypes can be used to define population parameters to a reasonable degree of accuracy. The average levels of variation, in terms of the mean proportion of polymorphic isozyme loci in the average population ranged from 2% to 11% in our data.

The greater proportion of variation attributable to between population differences than within population differences is consistent with the expected population structure for selfing taxa. RAPD analysis reveals a significant difference in variation between regions for *L.*

odemensis, 57.85% of variation being attributable to between regional differences. According to isozyme analysis and RAPD variation in *L. culinaris* subsp. *orientalis*, between population variation is significant, but regional differences are not. The sample size in terms of numbers of populations studied would, however, have to be increased before any firm conclusions could be drawn.

The discrepancy in the results obtained from isozyme and RAPD analysis in the case of *L. lamottei* is interesting and explanations based on species evolutionary history and the nature of the markers themselves are proposed. The partitioning of variation within and between populations was typical of the other taxa studied in the case of RAPD results, however isozyme results were contradictory. There is increasing evidence, based on eco-geography, ecology, morphology and RAPDs, that *L. lamottei* is an ancient relic of cultivation, if this is the case then it is likely to have gone through a genetic bottleneck. This is supported by previous RAPD studies of variation occurring between populations in relation to other species.

Questions then arise relating to the evolutionary rates of different parts of the genome and the nature of the markers used. Isozyme electrophoresis detects variation in enzyme sub-units and thus reflects coding DNA. There is growing evidence that isozyme variation may not be selectively neutral at certain loci and thus may not accurately reflect population sub-division. In addition, only mutations in amino acids which affect the mobility of proteins can be detected. The accumulation of variation after a bottleneck in such genomic regions may thus be slow. In addition, the resolution in detecting variation is limited by the number of informative isozymes which are available.

Isozymes reveal similar levels of variation as RFLPs but discrepancies between the two levels have also been found. RAPD, in contrast, reflects diversity in both coding and non-coding DNA throughout plant genomes, and thus has the potential to provide a high degree of resolution. RAPDs have been found to reveal greater variation than allozymes in outcrossing diploids. However this may largely be due to the dominant nature of RAPD markers. In *L. lamottei* non-coding DNA (selectively neutral) may have allowed the relatively rapid accumulation of mutations after the occurrence of a bottleneck. The combination of species history, marker resolution and

differences in selective neutrality could therefore serve to explain the observed discrepancies between isozyme and RAPD data in *L. lamottei*.

To conclude, it appears that low levels of polymorphism occur within populations, on average 89% of variation (excluding *L. lamottei* and averaged over both isozyme and RAPD results) being due to differences between populations. Levels of variation do however differ between populations and must be measured and considered prior to the establishment of *in situ* conservation reserves. The population structure of *L. lamottei* remains unclear due to contrasting results from isozyme and RAPD analyses. This study has shown that RAPDs may be useful for the measurement of population genetic parameters in highly inbreeding species.

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1.4.13. Faba bean pre-breeding for *Botrytis fabae* resistance

Nursery design

The material consisted as follows: Chinese germplasm collected in 1996 (63 lines, plots 97001 - 97079). Ecuadorian germplasm collected in 1996 (88 lines, plots 97080 - 97189). In 1966, selections were made for earliness from BPL 710 in the screen houses (6 entries, plots 97190 - 97197 and from BPL 1179 (20 lines, plots 97198 - 97222). Selections made in previous years for chocolate spot (*Botrytis fabae*) resistance or other desirable characters (126 lines, plots 97223 - 97379). New BPLs derived from 8 germplasm accs. from Spanish origin, received in 1981 (17 lines, plots 97380 - 97400). The nursery was unreplicated, with each entry sowed in a single 3m long row at 0.45m row distance. Every fifth plot was divided in two subplots of 1.5m long and planted with two check entries, Rebaya-40 (Egyptian breeding line, chocolate spot susceptible) and Icarus (pure line selection from an Ecuadorian landrace, chocolate spot resistant). The 400 plots (320 test entries and 80 check plots) were planted in two screen houses of 50 x 8m (200 plots each).

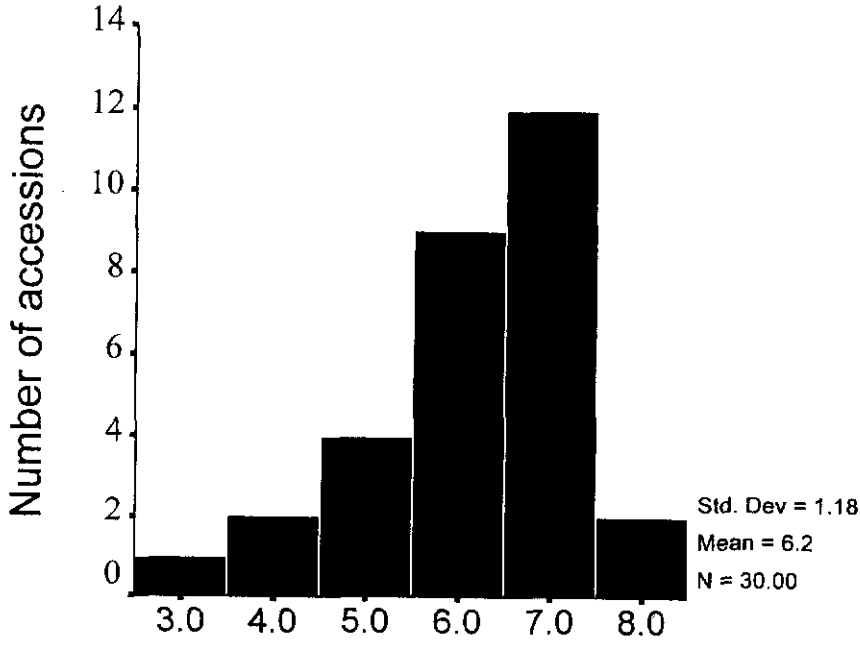

Fig. 39. *Botrytis fabae* scores (1-9) for faba bean collected in Yunnan province, China, in 1996

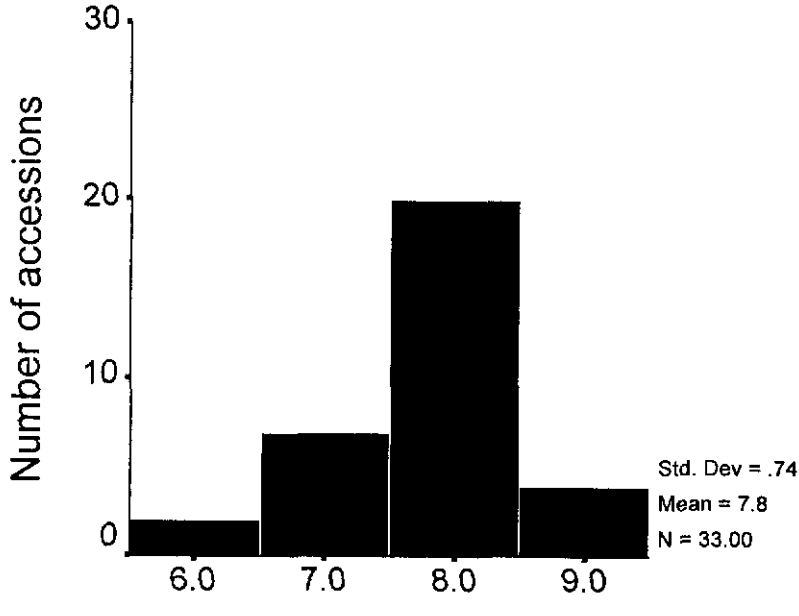

Fig. 40. *Botrytis fabae* scores (1-9) for faba bean collected in Sichuan province, China, in 1996

Inoculation and disease development

Inoculation with a mixture of Syrian *Botrytis fabae* isolates on 13 February 1997 resulted in a heavy initial infection. Although rather cold, the weather was in general favorable for chocolate spot development. Both a misting and a low-volume sprinkler system were installed in the screen houses to assist in the disease development by increasing humidity and prolonging leaf wetness periods. The nursery was rated for chocolate spot on 3 and 17 April, using a 0-9 scoring scale. The average score for the 320 entries significantly increased from 4.5 to 5.5 during this period ($P< 0.001$, using Wilcoxon's signed rank test for paired samples). Only the last score was used for further data analysis. Disease development on the checks appeared to be related to the level of disease in the surrounding plots; the average score of the four neighboring entries for the 76 check plots not placed on the border of the nurseries, was positively correlated with the score of both Icarus ($r= 0.39$, $P < 0.001$) and Rebaya-40 ($r= 0.25$, $P = 0.027$). However, scores on both checks were relatively uniform, indicating an even and severe chocolate spot development through the nursery. Days to flowering for Rebaya-40 ranged from 73 to 86 days with an average of 81 and a standard deviation of 3.1. Icarus was more uniform, with days to flowering ranging from 110 to 113 days, an average of 111 and a standard deviation of 1.3.

Performance of newly collected Chinese germplasm

The Chinese germplasm was early, but had a large proportion of very susceptible lines. However, a number of lines with a moderate level of resistance were present (Fig. 39 = Yunnan and Fig. 40 = Sichuan provinces). Scores for chocolate spot were negatively correlated with days to flowering ($r = -0.40$ $P = 0.001$) and the altitude of the collection site ($r = -0.68$, $P< 0.001$). Altitude and flowering date were positively correlated ($r = 0.49$, $P< 0.001$).

The Chinese material originated from two provinces; Sichuan (33 accs., Table 53) and Yunnan (30 accs., Table 54). The material from Sichuan was earlier than that of Yunnan (average days to flowering 82 vs. 86), but was more susceptible to chocolate spot (average score 7.8 vs. 6.2). The 7 lines with a score of 5 or less originated all from Yunnan, 2 from the county Guandu (the most resistant lines in

Table 53. Differences among counties of origin for Chinese faba bean germplasm collected in the Sichuan province (*Botrytis*)

		Chocolate spot		Days to flower		Altitude	
County	lines	ave	range	ave	range	ave	range
Bao Seng	2	8.0	8-8	81	79-83	330	320-340
Bei Pei	2	8.0	8-8	83	83-83	305	200-410
Bi Shan	3	7.7	7-8	82	79-85	220	210-240
Da Zhu	2	7.0	6-8	82	80-83	385	330-440
Gao Ping	1	9.0		75		365	
Guang Am	2	7.0	7-7	86	83-88	340	340-340
He Chun	1	8.0		85		340	
Jia Ling	2	8.5	8-9	79	79-79	448	415-480
Jian Yang	2	7.0	7-7	74	74-74	440	430-450
Lezhi	7	7.9	7-8	82	79-85	437	310-515
Peng Xi	1	8.0		83		380	
ShuangQiao	1	8.0		83		330	
Shui Ning	2	8.5	8-9	81	79-83	320	310-330
Yong Chun	2	8.5	8-9	84	83-85	250	250-250
Yue Chi	3	7.0	6-8	83	83-83	393	350-420

Table 54. Differences among counties of origin for Chinese faba bean germplasm collected in the Yunnan province (*Botrytis*)

		Chocolate spot		Days to flower		Altitude	
County	lines	ave	range	ave	range	ave	range
Cheng Gong	1	7.0		88		1985	
Guandu	2	3.5	3-4	87	85-88	2090	2090-2090
Hui Ze	8	6.9	6-8	89	80-94	1895	1690-2080
Lu Liang	3	7.3	7-8	85	80-91	1815	1780-1840
Lu Nan	1	7.0		85		1680	
Qu Jing6	6	5.2	4-6	88	79-92	1911	1795-2075
Shong Ming	3	5.7	5-6	85	85-85	1937	1930-1950
Tong Chuan	1	6.0		79		1320	
Xun Dian	4	6.5	6-7	82	79-89	1870	1860-1880
Yi Ling	1	7.0		75		1720	

the collection), 4 from Qu Jing and 1 from Shong Ming. Out of these 7 lines, 4 flowered within 90 days. If data were analyzed for both provinces separately, correlation between score and days to flowering was not significant. The relation between score and altitude remained significant (r= -0.40, *P*= 0.027) for the low-land province Sichuan, but was not present within the collection from the high-land province Yunnan. There appear to be differences among counties within each province (Table 53 and 54), but data were not further analyzed as the number of lines collected per county were rather small.

Performance of newly collected Ecuadorian germplasm

The Ecuadorian material showed a very high level of chocolate spot resistance (Fig. 41), but was in general late. However, 46 out of the 88 lines tested flowered in less than 111 days (average of the chocolate spot resistance check Icarus), and 5 lines flowered within 90 days. The collection originated from 10 provinces (Table 55). Differences for chocolate spot score, days to flowering and altitude were analyzed for the 8 provinces with more than 5 accs. Significant differences were found for disease and altitude, but not for flowering date.

Table 55. Differences among provinces of origin for Ecuadorian faba bean germplasm (*Botrytis*)

		Chocolate spot		Days to flower		Altitude	
Province	**lines**	**ave**	**range**	**ave**	**range**	**ave**	**range**
Azuay	13	3.2	2-5	109	92-119	2695	2460-2910
Bolivar	10	3.9	3-6	105	89-125	2849	2750-3130
Canar	8	4.0	3-5	109	89-121	3108	2835-3350
Carchi	12	4.3	3-5	113	89-128	3013	2865-3290
Chimborazo	13	3.7	2-5	111	98-125	3053	2270-3620
Cotopaxi	1	4.0		105		2950	
Imbabura	6	3.3	3-4	107	87-128	2636	2550-2840
Loja	4	4.3	4-5	102	90-116	2569	2540-2615
Pichincha	7	3.9	3-5	113	95-125	3036	2840-3260
Tungurahua	14	4.1	3-5	111	89-128	2960	2440-3300

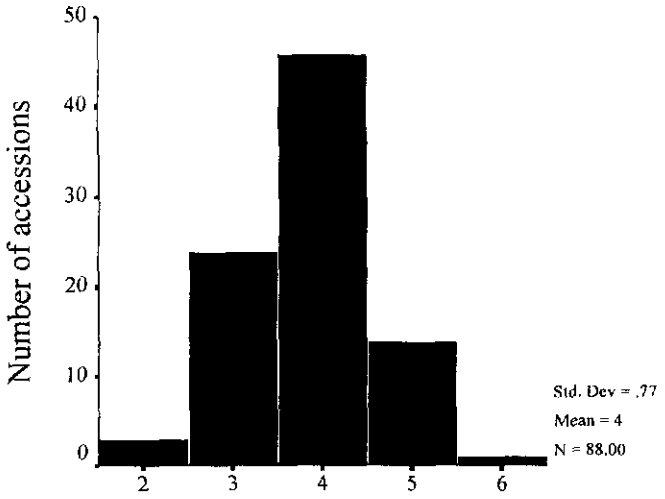

Fig. 41. *Botrytis fabae* scores (1-9) for faba bean collected in Ecuador in 1996

No correlation between flowering date, altitude and chocolate spot score was present, so selection for earlier material with a high level of chocolate spot resistance should be possible; Three out of the five lines that flowered within 90 days had a chocolate spot score of 4 or less. These five early and resistant lines originated from five different provinces and were collected in sites that ranged in altitude from 2750 to 3300m.

Selections from BPL-0710 and BPL-1179

BPL-0710 (Icarus) is a selection from ILB-0438 (originating from Ecuador), and BPL-1179 is a selection from ILB-0938 (originating from Colombia). Both lines have proved their resistance to chocolate spot in field trials with heavy disease pressure in different countries, but are rather late. Progenies of single plant selections made from both BPLs in the screen house during 1996 were grown in 1997. Differences in days to flowering were confirmed; Selections from BPL-0710 ranged from 92 to 119 days, selections from BPL-1179 ranged from 86 to 98. All progenies of BPL-0710 and 13 out of 20 BPL-1179 progenies retained a high level (score ≤ 4) of resistance to chocolate spot. Further single plant selections were made for testing in 1998. BPL-0710 is the only single plant selection made from the original ILB, while only two BPLs are derived from ILB-0938. It

could therefore be considered to re-test the original populations, as a wider range of variability would be expected.

Other germplasm tested

Of the total of 126 lines selected in previous years for different characters, only 7 lines had a chocolate spot score of 4, all others received higher scores. Two out of the 7 lines were selections made in 1981 from BPL-1179. However, these selections flowered in 116 days, while 10 out of the 20 selections made in 1996 flowered within 90 days. Very few of the lines selected in the early eighties looked as good for chocolate spot resistance as the newly tested material. However, selections in the 1996 Lattakia nurseries were mainly made for low levels of virus symptoms. These lines should therefore be re-tested in a special nursery, designed to test for virus resistance.

The newly developed BPLs from Spanish germplasm performed very well. Generally, they possessed an acceptable level of chocolate spot resistance (12 out of 17 lines ≤ 4 score), and were not too late (13 lines ≤ 95 days to flowering), had good pod setting and large pods.

Plans for the 1998-99 season

Table 56 shows the number of lines of which single plant selections were made and the total number of plants selected. The single plant progenies will be tested in the screen house during 1998-99. Proposal is to test single plant progenies next to the original populations.

Table 56. Number of selected lines and individual plants from different germplasm groups in the 1997 *Botrytis* nursery

Germplasm group	total lines	selected lines	selected plants
Chinese	63	24	36
Ecuadorian	88	51	114
BPL-0710 & -1179	26	19	59
Spanish BPL's	17	14	38
Other	126	39	60
Total	**320**	**147**	**307**

Because of lack of space and seed most nurseries were tested unreplicated in the past season. Comparison of individual entries was therefore not possible. It is proposed to shorten plot lengths to 1.5 m for the coming season. This will enable the testing of the same number of entries as in the past season, but using two replicates. Apart from the single plant selections from this year's nursery, it is likely that a new collection of Ethiopian germplasm will be included in the 1998 nurseries.

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1.4.14. Faba bean *Ascochyta fabae* disease screening

Nursery design

The material under testing consisted of the following groups; Chinese germplasm collected in 1996 (56 lines, plots 98002 - 98070). New BPLs derived from 27 germplasm accs. from Spanish origin, received in 1981 (76 lines, plots 98208 - 98302).

New BPLs derived from 34 germplasm accs. from Moroccan origin, received in 1981 (79 lines, plots 98303 - 98400). Single plant progenies made in 1996 (22 progenies from BPLs, 47 from other lines, plots 98072 - 98157). Other material (40 lines, plots 98158 - 98207). The nursery was unreplicated, with each entry sowed in a single 3m long row at 0.45m row distance. Systematic checks were included; Every fifth plot was divided in two subplots of 1.5m and planted with two check entries, Giza-4 (Egyptian breeding line, ascochyta blight susceptible) and Ascot (selection from Fiord, a BPL originating from Greece, ascochyta blight resistant). The 400 plots (320 test entries and 80 check plots) were planted in two screen-houses of 24 x 16m (200 plots each).

Inoculation and disease development

The nursery was inoculated with a mixture of Syrian *Ascochyta faba* (ascochyta blight) isolates on 13 February 1997. The screen houses were located next to the nurseries inoculated with *Botrytis fabae* and chocolate spot developed severely on some of the material, masking the development of Ascochyta blight on leaves. The nursery was rated on 18 and 19 April using an adapted scoring scale that gave priority to disease development on pods rather than on leaves (Table 57).

Plant selections were not yet made as another disease rating was planned for early May. The scoring for ascochyta blight might have been influenced by chocolate spot, but the consistently high score of the susceptible check Giza-4 showed that the inoculation was successful.

Table 57. Scoring scale for Ascochyta blight

Score	Disease development
1	no disease
2	some lesions on stem or pod
3	discrete lesions on stem
4	more than 4 lesions / stem or start of lesions on pods
5	large lesions on stem and/or > 10% disease on pods
6	clear lesions on pods, no broken stems
7	pods heavily affected, < 10% stems broken
8	10 - 90% stems broken
9	>90% stems broken, leaves dead

Performance of newly collected Chinese germplasm

A large proportion of the Chinese material appeared to be susceptible (but less so than the check Giza-4), while being early (Tables 58 and 59). All of the 56 newly collected Chinese germplasm lines were as well present in the FBBOT97. As with chocolate spot, score was negatively correlated with flowering date ($r = -0.74$, $P < 0.001$). Scores on both diseases (taken in two different nurseries/screen houses) were positively related with each other ($r = 0.53$, $P < 0.001$). From the 56 lines in the ascochyta nursery, 33 originated from the province Sichuan (same lines as tested in the botrytis nursery) and 23 from the province Yunnan (7 less than in the botrytis nursery). Ascochyta blight followed partly the same pattern as chocolate spot; The material from Sichuan was more susceptible than that of Yunnan (average score 6.4 vs. 4.0). The performance of different counties in each province was different

Table 58. Differences among counties of origin for Chinese faba bean germplasm collected in the Sichuan province (*Ascochyta*)

		Ascochyta blight		Days to flowering	
County	**lines**	**ave**	**range**	**ave**	**range**
Bao Seng	2	6.5	6-7	79	79-79
Bei Pei	2	4.5	4-5	81	79-82
Bi Shan	3	5.3	4-6	82	82-82
Da Zhu	2	7.0	7-7	79	79-79
Gao Ping	1	7.0		79	
Guang Am	2	5.5	5-6	81	79-82
He Chun	1	4.0		85	
Jia Ling	2	7.5	7-8	78	76-79
Jian Yang	2	8.0	8-8	78	76-79
Lezhi	7	7.4	5-9	80	79-82
Peng Xi	1	6.0		79	
Shuang Qiao	1	6.0		79	
Shui Ning	2	7.0	7-7	79	79-79
Yong Chun	2	5.5	5-6	79	76-82
Yue Chi	3	5.7	5-6	81	79-82

Table 59. Differences among counties of origin for Chinese faba bean germplasm collected in the Yunnan province (*Ascochyta*)

		Ascochyta blight		Days to flowering	
County	**lines**	**ave**	**range**	**ave**	**range**
Guandu	2	3.5	3-4	87	85-88
Hui Ze	6	3.5	3-5	88	85-91
Lu Liang	2	3.0	3-3	85	82-88
Lu Nan	1	4.0		85	
Qu Jing	6	3.7	3-5	87	82-88
Shong Ming	2	4.5	4-5	87	85-88
Tong Chuan	1	6.0		82	
Xun Dian	3	5.7	3-7	87	85-88

than in the chocolate spot testing; Lines with a relatively low score were found in counties Bei Pei and Bi Shan from Sichuan province,

while these lines were highly susceptible to chocolate spot. Two lines from the county Guandu (Yunnan province) appeared to be resistant to both diseases, but some lines from other counties in this province rated low for ascochyta blight, while being susceptible for chocolate spot.

Performance of new BPLs from Moroccan and Spanish origin

Most of the new BPLs showed a moderate level of resistance to ascochyta blight. Moroccan and Spanish germplasm performed well in the uninoculated Faba Bean Evaluation Nursery (FBEVA97) for three diseases and agronomic characteristics. The 76 new BPLs from Spanish origin were derived from 27 ILBs. Out of these, 15 ILBs were present in the FBEVA97. The 79 Moroccan BPLs originated from 34 ILBs, of which 33 were tested in the FBEVA97. The average ascochyta blight score in the FBASC97 of the BPLs derived from the 48 ILBs in the FBEVA97 was weakly correlated with the ascochyta blight score on the ILBs in the FBEVA97 ($r = 0.283$, $P = 0.05$). There was no relation for the flowering date. The relatively high level of ascochyta blight resistance in the material could explain the low level of correlation. It will be worthwhile to retest these BPLs in next year's nurseries.

Performance of other germplasm

Few of the lines originating from single plant selections made in 1996 and other lines were susceptible to ascochyta blight. The selections made in 1996 were mainly made for a relative good performance during a heavy virus epidemic. First priority for this material therefore is to confirm their virus resistance.

Plans for the 1998 season

Apart from the susceptible checks and 28 of the newly collected Chinese accs., only one line (BPL-4172) showed a high level of susceptibility (score ≥ 6). Therefore, either the disease screen was not sufficiently high (even though plots with the susceptible check received mostly a high score), or the Syrian *Ascochyta fabae* isolates were not very virulent (the apparent resistance of Icarus in the FBEVA97 could be an indication for this), or ascochyta blight susceptibility is uncommon within the faba bean germplasm pool.

In order to improve the reliability of screening for ascochyta blight, development of chocolate spot has to be avoided. The best possibility

to do so might be to locate the future nursery in another location than the one for the chocolate spot screening, possibly at Tel Hadya. Another possibility could be to protect the nursery by using fungicides with a specific action against *Botrytis fabae*. The same modifications as suggested for the chocolate spot screening nursery (shorter rows, replications) could be followed.

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1.4.15. Anti-nutritional factors in the *Vicieae*

Legumes contain a wide range of secondary metabolites that can act as anti-nutritional factors (ANF) when ingested by a range of predators from insects to humans. Of particular significance are compounds that reduce the digestibility of plant material such as the polyphenolics, especially the condensed tannins, and proteinase inhibitors targeted against enzymes such as trypsin. Non-protein amino acids, which are particularly prevalent in the *Vicieae,* have the potential to interfere with animal metabolism by substituting their native amino acid analogues causing the production of dysfunctional proteins. Potentially problematic non-protein amino acids which have been detected in the *Vicieae* include γ-glutamyl-β--cyanoalanine in *V. sativa*, canavanine in *V. ervilia*, and glutamyl-ethenyl cysteine (GEC) in *V. narbonensis*. All these compounds has been shown to reduce the performance of livestock, in particular monogastrics, reducing weight gain, feed conversion efficiency, and in some cases causing death: chicks fed as little as 0.075% γ-glutamyl-β-cyanoalanine, the alanine analogue found in *V. sativa* seeds, die within 11 days.

While there have been a number of studies measuring single anti-nutritional factors in various legume species, there have been very few attempts to measure a range of compounds in a range of species collected over a wide variety of habitats. The substantial legume collection housed at GRU, ICARDA combined with the analytical

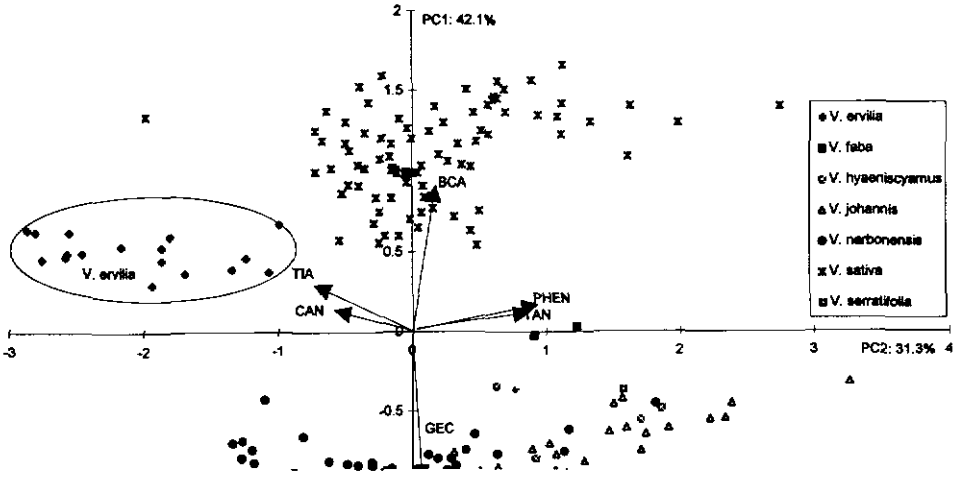

Fig 42. Principal component analysis of ANF found in the seeds of *Vicia* spp.

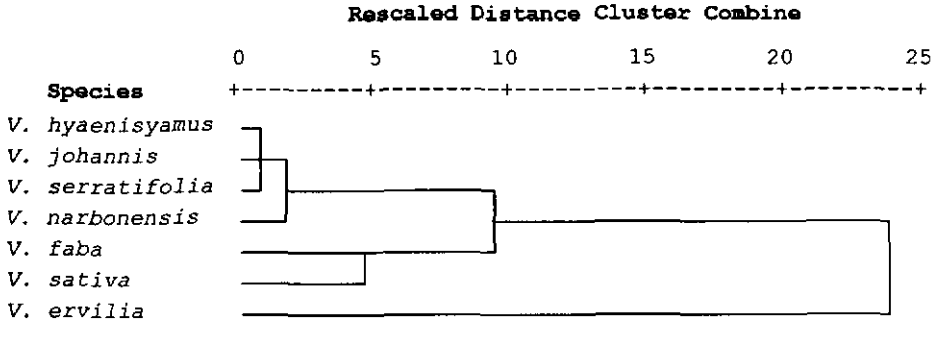

Fig. 43. Cluster analysis of *Vicia* spp. using group centroids calculated by discriminant analysis of ANF concentrations

chemistry capacity of the Chemistry Center, Western Australia and the Waite Institute, SA enabled such a study to take place. Sympatric accs. of three *Vicia* spp.: *V. narbonensis* (n= 88), *V. sativa* (n= 71) and *V. ervilia* (n= 17), as well as two local varieties of *V. faba* and the complete range of *V. narbonensis* relatives in the GRU collection were grown out in two trials at Tel Hadya. The material was largely collected from the Eastern Mediterranean covering a broad range of altitude (20-1500m) and rainfall (200-1700mm per annum).

Principal components analysis reveals that there are substantial differences in the range of anti-nutritional factors found in the seeds of *Vicia* spp. housed in the GRU collection (Fig. 42). *V. ervilia* seeds are typified by the presence of canavanine, low concentrations of phenolic secondary metabolites, coupled with high concentrations of proteinase inhibitors (Table 60). In contrast *V. faba* contains high concentrations of phenolic secondary metabolites, but low levels of proteinase inhibitors (Table 60). Neither *V. ervilia* or *V. faba* seeds contain GEC or include γ-glutamyl-β--cyanoalanine. *V. sativa* and *V. narbonensis* seeds contain intermediate levels of both phenolic secondary metabolites and proteinase inhibitors, but are separated by the presence of include γ-glutamyl-β--cyanoalanine in the former, and GEC in the latter (Fig. 42). *V. johannis*, *V. hyaeniscyamus* and *V. serratifolia* are differentiated from their near relative, *V. narbonensis*, by significantly lower levels of GEC and proteinase inhibitors ($p<0.001$), and significantly higher levels of phenolic secondary metabolites (Table 60).

Fig. 42 shows that for all species there is considerable intra-specific variation for anti-nutritional factors, suggesting that the GRU collection is comprised of a diverse range of germplasm, giving breeders substantial scope for selection. This is important because selection on the basis of anti-nutritional factors is unlikely to be unidirectional. While anti-nutritional factors have been demonstrated to reduce the performance of monogastrics in particular, intermediate to high levels of condensed tannins may increase wool production and weight gain in sheep due to the increased flow of proteins from the rumen into the abomasum (the fourth or digesting chamber of the stomach of a cud-chewing animal, such as the cow). Moreover, there is a large body of circumstantial evidence suggesting tannins play a

Table 60. Anti-nutritional factor concentrations recorded in *Vicia* spp. from the GRU-ICARDA collection

Species	Mean	SD	Min	Max
Non-protein amino acids				
V. ervilia (Canavanine)	0.83	0.04	0.33	1.16
V. hyaeniscyamus (GEC)	1.39	0.10	1.19	1.76
V. johannis (GEC)	1.56	0.05	0.98	2.21
V. narbonensis (GEC)	1.93	0.02	1.16	2.60
V. serratifolia (GEC)	1.44	0.47	0.96	1.91
V. sativa (γ-Glutamyl-β-cyanoalanine)	0.83	0.02	0.41	1.36
Total phenolics (mg/g)				
V. ervilia	4.78	0.30	2.55	8.88
V. faba	10.11	0.74	6.63	11.67
V. hyaeniscyamus	9.47	0.98	5.95	11.24
V. johannis	10.43	0.44	5.25	15.88
V. narbonensis	6.37	0.13	3.23	12.52
V. serratifolia	12.17	0.82	11.35	12.99
V. sativa	8.08	0.17	3.25	16.42
Condensed tannins (Leucocyanidin equivalents w/w%)				
V. ervilia	0.41	0.03	0.16	0.83
V. faba	0.80	0.08	0.41	0.96
V. hyaeniscyamus	0.92	0.16	0.39	1.29
V. johannis	1.02	0.06	0.39	1.89
V. narbonensis	0.51	0.02	0.11	1.25
V. serratifolia	1.20	0.10	1.10	1.29
V. sativa	0.65	0.02	0.09	1.39
Trypsin inhibitors (mg trypsin inhibited per mg protein)				
V. ervilia	2.14	0.08	0.71	2.88
V. faba	0.25	0.02	0.17	0.31
V. hyaeniscyamus	0.55	0.22	0.28	1.44
V. johannis	0.50	0.06	0.11	1.67
V. narbonensis	1.24	0.04	0.46	3.20
V. serratifolia	0.40	-	0.40	0.40
V. sativa	1.29	0.04	0.18	2.88

role in crop establishment and disease resistance, and anti-nutritional factors may protect the both the growing plant and seed from herbivory, particularly from insects.

Indeed anti-nutritional factor concentrations can be used to successfully demonstrate species taxonomic relationship (Fig. 43). Hierarchical cluster analysis using group centroids calculated by discriminant function analysis of anti-nutritional factor concentrations shows that *V. narbonensis* and its relatives are very closely related, reflecting the fact that common compounds were detected in all four species (Fig. 43). The remaining *Vicia* spp. cluster further from *V. narbonensis* and relatives as a result of the qualitative and quantitative differences in anti-nutritional factor makeup of the seed outlined above.

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1.5. DOCUMENTATION OF GENETIC RESOURCES

1.5.1. Genetic resources documentation on Internet - the SINGER project

Access to genetic resources database to as wide a range of users as possible is important to easily select and use conserved germplasm in gene banks. The GRU's database was set up on an ICARDA-wide network, so that all scientists can readily query the database. However, prospective users outside ICARDA could not access the database directly; they had to request their colleagues at ICARDA to query the database for them. This situation changed when the CGIAR's System-wide Information Network for Genetic Resources (SINGER) project was completed and put into operation in 1997. The SINGER project of the System-wide Genetic Resources Program (SGRP) was initiated at the end of 1994. The objectives were (i) to effectively link together the common data from all genetic resources databases in the CGIAR, and (ii) to allow searches across the Centers' databases through a common user interface. During 1995, extensive consultations within the CGIAR, and also with prospective users of the system, were carried out. Subsequently, the agreed model of a wide-area database was implemented in 1996 and 1997.

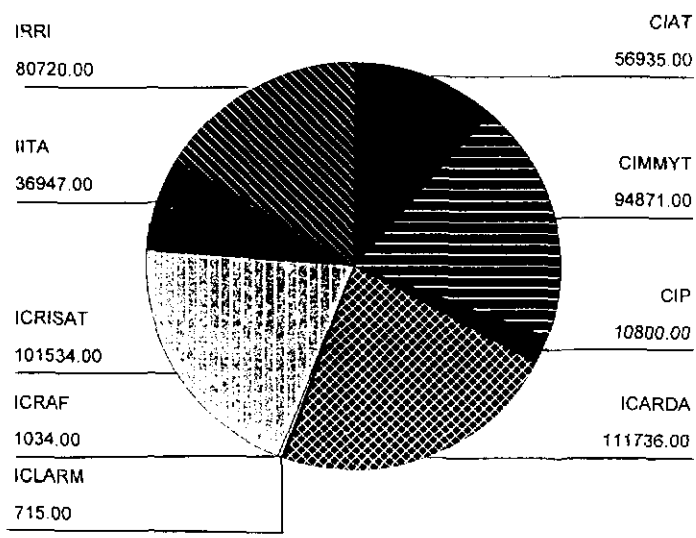

Fig. 44. Pie-chart showing the number of accs. under conservation at CGIAR centers according to data from SINGER

At the heart of SINGER lies the Network Operation Center (NOC) with the central server storing the data transferred from all Centers dealing with genetic resources. NOC's server is a powerful computer which is accessible via very fast Internet line(s); thus allowing quick searches simultaneously for a large number of users. Each Center replicates its data to the NOC at scheduled intervals. The automation of replication requires that each Center has to run its own SINGER server with identical database software as at NOC. Microsoft SQL Server, running under Microsoft NT operating system, is currently being used.

Implementing the project at ICARDA involved installating the NT server, building the SQL Server database to match the agreed schema, and off-line replication of data to NOC. Automated, on-line replication will be possible after installing the Integrated Voice and Data Network (IVDN) in the Center. Much effort was directed towards checking the quality of the data and structurally changing the ICARDA germplasm database in order to automate future replication of information to the SINGER database.

Over 500,000 accs. maintained in the CGIAR centers are now included in the SINGER database, which is available on Internet. ICARDA has contributed the passport and evaluation data of 111,740 accs. (Fig. 44). Recognizing that significant part of our collaborators do not have ready access to Internet, CD-ROMs were also produced and distributed. Such wide availability of germplasm documentation enhances the transparency of evaluating collections, and helps to fulfill the trusteeship obligations.

The inter-center collaboration was also useful with regard to documentation standards and harmonization of germplasm documentation systems used in different Centers.

J. Konopka and S. Jankieh

1.5.2. Vavilov Institute's database at ICARDA

The world's longest established major germplasm collection is maintained at the N.I. Vavilov Scientific Research Institute of Plant Industry (VIR), St. Petersburg, Russia. Initiation of the Australia-funded Grains Research and Development Corporation (GRDC)/CLIMA/ICARDA project on the preservation and utilization

of the unique pulse and cereal genetic resources of the Vavilov Institute necessitated an access to VIR crop databases in order to select the genetic resources for further research. Taking into consideration the germplasm exchange between VIR and ICARDA in the past, current project needs as well as future collaboration, the establishment of a working linkage between the database systems of VIR and ICARDA was a priority. As a first step, during a short visit to St. Petersburg in August 1997, the VIR database of approx. 79,000 accs. (cereals: 56,600 accs. and legumes: 22,600 accs.) was obtained from VIR's computerization department and transferred to ICARDA.

The data were reformatted to fit the standards used in GRU database and hence, the VIR database can now be queried on ICARDA's network. Essential linkages to germplasm identifiers (cultivar or local names and/or numbers) in GRU database were developed. The system was then used to request the legume and cereals genetic resources from VIR for multiplication and evaluation at ICARDA (which is reported elsewhere in this report).

The contacts with VIR scientists dealing with the germplasm documentation and databases were very fruitful and subsequent collaboration should lead to periodical exchange of updated records of germplasm collections.

J. Konopka, S. Jankieh (GRU-ICARDA) and A. Omelchenko (VIR, St. Petersburg, Russia)

1.5.3. Database of microbial genetic resources in CGIAR Centers

The SGRP project on a "Development of a System-wide Microbial Genetic Resources Database" was initiated in ICARDA in 1997 with the following objectives: (i) to develope standardized passport and evaluation descriptors, (ii) to put in order and computerize data at the Centers, (iii) to develope a central database in ICARDA, and (iv) to produce CD-ROMs to facilitate access to the database.

In addition, the project will attempt to: (i) initiate the process leading to the development of a strategy and standards for microbial collection and conservation at the CGIAR centers, (ii) placement of the CGIAR microbial collections under the auspices of FAO, and (iii) the development of a CGIAR policy on collections and distribution in line with the Convention on Biological Diversity (CBD).

ICARDA (the lead center), the International Institute for Tropical Agriculture (IITA), the International Livestock Research Institute (ILRI), the International Rice Research Institute (IRRI) and the International Center for Tropical Agriculture (CIAT) are participating in this project.

In October 1997, ICARDA hosted the project's first workshop which was attended by the representatives from IITA, ILRI, IRRI and ICARDA. The meeting reviewed the work of Centers in collection, research and maintainanace of nitrogen fixing organisms. Subsequently, a set of recommendations were formulated.

A major part of the time of the meeting was devoted to deliberations on the development of descriptors and schema for the system-wide database. Attempts to maintain the schema of the database as close as possible to SINGER in order to facilitate possible future integration were made. However, compared to SINGER, the nitrogen fixing organisms database has many new fields of information, which are essential to accurately document the collections maintained by the CGIAR Centers.

Based on the data files submitted to ICARDA, the pilot version of a database was developed and demonstrated during the SGRP meeting in Nairobi, Kenya, in January 1998. The final version should be in place during second half of 1998.

Jan Konopka and S. Jankieh

1.6. GERMPLASM MANAGEMENT

1.6.1. Multiplication and rejuvenation

Whenever routine seed stock monitoring shows that the quantity of seed for distribution is below 50g and/or viability falls below 85% the acc. is planted in the field, and thereby multiplied and rejuvenated. The material for rejuvenation (and multiplication at the same time) was planted in two rows of one meter each with a distance of 0.45 m between the two rows and 1.35 m between plots. In the case of *Aegilops* spp. a greater distance was maintained between plots. Triticale plants were planted as borders all around to prevent cross pollination and to preserve the genetic purity of the material. After harvest the germplasm was cleaned and seed stock replenished in the base collection. The excess seed were set aside for distribution upon request in the medium-term cold store. A total of 1,510 cereal accs. were rejuvenated and multiplied during 1995-96. During 1996-97 a further set of 966 accs. were multiplied and rejuvenated. The details of rejuvenation and multiplication during both seasons is given in Table 61.

Table 61. Multiplication and rejuvenation of cereal germplasm during 1996 and 1997

Species	1996	1997
Barley	513	119
Durum wheat	408	300
Bread wheat	368	379
Aegilops spp.	221	--
Wild *Triticum* spp.	--	198
Totals	**1510**	**996**

Table 62. Food legume germplasm multiplication and characterization during 1996 and 1997

Crop	Multi. (accs.)	Charact. (accs.)	Traits
Chickpea	1568	-	-
Wild *Cicer* spp.	310	-	-
Lentil	1671	2299	34
Wild *Lens* spp.	450	-	-
Faba beans	1857	113	25
Totals	**5856**	**2412**	-

In all, 5,856 food legume accs. were rejuvenated and multiplied and 2,412 accs. were characterized during 1996 and 1997. The details are given in Table 62. The figures for forage legumes are given in Table 2 (see under Introduction and Highlights).

1.6.2. Viability testing

Viability testing of seed genetic resources stored in the cold room of the gene bank of ICARDA's mandate crops is an on-going activity through out the year. During 1996 and 1997, a total of 6,596 and 7,201 accs., respectively, were tested for viability in special cabinets in the germination room at GRU. Typically 40 seeds, selected at random, were placed on four petri dishes and incubated in special germination chambers at 25°C for a maximum of seven days. Illumination to simulate daylight is provided throughout the period. Germination was recorded in each dish after the second day. The accs. which showed viability of less than 85% were ticked off for rejuvenation and multiplication in the next available season. The details of this activity is given in Table 63.

B. Humeid & GRU staff

Table 63. Viability testing during 1996 and 1997

Species	1996	1997
Bread wheat	2006	5510
Durum wheat	3564	1566
Lentil	112	125
Chickpea	647	--
Pisum	267	--
Totals	**6596**	**7201**

1.6.3. Long-term preservation and safety duplication

The base collection build up of the ICARDA's germplasm holdings is also an ongoing activity. During 1996 and 1997 a total of 3,099 accs. of ICARDA mandate crops were dried in a special room and vacuum sealed in laminated aluminum foil packets. They were subsequently deposited in the long-term cold room which is maintained at a constant temperature of -20°C. The status of the ICARDA base collection is given in Table 64.

Since a great deal of genetic erosion has taken place in almost all centers of origin and diversity, genetic resources which were collected in the past in these areas would perhaps not be available today. Several mission reports in recent years speak about the loss of biodiversity. Hence, it would be prudent to duplicate unique collections in other gene banks for safety from destruction due to man-made or natural disastrous. In keeping with past practice GRU-ICARDA continued to despatch its unique germplasm for safety duplication in gene banks with similar storage conditions under cooperative agreements. Wheat and barley and their wild relatives were sent to the International Maize and Wheat Improvement Center (CIMMYT), Mexico. The lathyrus were sent to the Station Federale de Recherche Agronomique de Changins (SFRAC), Nyon, Switzerland, and faba bean, *medicago* and vicia were sent to the Federal Institute of Agrobiology (FIA), Linz, Austria (Table 65).

B. Humeid & GRU staff

Table 64. Status of ICARDA base collection (as of Dec. 1997)

Crop	Total held	In base collection	%
Barley	22923	22261	97.1
Wild *Hordeum* spp.	1737	606	34.9
Durum wheat	18717	16897	90.3
Bread wheat	7906	7588	96.0
Wild wheat relatives	5060	4237	83.7
Total Cereals	**56343**	**51589**	**91.6**
Chickpea	9762	8633	88.4
Lentil	7759	7478	96.4
Faba bean	5030	59	1.20
Total Food Legumes	**22551**	**16170**	**71.7**
Vicia	5558	2910	52.4
Medicago	7753	5181	66.8
Lathyrus	3039	1175	38.6
Total Forages	**16350**	**9266**	**56.7**
GRAND TOTALS	**95244**	**77025**	**80.9**

Table 65. Safety duplication of ICARDA's genetic resources in 1996 and 1997

Crop	Accs.	Institute where duplicated
1996		
Lathyrus	1268	SFRAC, Switzerland
Faba bean	1002	FAI, Austria
Medicago	2000	FIA, Austria
Vicia	2025	FIA, Austria
Total	**6295**	
1997		
Barley	2124	CIMMYT, Mexico
Wild *Hordeum* spp.	271	CIMMYT, Mexico
Bread wheat	2772	CIMMYT, Mexico
Durum wheat	863	CIMMYT, Mexico
Wild *Triticum* spp.	897	CIMMYT, Mexico
Aegilops spp.	1141	CIMMYT, Mexico
Total	**8068**	

1.6.4. Rhizobium diversity conservation at ICARDA

Collection and conservation of beneficial micro-organisms associated with mandate legumes is essential for development and implementation of sustainable farming systems in which atmospheric nitrogen fixation by *Rhizobium* spp. plays an important role. Consequently, large rhizobia collections have been assembled and held at ICARDA. The collection consists of a total of 1,512 accs. consisting of 99 *Rhizobium ciceri*, 481 *R. leguminosarum*, 700 *R. meliloti* and 232 *R. trifolii* accs. The collection is maintained separately for food and forage legumes at the Germplasm Program (GP) and for pasture legumes at the Natural Resource Management Program (NRMP).

Table 66. Geographical origin of ICARDA rhizobia collections

Country	No. of acc.	%Total
Syria	400	26.5
Morocco	319	21.1
Jordan	238	15.7
Turkey	190	12.6
Egypt	80	5.3
Lebanon	71	4.7
USA	42	2.8
Tunisia	30	2.0
Cyprus	17	1.1
India	16	1.1
Sudan	12	0.8
Ethiopia	10	0.7
Other countries	65	4.3
Unknown	22	1.5
Total	**1512**	**100.0**

Table 67. Crop specificity of ICARDA rhizobia collections

Crop/Genus	No. of accs.	%Total
Lentil	236	15.6
Chickpea	99	6.5
Faba bean	132	8.7
Medicago	692	45.8
Trifolium	232	15.3
Vetch	57	3.8
Trigonella	36	2.4
Pea	14	0.9
Lathyrus	1	0.1
Astragalus	1	0.1
Unknown	12	0.8
Total	**1512**	**100.0**

Table 68. Status of passport information of ICARDA rhizobia collections

Descriptor	No. of cases	%Total
Originator	1270	84.0
Form received	351	23.2
Collection date	769	50.9
Isolation date	1175	77.7
Rhizobium species	1512	100.0
Geographic origin	1490	98.5
Collection site	1287	85.1
Latitude/Longitude	677	44.8
Altitude	314	20.8
Crop specificity	1500	99.2
Trap species	709	46.7
Evaluation	1021	67.5
Ampules (long-term storage)	409	27.0

The Genetic Resources Unit (GRU) has developed, in collaboration with GP and NRMP staff, an ICARDA *Rhizobium* database which includes both passport and evaluation data. The database is now maintained at GRU and will be updated periodically. Geographic origin of ICARDA rhizobia collections is mostly in WANA countries (Table 66). The best geographical coverage is for *R. meliloti* in WANA countries of Syria, Morocco, Turkey, Jordan and Lebanon. ICARDA staff, in collaboration with NARS, collected 70% of the accs. The rest were received from other organizations. Legume rhizobia are collected as host plant root nodules in collection missions specific for rhizobia, or both nodules and soil samples during legume collection missions. Almost half of the total *Rhizobium* holdings are specific for medics, followed by those for lentil (15.6%) and *Trifolium* (15.3) (see Table 67). Status of passport information is shown in Table 68.

The information available for 14 descriptors varies from 20.8% for altitude to 100% for *Rhizobium* species. The country of origin is known in 98.5% cases. The evaluation data on nitrogen fixation efficiency are available for two thirds of accs. A total of 409 accs. (27.0%) have been lyophilized and long-term stored in ampules at 4°C. Duplicate dry-freezed samples will be held at GRU in the long-term store room at -20°C.

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2. SEED HEALTH ACTIVITIES

Barley stripe is a major seed-borne disease in the WANA region, where its agent pathogen has quarantine significance in many countries. Prior to 1995, the disease had seriously spread in barley plots grown in Tel Hadya experimental station, but for the last few years the disease has been occurring sporadically. For barley seed treatment, ICARDA replaced Vitavax 200 (Carboxin + Thiram) with Vitavax Extra (Carboxin + Imazalil + Thiadendazole), where Imazalil is very effective against *Pyrenophora graminea*. This was done from the 1994-95 season onwards. Ever since, barley stripe has very considerably decreased in treated seed plots. For example, in Block A of the station only 47, 64 and 44 infected plants were inspected and rogued during the 1995, 1996 and 1997 seasons, respectively. This is lower compared to 1,558 infected plants found in 1994.

Furthermore, a total of 9 and 5 plants infected with flag smut (*Urocystis agropyri*) were identified and rogued early in the season of 1995-96 and 1996-97, respectively. During the 2-year period, the Seed Health Laboratory (SHL) has had tested for seed health status of imported and exported seed plots of cereal and food and feed legume crops, and carried out field inspection and roguing of infected plants. The SHL has also conducted and/or participated in training courses, and carried out research subjects.

2.1. Activities on incoming seeds

During the 1995-96 and 1996-97 seasons, 44 and 41 seed consignments were received from 22 and 20 countries, respectively. This is higher compared to 34 consignments handled by the SHL in the previous year (1994-1995). All incoming seeds were immediately either fumigated or treated to temperatures of −18°C for seven days.

2.1.1. Laboratory testing

After visual inspection, several laboratory procedures were used to detect seed-borne pathogens in seeds. During the 1995-96 and 1996-97 seasons, 9,445 and 11,502 seed samples, respectively, were tested for seed-borne pathogens in cereals (Table 69) and food and forage legumes (Table 70). The percentage of samples found contaminated with seed-borne pathogens was only 3.5% and 6.1%, respectively,

compared to 12.1% in 1994-95. The most frequent pathogens, associated with the incoming seed material in both seasons, were *Tilletia caries/T. foetida* in wheat, and *Helminthosporium* spp. and *Fusarium* spp. in barley seed lots. *Ustilago* spp. was detected only in the 1996-97 seed consignments. *T. contravresa* and *Urocystis agropyri* were found in both seasons, whereas *T. indica* was found in the 1995-96 seed samples. The contaminated samples with the latter three quarantine pathogens were destroyed.

In both seasons, imported seeds of lentil were lightly contaminated with *Ascochyta* spp. In addition, *Fusarium* spp. was found in some lentil and faba bean samples. However, most *Lathyrus* seed samples were contaminated with *Fusarium* spp. Chickpea (1995-96) and peas (1995-96 and 1996-97) seed consignments were free from seed-borne pathogens and pests. However, about 9% of seed samples of chickpea were found contaminated with *Fusarium* spp. in the 1996-97 season (Table 70).

2.1.2. Field inspection

All incoming seeds, that were found to be free from quarantine pathogens in the laboratory, were grown for one generation in the post-quarantine area at Tel Hadya for observation. This incoming seed material usually covers approximately 16 ha/season. A single field inspection carried out during the 1995-96 season in this area showed that one plant of bread wheat was found to be infected with flag smut (*U. agropyri*). Whereas in the 1996-97 season exotic pathogens were absent in cereal and legume plots. In addition, very few plants of cereal and legumes were infected with one of the following pathogens: *T. caries/T. foetida*, *Ascochyta rabiei*, *A. fabae*, *Botrytis fabae* and virus – like symptoms. All infected plants were rogued and burned as per normal quarantine regulations.

2.2. Activities on seed dispatch

Seed samples despatch to users is a crucial task of the GRU. During the 1995-96 and 1996-97 seasons, 397 and 410 seed consignments were examined, issued phytosanitary certificates, and dispatched internationally or distributed to cooperators in 75 and 74 countries, respectively.

2.2.1. Laboratory testing

The total number of seed samples tested at the SHL, by the different techniques, decreased from 5,468, in 1995-96 to 4,695 in 1996-97. About 16.6% and 11% were found to be contaminated, respectively. Table 71 shows that *T. caries/T. foetida* (wheat) and *Fusarium* spp. and *Heminthosporium* spp. (barley) were the most common pathogens detected in seed lots of these two crops. In both seasons, some teliospores of *U. agropyri* were detected in few wheat seed samples. Consequently such samples were discarded.

Results from laboratory tests confirm absence of *Ascochyta* spp. and *Pseudomonas pisi* from all tested legume seed samples in both seasons. In the 1995-96 and 1996-97 seasons, *Fusarium* spp. were detected in 31% and 14% of tested seed samples of lentil and in 8.8% and 3.1% in chickpea seed lots, respectively.

2.2.2. Field inspection

During each of the two seasons, field inspections were carried out twice in the legume plots, but only once in the cereal plots. However, a single inspection is not sufficient for efficient detection of infected plants. These will have to be more frequent in the future. Eight and five plants infected with flag smut disease were found during the 1995-96 and 1996-97 seasons, respectively. Certain seed-borne diseases, such as, common bunt of wheat, covered smut of barley, scald of barley, barley stripe disease, loose smut, barley stripe mosaic virus, wilt/root rot of chickpea and lentil, and *Ascochyta* blight of chickpea and faba bean were infrequent in the seed rejuvenation/multiplication fields. *Orobanche* and *Cuscuta* (pest plants) were also detected in some food and forage legume plots. All infected plants were rogued and fully destroyed by burning.

A. El-Ahmed and S. Asaad

Table 69. Seed health tests conducted on cereal seeds newly introduced to ICARDA in the 1995-96[a] and 1996-97[b] seasons

Crop	Number of lines		Tests carried out	Pathogens observed*
	Tested	Found Infected		
Durum wheat	1296[a]/814[b]	92[a]/0[b]	Karnal bunt test or centrifuge wash test	*Tilletia caries* and/or *T. foetida* (92[a]/0[b])
Bread wheat	5659/6524	117/499	Karnal bunt test, Centrifuge wash test	*Tilletia caries* and/or *T. foetida* (63/441), *T. indica* (41/0), *Urocystis agropyri* (2/42); *T. contraversa* (11/1), *Ustilago* spp. (0/15).
Barley	1209/943	69/36	Centrifuge wash test, Freezing blotter test	*Helminthosporium* spp. (22/5), *Fusarium* spp. (44/28). *Urocystis agropyri* (3/1), *Tilletia* spp. (0/2).
Triticale	369/481	0/0	Centrifuge wash test	----
Wild wheat	52/417	11/34	Centrifuge wash test	*Tilletia caries* and/or *T. foetida* (5/5), *Urocystis agropyri* (6/14), *Ustilago* spp. (0/15).
Wild barley	3/50	0/0	Centrifuge wash test	----
Avena	0/14	0/0	Centrifuge wash test	----
Total	**8588/9243**	**289/569**		

* Numbers in parenthesis refer to infested entries.

Table 70. Seed health tests conducted on food and forage legumes newly introduced to ICARDA during the 1995-96[a] and 1996-97[b] seasons

Crop	Number of lines Tested	Found Infected	Tests carried out	Pathogens observed*
Lentil	280[a]/576[b]	36[a]/41[b]	Freezing blotter test	*Fusarium* spp. (31[a]/36[b]) *Ascochyta* spp. (5/5)
Faba bean	203/471	2/27	Freezing blotter test test for stem nematode	*Fusarium* spp. (2/27)
Chickpea	348/538	0/49	Freezing blotter test	*Fusarium* spp. (0/49)
Pea	19/578	0/0	Slide agglutination test	----
Bean	1/0	0/0	Freezing blotter test	----
Vetch	0/9	0/0	Freezing blotter test	----
Medic	3/0	0/0	Freezing blotter test	----
Lathyrus	1/19	1/18	Freezing blotter test	*Fusarium* spp. (1/18)
Fenugreek	1/0	0/0	Freezing blotter test	----
Chickling	1/0	0/0	Freezing blotter test	----
Carthamus	0/38	0/0	Freezing blotter test	----
Total	**857/2259**	**39/135**		

* : Numbers in parenthesis refer to infested entries.

Table 71. Seed health tests conducted on seeds dispatched internationally from ICARDA during the 1995-96[a] and 1996-97[b] seasons

Crop	Number of lines Tested	Found Infected	Tests carried out	Pathogens observed*
Durum wheat	594[a]/478[b]	270[a]/157[b]	Centrifuge wash test	*Tilletia caries* and/or *T. foetida* (270[a]/151[b]), *Urocystis agropyri* (2/6)
Bread wheat	1407/806	414/187	Centrifuge wash test	*Tilletia caries* and/or *T. foetida* (414/184), *Urocystis agropyri* (9/3)
Barley	2679/2365	386/122	Centrifuge wash test Freezing blotter test	*Helminthosporium* spp. (11/8) *Fusarium* spp. (375/114)
Lentil	232/301	72/42	Freezing blotter test	*Fusarium* spp. (72/42)
Chickpea	364/287	32/9	Freezing blotter test	*Fusarium* spp. (32/9)
Faba bean	0/73	0/0	Freezing blotter test	--
Pea	84/156	0/0	Slide agglutination test	--
Lathyrus	45/0	0/0	Freezing blotter test	--
Vetch	63/184	0/0	Freezing blotter test	--
Medic	0/5	0/0	Freezing blotter test	--
Oil seeds	0/40	0/0	Freezing blotter test	--
Total	**5468/4695**	**1174/517**		

* : Numbers in parenthesis refer to infested entries.

3. TRAINING

Training activity received a great boost in 1996 and 1997. Compared to 52 trainees during the two previous years (see GRU Annual Report 1994 and 1995), 122 trainees (an increase of over 100%) attended, in all, 14 training courses conducted by GRU scientists and support staff in the years 1996 and 1997 (Table 72).

3.1. Training in genetic resource conservation

3.1.1. Short courses

ICARDA, IPGRI, GTZ, and IAV Hassan II jointly organized an advanced in-country training course on "Genetic Resources of Grain Legumes" in Rabat, Morocco. The duration of the course was two weeks in February-March 1997. The course was attended by 20 participants representing three North African countries: Algeria, Tunisia and Morocco.

A specialized training course on "Faba Bean Improvement with Emphasis on Host Plant Resistance" was jointly organized by GRU and GP at ICARDA. The two-week course in March-April 1997 was attended by nine participants from six countries.

ICARDA and IPGRI jointly organized a short course on "Conservation and Use of Plant Genetic Resources in Central Asia" in Tashkent, Uzbekistan. Fifteen participants from five Central Asian Republics, viz., Kazakhstan, Kyrgystan, Tadjikistan, Turkmenistan, and Uzbekistan attended this course. The course lasted two weeks in September-October 1997.

Another in-country training course on "Collection and Conservation of Plant Genetic Resources" was conducted in Islamabad, Pakistan. Eighteen participants from the Pakistan attended the two-week course 20-30 October 1997. This training was conducted as a joint activity between ICARDA, CWANA-IPGRI and the Pakistan Agricultural Research Center (PARC).

3.1.2. Individual training

On request from the national agricultural research systems (NARS) in the WANA region, a number of candidates received individual training in various aspects of genetic resources conservation work at the GRU. The training was related to: (i) documentation of germplasm collections, (ii) identification of wild and cultivated species, (iii) use

of electrophoretic techniques in studying variation in germplasm collections, and (iv) seed bank management.

GRU scientists and support staff

3.2. Training in seed health activities

3.2.1. Short courses

Training, in seed health testing and field inspection of national scientists in WANA countries, is becoming an essential need for quarantine and seed certification purposes. The SHL staff conducted two in-country short training courses in Iran, viz., the "General Seed Technology", July 1996, at the Dryland Agricultural Research Institute (DARI) in Marageh and the "Seed Quality Control", June 1997, at the Seed and Plant Improvement Institute (SPII) in Karaj. The objective of the latter course was to train NARS scientists in the basic principals of seed quality control. The course emphasized seed-borne diseases and seed health testing for the purposes of phytosanitary certification and quarantine. The two-week short course covered, through lectures and practical demonstrations, all aspects related to: (i) seed-borne diseases normally encountered, (ii) their identification in the laboratory, (iii) their importance in seed production, (iv) requirements for production of healthy seeds, (v) methodology of field inspections, and (vi) levels of tolerances, and quarantine regulations to be observed during seed receipt and despatch. The 19 Iranian scientists, who participated in the course, came from all over the country. They benefitted from learning, first-hand from experts, the most up-to-date seed health testing techniques in use at ICARDA.

3.2.2. Individual training

During the 1995-96 and 1996-97 seasons, one scientist each from Algeria, Jordan and Syria were individually trained in seed health testing and quarantine procedures for a period of one to four weeks at the SHL. In addition, SHL personnel also covered, through lectures, field demonstrations and laboratory practicals, the seed health component of the long-term residential course and other short courses conducted by crop improvement programs and held by ICARDA at the headquarters. The main features of the above training activities are summarized in Table 72.

A. El-Ahmed and S. Asaad

Table 72. Summary of training courses conducted by GRU staff in Genetic Resources Conservation and Seed Health Testing during 1996 and 1997

Topic of course	Type of training	No. of trainees	Country	Duration
Genetic Resources of Grain Legumes (Morocco)	Short course	7 11 2	Algeria Morocco Tunisia	2 weeks
Faba Bean Improvement - with Emphasis on Host Plant Resistance	Short course	1 3 2 1 1 1	Algeria China Egypt Libya Morocco Syria	2 weeks
Conservation and Use of Plant Genetic Resources in Central Asia (Uzbekistan)	Short course	2 2 1 2 8	Kazakhstan Kyrgystan Tadjikistan Turkmenistan Uzbekistan	2 weeks
Collection and Conservation of Plant Genetic Resources (Pakistan)	Short course	18	Pakistan	2 weeks
General Seed Technology (Iran)	Short course	17	Iran	2 weeks
Seed Quality Control (Iran)	Short course	19	Iran	2 weeks

Table 72 (Cont'd)

Documentation Systems for for Plant Genetic Resources	Individual	1	Iran	2 weeks
		2	Jordan	2 weeks
		2	Iraq	2 weeks
		1	Morocco	2 weeks
		2	Syria	2 weeks
Identification of Forage Legumes	Individual	2	Syria	1 week
Electrophoretic Techniques (Cereals)	Individual	2	Syria	1 week
Seed Bank Management	Individual	2	Syria	1 week
		1	Morocco	2 weeks
Seed Health Testing and Field Inspection	Individual	1	Syria	5 weeks
		1	Algeria	4 weeks
		1	Jordan	2 weeks
Germplasm Cataloging	Individual	1	Morocco	4 weeks
Wild Wheat Evaluation	Individual	1	Syria	1 week
In-situ Conservation	Individual	4	Syria	1 week
TOTAL		**122**		

4. GENETIC RESOURCES RELATED ACTIVITY

4.1. "Origins of Agriculture and the Domestication of Crop Plants in the Near East (*The Harlan Symposium*)"

The Genetic Resources Unit organized an International Symposium on the "Origins of Agriculture and the Domestication of Crop Plants in the Near East". The Symposium was held at ICARDA from 10 to 14 May 1997. Director Generals of two CGIAR Centers honored the inaugural session by their presence; Professor Dr Adel El-Beltagy, ICARDA, Dr Geoffrey Hawtin, the International Plant Genetic Resources Institute (IPGRI).

The symposium was dedicated to Emeritus Professor Jack R. Harlan. Professor Harlan contributed considerably towards our understanding of crop evolution and domestication processes at work in the early years of agriculture in West Asia and North Africa (WANA). Hence, is being referred to as the "*Harlan Symposium*". The symposium recognized Professor Harlan's contribution with an award for his lifelong work in the field of domestication and crop evolution, especially for his research in this region. Unfortunately, despite valiant efforts, Harlan could not attend as the injuries received in a car accident during December 1996 were not fully healed. The plaque, that was presented to him *in absentia,* was in the form of a mosaic depicting an outline map of WANA. The map was made from seeds which were derivatives of the actual accs. that he had himself collected during his explorations in Syria, Lebanon and Turkey nearly 50 years ago (see Damania and Valkoun in *Diversity* 1997).

The GRU-ICARDA; IPGRI's Regional Office for CWANA; Genetic Resources Conservation Program (GRCP), University of California, USA; Institut de Prehistoire Orientale Center National de la Recherche Scientifique (CNRS), France; Department of Antiquities and Museums, Damascus, Syria; Institut Français de Archéologie au Proche Orient (IFAPO), Damascus, Syria; and the Embassy of France, Damascus, Syria, co-sponsored the symposium.

The *Harlan Symposium* was organized so that plant breeders, geneticists, ecologists, and palaeobotanists could, bridge the gap between their respective disciplines, by personal contact and discussion. They could also critically examine the state of the evidence from these different disciplines vis-a-vis crop evolution and domestication. As one participant observed, "in order to learn more

about our future and the direction in which we are heading (as far as food production was concerned) it is perhaps necessary to know as much as we can about our past".

The main objective of the *Harlan Symposium* was to investigate and discuss the various fresh discoveries which have been made and new research results published during the last decade or so. There is mutual realization among pure archaeologists, on one hand, and biological scientists on the other, that each held only a part of the key necessary to unravel the mysteries of the origins of agriculture, domestication of crop plants and the major changes that took place in life styles as a consequence.

The *Harlan Symposium* attracted about 60 Plant Biologists and Archaeologists from 23 countries (Fig. 45). Nearly 30 papers were presented and six posters were exhibited throwing new light on several topics. Professor David R. Harris of the Institute of Archaeology, University College London delivered the keynote address on "Agricultural Origins: Retrospect and Prospects". Professor Harris observed that, when mankind was surviving on hunting and gathering, the human population was increasing very slowly. Therefore, a fundamental question often overlooked: why did the advent of agriculture lead to a rapid growth in human population? It has been deduced from recent anthropological studies of former hunter/gatherers, who have settled down to a sedentary life-style, that there is a direct link between a reduction of mobility and an increase in population. This is mainly because the average birth interval was reduced.

This was the first time that archaeologists, ethnobotanists, and plant scientists came together, in West Asia, to forge a link between the beginnings of agriculture during the Neolithic Age and the current plant breeding efforts. Indeed, the work begun by the early agriculturists in the near eastern arc continued with the conscious selection of superior genotypes by farmers leading to the creation of the landraces with their specific attributes. This genetic diversity has a vital role to play in meeting the challenge of global food supply.

The deliberations of the symposium focussed mainly on the following seven topics. Some of the discussions that took place are summarized below:

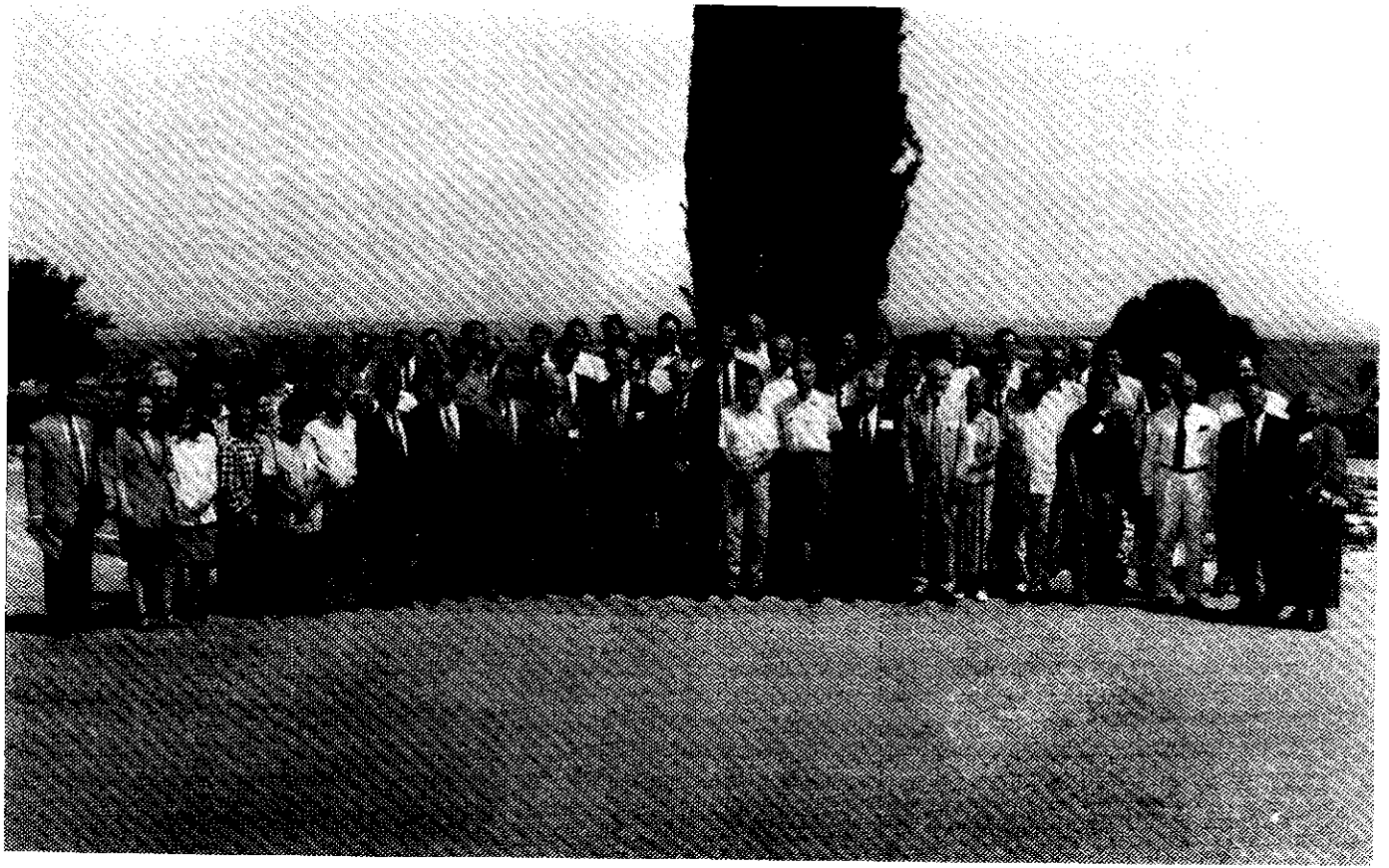

Fig. 45. Participants of the Harlan Symposium at ICARDA 10-14 May, 1997

1. *Climate and vegetation change at the origins of agriculture*: The origins of agriculture coincided with certain changes in climate and vegetation in the Near East. What were these changes and did they favor domestication of grasses? Evidence suggests that supplies of wild grains coupled with aquatic resources were abundant following favorable post-Pleistocene environmental changes around 11000 years before present (BP). These could have led to a population explosion in Southwest Asia. Increasingly sedentary lifestyle may have further accelerated population growth through: (i) closer spacing of births, (ii) a higher rate of infant survival, and (iii) perhaps a lower rate of adult mortality. However, it was observed that hunters (incl. fishermen) and gatherers have survived till today in other parts of the world where agriculture is unrewarding.

2. *Wild progenitors of crop plants*: Evidence of the role of wild progenitors in the domestication of major cereals and legumes from both distribution and cytogenetics aspects was presented. Fresh cytological and electrophoretic evidence presented seems to suggest that there can be alternate theories to the origins of wheat genomes. Wild progenitors play a crucial role in crop evolution even after domestication. As seen in West Asia, cultivated durum wheat (*Triticum durum*) continuously exchanges genes with wild emmer (*T. dicoccoides*) and cultivated barley (*Hordeum vulgare*) with wild barley (*H. spontaneum*); thus infusing the cultivated gene pool with hardy stress-tolerating genes.

Besides the three wild cereals *Triticum baeoticum*, *T. dicoccoides* (wild wheat) and *Hordeum spontaneum* (wild barley), there were other so called "founder crops" which were also domesticated from their wild progenitors in the Fertile Crescent. They are green pea (*Pisum sativum*, domesticated from the wild pea *P. humile*), lentil (*Lens culinaris*, domesticated from *L. orientalis*), bitter vetch (*Vicia ervilia*, from wild forms of *V. ervilia*, and flax (*Linum usitatissimum*, from *L. bienne*). For example, *L. orientalis* is distributed from Greece to Uzbekistan. Its oldest carbonized remains, dating from 13000 BP, were found in the Franchthi cave in Greece. Its domesticated forms were found in aceramic villages from 9000 BP. It is, however, extremely difficult to distinguish between cultivated and wild types among carbonized seeds in food legumes.

3. *Genetic, physiological and morphological aspects of domestication*: Changes in morphology of the wild progenitors, once they are domesticated, were presented. The mechanisms of genetic, morphological and physiological changes that occur due to domestication were discussed. Besides the evolution of a non-brittle rachis, which led to the domestication of wild cereals, there is also the fact that persistent glumes made threshing difficult. At what stage, after domestication, did the cereal spikes develop into free-threshing types so that the grains could be easily obtained? Even today in some of the subsistence farming communities in WANA the most primitive methods of separating grains from chaff is utilized. One such method is the repeated trampling of harvested stems by horses, mules and donkeys. Hence, it is probable that domestication took place in two stages. First, the selection for a non-brittle rachis, followed by selection for plants with free-threshing grains from spikelets. In fact, the two most ancient forms of cultivated wheats, einkorn (*Triticum monococcum*) and emmer (*T. dicoccum*), have persistent glumes on their grains. Their flour and dough properties are very different from those of macaroni wheat (*T. durum*) and bread wheat (*T. aestivum*) which evolved several centuries later.

4. *Palaeobotanical evidence for agricultural transitions*: Excavations, in recent years, have produced important new evidence for plant use in the past, at both pre-agrarian hunter-gatherer sites and early farming settlements. They also reveal glimpses of the cultural practices of these earliest settlers in the Fertile Crescent. Tools used by early cultivators to harvest domesticated cereals were discussed. Wooden handles were studded with sharp stones or bones to give them the sharpness needed to cut cereal stems. Studies carried out in Spain showed how early farmers may have harvested their crops with the primitive tools at their disposal. Problems in identifying carbonized remains of early domestication persist. For example, in lentils, it is extremely difficult to know, from examining carbonized seeds, as to whether they belonged to the wild species or the domesticated ones. Does the presence of crop plant remains indicate an agricultural community? Or were other aspects of the economy which were not well preserved and hence not taken into consideration? The symposium heard evidence from Turkey which

suggested that there were over 42 leafy plants which are consumed even today, by gathering them from the wild. Since these plants do not leave behind carbonized evidence, as do cereals and most legumes, their role in the food supply of early settlers in the Fertile Crescent has been ignored.

5. *The archaeology and explanations for the origin of agriculture*: Information available regarding the chronology and distribution of the early farming villages and the implements used in the Near East were discussed. Participants observed that while a great deal was known about the southern arc, and the mid section of the Fertile Crescent. However, little recent information about the north eastern arc, which transgressed into south eastern Turkey and north eastern Iraq and western Iran, was available. This was perhaps due to the politically disturbed situation prevailing in that region after the second world war. Early agriculture must be seen in its cultural framework. What information is available regarding the chronology and distribution of the early farming villages in the Near East? How well do the current theories of agricultural origins match with palaeobotanical evidence? Can cultural changes be identified in parallel with changes in subsistence farming? These were some of the other topics discussed.

But why did agriculture first develop in the Fertile Crescent? Not because its inhabitants figured out how it was done before anyone else, but because the region had several wild plant and animal species that were ready for domestication. It has been recently concluded that history unfolded differently for different sets of people because of differences among people's environment, and not because of any biological differences among the peoples themselves.

6. *Spread of crops from the Near East to other parts of the world*: Once domesticated, crops diffused from their nuclear area in the western part of the Fertile Crescent to other parts of the world was related to migrations and cultural diffusion along trade routes and colonial conquests. This spread of agriculture correlates also to a certain extent with the spread of languages. Crops radiated eastwards to the Indus Valley and from there to the Indian sub-continent. Buddhist travelling monks also helped germplasm exchange between India and China and later Japan. One of the reasons why domesticated crop plants spread rapidly from the nuclear area was that, they were

already well adapted to the climates of the regions to which they were spreading. From the Mediterranean basin crops entered Europe and from there colonists introduced them into the New World. In the south they spread as far as Ethiopia but could not go further due to the unsuitable tropical climate of Central Africa. By 2000 BP cereals of Near Eastern origin were growing over a 10,000 mile expanse, from the Atlantic Coast of Ireland to the Pacific Coast of Japan.

7. *In situ conservation of wild relatives of crop plants in relation to their history*: Palaeobotanical information can assist in the conservation of the wild relatives of crop plants in their natural habitats. What would be the areas deserving this type of conservation such that the wild relatives continue to evolve in relation to environmental changes brought about by global warming or the "greenhouse" effect? Efforts at conserving *in situ* wild progenitors of wheat and barley, viz., *Triticum baeoticum* (wild einkorn), *T. dicoccoides* (wild emmer) and *Hordeum spontaneum* (wild barley) and their domesticates are underway at a few sites in the western part of the Near East arc, the center of diversity for these ancient and very important world crops.

One of the highlights of the Symposium was the participants' visit to some of the archaeological sites: Tell Halula (*ca.* 8000 BP) studied by a team from Spain, D'jade (on the banks of the middle Euphrates river, *ca.* 10,000 BP) studied by a team from France, and Tell Banat (a Bronze Age site complete with an underground royal tomb) studied by an Australian team.

Recent palaeobotanical finds at Tell Halula and D'jade in Syria indicate that morphologically wild plants were harvested for a long period before their domestication into cultivated forms. And surprisingly, they continued to be grown even after domestication, with harvest taking place while the plants were still green and the grains in the milky stage of development. This was done to preclude the shattering of the ears at maturity due to dryness of a brittle rachis; hence, loss of grains which fall on the ground, eaten by ruminants, or blown away by wind.

GRU-ICARDA organized visits to fields, in the vicinity of Azaz, near Aleppo, where *in situ* conservation of wild progenitors of cereals and legumes is being practiced.The participants also appreciated visit

to the San Simeon citadel and its environs, where several wild progenitors also abound in their natural habitats during that time of the year.

The *Harlan Symposium* ended with several open discussion sessions where participants were encouraged to fully air their views and observations. A "*Book of Abstracts*" of the papers presented at the symposium was compiled and edited by A.B. Damania and J. Valkoun and published by ICARDA in 1997. The conclusions and recommendations emanating from the symposium can be found in the Book of Abstracts.

The full proceedings volume under the title "*Origins of Agriculture and Crop Domestication - The Harlan Symposium*" was published by ICARDA at the end of December 1998. This publication was co-sponsored by ICARDA/IPGRI/GRCP/FAO. Copies and further details regarding the above two publications can be obtained from the Head, Communication, Documentation and Information Services (CODIS) at ICARDA.

J. Valkoun, A.B. Damania (GRU-ICARDA), G. Willcox (IPO, CNRS, France), C.O. Qualset (GRCP-UC, USA), Y. Adham, A. Bari (IPGRI-CWANA) and GRU staff

5. PUBLICATIONS

5.1. Books

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6. GRU STAFF LIST (as at December 1997)

Jan Valkoun	Unit Head
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Dr Larry D. Robertson	Legume Germplasm Curator
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Mr Ali Abdullah Ismail	Research Assistant III
Mr Ali Shehadeh	Research Assistant III
Mr Munzer Kabakebji**	Research Assistant II
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Ms Jankieh Sumaia**	Data Assistant
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*** Joined during 1997

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We would also like to acknowledge the assistance of the staff of Communications, Documentation and Information Services (CODIS) at ICARDA, and particularly the Art Unit who, once again, did an excellent job creating a very readable Annual Report.

Table A1. Monthly precipitation (mm) during the 1995-96 season at Tel Hadya

	Sep.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Total
1995-96 season	0.0	10.3	68.3	35.5	73.7	44.6	137.0	32.2	2.9	0.0	0.0	0.0	404.5
Long term aver. (18 seasons)	0.5	24.0	51.0	51.3	63.4	56.2	44.7	25.9	15.8	2.5	0.0	0.8	336.1
%of long term average	0	43	134	69	116	79	306	124	18	0	-	0	120

Table A2. Monthly air temperature (°C) during the 1995-96 season at Tel Hadya

	Sep.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May.	Jun.	Jul.	Aug.
Mean maximum	34.3	28.3	17.2	12.4	11.2	14.4	15.8	20.6	32.2	35.6	39.1	38.3
Mean minimum	18.0	10.5	4.6	2.0	3.3	4.3	6.6	6.7	12.3	17.6	21.8	21.2
Average	26.2	19.4	10.9	7.2	7.2	9.3	11.2	13.6	22.2	26.6	30.5	29.7
Absolute maximum	41.2	33.8	25.2	17.9	15.6	19.4	20.7	29.4	27.5	42.0	43.0	41.0
Absolute minimum	8.1	5.0	-4.4	-5.5	-2.6	-6.6	0.9	1.7	4.8	12.3	17.3	17.6

Table A3. Frost events during the 1995-96 season at Tel Hadya

	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Season
Number of frost days	8	10	6	4	0	0	0	28
Absolute minimum (°C)	-4.4	-5.5	-2.6	-6.6	-	-	-	-6.6
No. of frost events at 5 cm above ground	10	12	9	7	0	0	0	38
Absolute minimum (°) at 5 cm above ground	-5.5	-4.5	-3.7	-7.2	-	-	-	-7.2

Table A4. Monthly precipitation (mm) during the 1996-97 season at Tel Hadya

	Sep.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.	Total
1996-97 season	22.9	35.3	17.4	92.5	46.84	24.85	76.3	111.7	6.0	0.0	0.0	0.0	433.7
Long term aver. (19 seasons)	3.0	21.5	51.0	52.2	59.48	59.13	46.4	30.8	14.9	2.4	0.0	7.0	347.7
%of long term average	763	164	34	177	79	42	164	363	40	0	-	0	125

Table A5. Monthly air temperature (°C) during the 1996-97 season at Tel Hadya

	Sep.	Oct.	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Jun.	Jul.	Aug.
Mean maximum	33.1	26.1	20.1	15.2	12.0	12.9	15.3	20.0	31.9	34.8	36.8	34.5
Mean minimum	17.1	11.0	7.1	7.3	2.6	-1.0	2.2	6.3	11.6	17.7	21.4	21.4
Average	25.1	18.6	13.6	11.3	7.3	6.0	8.8	13.2	21.8	26.3	29.1	28.0
Absolute maximum	38.5	33.0	25.0	19.6	17.3	19.6	20.2	31.2	37.6	41.1	40.2	37.4
Absolute minimum	11.6	3.8	-2.9	4.1	-7.1	-8.3	-5.2	-3.2	6.6	10.2	16.2	17.0

Table A6. Frost events during the 1996-97 season at Tel Hadya

	Nov.	Dec.	Jan.	Feb.	Mar.	Apr.	May	Season
Number of frost days	4	11	17	10	3	-	-	45
Absolute minimum (°C)	-2.9	-7.1	-8.3	-5.2	-3.2	-	-	-8.3
No. of frost events at 5 cm above ground	6	11	16	11	4	-	-	48
Absolute minimum (°) at 5 cm above ground	-5.1	-7.9	-9.1	-6.5	-4.8	0	-	-9.1

Table A7. Status of ICARDA collections by origin (December 1997)

	Cereals	Food legumes	Forage legumes	Total
WANA	**37418**	**17387**	**20945**	**75750**
Afghanistan	540	1254	320	2114
Algeria	1756	166	1695	3617
Armenia	97	13	37	147
Azerbaijan	259	27	38	324
Bahrain	-	-	2	2
Cyprus	165	435	406	1006
Egypt	501	376	180	1057
Eritrea	12	-	-	12
Ethiopia	9802	1741	808	12351
Iran	1808	2690	693	5191
Iraq	506	235	277	1018
Jordan	1325	608	2058	3991
Kazakhstan	89	3	21	113
Kyrgystan	20	4	8	32
Lebanon	386	265	284	935
Libya	254	17	249	520
Morocco	1334	1240	2416	4990
Oman	113	4	105	222
Pakistan	1066	608	226	1900
Palestine	1048	83	127	1258
Saudi Arabia	35	3	8	46
Syria	2045	4259	5615	11919
Tadjikistan	58	29	89	176
Tunisia	2343	381	1550	4274
Turkey	5429	2010	3599	11038
Turkmenistan	198	3	45	246
United Arab Emirates	4	-	-	4
Uzbekistan	133	31	73	237
Yemen	193	100	16	309
ICARDA lines	5899	802	-	6701
EUROPE	**8794**	**3703**	**5988**	**18485**
Albania	32	2	19	53
Austria	311	3	2	316
Belarus	5	1	1	7
Belgium	10	3	25	38
Bulgaria	268	259	88	615
Croatia	3	-	1	4
Czechoslovakia	164	63	116	343
Denmark	43	-	23	66
Estonia	3	-	1	4
Finland	29	-	23	52
France	206	64	238	508
Georgia	172	4	38	214
Germany	586	185	473	1244
Greece	1300	208	612	2120
Hungary	201	56	366	623

Ireland	1	-	-	1
Italy	416	217	1136	1769
Latvia	3	3	4	10
Lithuania	3	4	6	13
Malta	5	-	26	31
Moldova	17	10	3	30
Netherlands	41	41	124	206
Norway	6	1	3	10
Poland	141	74	86	301
Portugal	811	259	266	1336
Romania	84	52	37	173
Russian Federation	1194	102	125	1421
Slovakia	-	-	1	1
Slovenia	1	1	-	2
Soviet Union	323	114	481	918
Spain	432	1593	824	2849
Sweden	77	17	420	514
Switzerland	787	8	7	802
Ukraine	448	75	32	555
United Kingdom	158	191	316	665
Yugoslavia	513	93	56	662
Europe	-	-	9	9
ASIA	**5026**	**3588**	**1844**	**10458**
Bangladesh	-	116	1127	1243
Bhutan	29	-	-	29
China	3147	672	90	3909
India	665	2267	262	3194
Indonesia	-	2	-	2
Japan	448	18	49	515
Korea	195	-	-	195
Maldives	-	-	-	-
Mayanmar	1	-	-	1
Mongolia	34	-	10	44
Nepal	507	507	305	1319
Sri Lanka	-	6	-	6
Thailand	-	-	1	1
AFRICA	**228**	**180**	**67**	**475**
Central African Republic	2	-	-	2
Gabon	-	-	1	1
Kenya	24	-	11	35
Malawi	-	3	-	3
Nigeria	-	1	5	6
Rwanda	2	-	-	2
Senegal	-	-	3	3
Somalia	-	1	-	1
South Africa	178	3	7	188
Sudan	8	172	31	211
Swaziland	-	-	4	4
Tanzania	2	-	-	2
Uganda	-	-	4	4
Zaire	-	-	1	1
Zimbabwe	12	-	-	12

AMERICA	**3995**	**2084**	**911**	**6990**
Argentina	79	16	5	100
Bolivia	27	2	15	44
Brazil	35	3	6	44
Canada	326	307	85	718
Chile	57	695	30	782
Colombia	577	147	2	726
Costa Rica	-	2	1	3
Ecuador	64	449	36	549
Guatemala	4	2	1	7
Mexico	113	183	4	300
Netherlands Antilles	-	-	3	3
Paraguay	2	-	1	3
Peru	123	102	8	233
USA	2566	172	700	3438
Uruguay	15	4	12	31
Venezuela	7	-	2	9
OCEANIA	**154**	**50**	**269**	**473**
Australia	153	49	250	452
New Zealand	1	1	19	21
Unknown	728	1539	910	3177
TOTAL	**56343**	**28531**	**30934**	**115808**

Table A8. Status of cereals collections by origin (December 1997)

Origin	Barley	Wild Barley	Durum Wheat	Bread Wheat	Wild Wheat	Other Cult. Wheat	*Aeg*	Total
WANA	**10461**	**1613**	**14054**	**7199**	**1411**	**222**	**2458**	**37418**
Afghanistan	285	7	235	5	-	1	7	540
Algeria	127	12	1085	459	-	2	71	1756
Armenia	26	-	5	6	11	6	43	97
Azerbaijan	75	2	109	20	4	1	48	259
Cyprus	7	4	102	1	-	-	51	165
Egypt	197	8	216	60	-	-	20	501
Eritrea	8	-	1	3	-	-	-	12
Ethiopia	2691	-	4966	2119	-	26	-	9802
Iran	428	76	790	96	78	28	312	1808
Iraq	173	21	135	132	10	-	35	506
Jordan	144	146	279	20	522	1	213	1325
Kazakhstan	18	2	29	25	-	-	15	89
Kyrgystan	15	-	3	2	-	-	-	20
Lebanon	16	25	65	27	49	-	204	386
Libya	204	11	6	1	-	-	32	254
Morocco	743	11	256	260	-	2	62	1334
Oman	44	-	-	60	-	9	-	113
Pakistan	249	3	19	744	-	2	49	1066
Palestine	2	926	50	-	45	2	23	1048
Saudi Arabia	16	-	13	6	-	-	-	35

Syria	443	263	404	90	343	9	493	2045
Tadjikistan	19	4	2	18	-	-	15	58
Tunisia	601	-	1348	385	-	-	9	2343
Turkey	1390	51	1892	993	349	131	623	5429
Turkmenistan	71	31	9	10	-	-	77	198
United Arab Emirates	4	-	-	-	-	-	-	4
Uzbekistan	23	10	18	24	-	2	56	133
Yemen	106	-	58	29	-	-	-	193
ICARDA lines	2336	-	1959	1604	-	-	-	5899
EUROPE	**4211**	**24**	**3395**	**386**	**19**	**133**	**626**	**8794**
Albania	28	-	3	-	-	1	-	32
Austria	238	-	50	18	-	5	-	3112
Belarus	4	-	1	-	-	-	-	5
Belgium	6	-	2	1	-	1	-	10
Bulgaria	38	-	80	1	8	7	134	268
Croatia	1	-	2	-	-	-	-	3
Czechoslovakia	97	-	11	40	-	16	-	164
Denmark	43	-	-	-	-	-	-	43
Estonia	2	-	-	1	-	-	-	3
Finland	29	-	-	-	-	-	-	29
France	72	-	122	12	-	-	-	206
Georgia	106	-	55	1	-	8	2	172
Germany	493	-	58	21	-	14	-	586
Greece	339	-	708	4	1	3	245	1300
Hungary	83	2	62	52	-	2	-	201
Ireland	1	-	-	-	-	-	-	1
Italy	29	-	363	3	-	21	-	416
Latvia	2	-	-	1	-	-	-	3
Lithuania	3	-	-	-	-	-	-	3
Malta	-	-	5	-	-	-	-	5
Moldova	2	-	2	13	-	-	-	17
Netherlands	37	1	-	3	-	-	-	41
Norway	6	-	-	-	-	-	-	6
Poland	116	-	25	-	-	-	-	141
Portugal	18	-	671	17	-	1	104	811
Romania	36	-	40	6	-	2	-	84
Russian Federation	410	5	519	101	3	17	139	1194
Slovenia	-	-	-	-	-	1	-	1
Soviet Union	93	14	187	15	7	5	2	323
Spain	230	2	194	3	-	3	-	432
Sweden	68	-	-	9	-	-	-	77
Switzerland	689	-	91	-	-	7	-	787
Ukraine	330	-	73	44	-	1	-	448
United Kingdom	140	-	13	4	-	1	-	158
Yugoslavia	422	-	58	16	-	17	-	513
ASIA	**4484**	**52**	**209**	**252**	**-**	**7**	**22**	**5026**
Bhutan	29	-	-	-	-	-	-	29
China	3039	47	33	6	-	2	20	3147
India	432	-	161	67	-	4	1	665
Japan	262	5	11	168	-	1	1	448
Korea	195	-	-	-	-	-	-	195

Mayanmar	-	-	-	1	-	-	-	1
Mongolia	34	-	-	-	-	-	-	34
Nepal	493	-	4	10	-	-	-	507
AFRICA	**158**	**-**	**66**	**4**	**-**	**-**	**-**	**228**
Central African Republic	1	-	1	-	-	-	-	2
Kenya	-	-	22	2	-	-	-	24
Rwanda	-	-	2	-	-	-	-	2
South Africa	146	-	30	2	-	-	-	178
Sudan	8	-	-	-	-	-	-	8
Tanzania	-	-	2	-	-	-	-	2
Zimbabwe	3	-	9	-	-	-	-	12
AMERICA	**3241**	**21**	**699**	**33**	**-**	**1**	**-**	**3995**
Argentina	16	13	49	1	-	-	-	79
Bolivia	23	1	3	-	-	-	-	27
Brazil	3	-	32	-	-	-	-	35
Canada	182	-	141	3	-	-	-	326
Chile	9	-	48	-	-	-	-	57
Colombia	569	-	8	-	-	-	-	577
Ecuador	60	-	4	-	-	-	-	64
Guatemala	2	-	2	-	-	-	-	4
Mexico	18	1	93	1	-	-	-	113
Paraguay	2	-	-	-	-	-	-	2
Peru	101	-	21	1	-	-	-	123
USA	2244	6	288	27	-	1	-	2566
Uruguay	5	-	10	-	-	-	-	15
Venezuela	7	-	-	-	-	-	-	7
OCEANIA	**85**	**-**	**64**	**5**	**-**	**-**	**-**	**154**
Australia	85	-	63	5	-	-	-	153
New Zealand	-	-	1	-	-	-	-	1
Unknown	283	27	230	27	21	115	25	728
TOTAL	**22923**	**1737**	**18717**	**7906**	**1451**	**478**	**3131**	**56343**

Table A9. Status of food legumes collections by origin (December 1997)

	Lentil	Wild Lens	Chick pea	Wild Cicer	Faba Bean	Faba BPL	Total
WANA	**4313**	**417**	**7648**	**262**	**2558**	**2189**	**17387**
Afghanistan	142	-	891	14	96	111	1254
Algeria	35	-	49	-	41	41	166
Armenia	9	-	4	-	-	-	13
Azerbaijan	5	-	22	-	-	-	27
Cyprus	28	4	46	-	106	251	435
Egypt	99	-	57	-	93	127	376
Ethiopia	406	2	120	8	522	683	1741
Iran	912	7	1737	-	16	18	2690

Iraq	26	1	32	-	62	114	235
Jordan	390	12	143	8	22	33	608
Kazakhstan	-	-	3	-	-	-	3
Kyrgystan	-	-	4	-	-	-	4
Lebanon	76	19	28	18	36	88	265
Libya	2	1	2	-	12	-	17
Morocco	92	-	225	-	741	182	1240
Oman	-	-	-	-	4	-	4
Pakistan	268	-	256	-	34	50	608
Palestine	2	9	40	17	5	10	83
Saudi Arabia	3	-	-	-	-	-	3
Syria	1246	184	2095	42	516	176	4259
Tadjikistan	7	5	16	-	-	1	29
Tunisia	22	-	264	-	30	65	381
Turkey	412	159	864	154	209	212	2010
Turkmenistan	1	2	-	-	-	-	3
Uzbekistan	1	12	17	1	-	-	31
Yemen	60	-	-	-	13	27	100
ICARDA lines	69	-	733	-	-	-	802
EUROPE	**605**	**46**	**849**	**-**	**952**	**1251**	**3703**
Albania	2	-	-	-	-	-	2
Austria	-	-	-	-	1	2	3
Belarus	1	-	-	-	-	-	1
Belgium	2	-	-	-	1	-	3
Bulgaria	49	-	194	-	14	2	259
Czechoslovakia	23	-	10	-	30	-	63
France	11	5	18	-	15	15	64
Georgia	-	-	3	-	-	1	4
Germany	36	-	1	-	83	65	185
Greece	107	-	18	-	29	54	208
Hungary	27	-	2	-	15	12	56
Italy	13	6	68	-	57	73	217
Latvia	-	-	-	-	2	1	3
Lithuania	-	-	-	-	1	3	4
Moldova	-	-	9	-	1	-	10
Netherlands	1	-	-	-	30	10	41
Norway	1	-	-	-	-	-	1
Poland	11	-	-	-	42	21	74
Portugal	14	-	121	-	109	15	259
Romania	3	-	2	-	33	14	52
Russian Federation	45	-	44	-	9	4	102
Slovenia	-	1	-	-	-	-	1
Soviet Union	36	1	36	-	21	20	114
Spain	179	11	284	-	337	782	1593
Sweden	-	-	-	-	6	11	17
Switzerland	-	-	-	-	2	6	8
Ukraine	18	4	25	-	16	12	75
United Kingdom	1	-	8	-	84	98	191
Yugoslavia	25	18	6	-	14	30	93
ASIA	**2335**	**-**	**425**	**1**	**457**	**370**	**3588**
Bangladesh	80	-	1	-	35	-	116

China	3	-	21	-	306	342	672
India	1850	-	397	-	10	10	2267
Indonesia	-	-	-	-	1	1	2
Japan	-	-	-	-	6	12	18
Nepal	402	-	6	1	97	1	507
Sri Lanka	-	-	-	-	2	4	6
AFRICA	3	-	15	-	115	47	180
Malawi	-	-	3	-	-	-	3
Nigeria	-	-	1	-	-	-	1
Somalia	1	-	-	-	-	-	1
South Africa	-	-	-	-	-	3	3
Sudan	2	-	11	-	115	44	172
AMERICA	**467**	**-**	**591**	**-**	**606**	**420**	**2084**
Argentina	11	-	-	-	1	4	16
Bolivia	-	-	-	-	-	2	2
Brazil	3	-	-	-	-	-	3
Canada	4	-	-	-	294	9	307
Chile	349	-	346	-	-	-	695
Colombia	8	-	1	-	43	95	147
Costa Rica	2	-	-	-	-	-	2
Ecuador	6	-	2	-	205	236	449
Guatemala	2	-	-	-	-	-	2
Mexico	45	-	117	-	7	14	183
Peru	2	-	4	-	49	47	102
USA	34	-	121	-	6	11	172
Uruguay	1	-	-	-	1	2	4
OCEANIA	**3**	**-**	**4**	**-**	**14**	**29**	**50**
Australia	2	-	4	-	14	29	49
New Zealand	1	-	-	-	-	-	1
Unknown	33	-	230	1	328	947	1539
TOTAL	**7759**	**463**	**9762**	**264**	**5030**	**5253**	**28531**

Table A10. Status of forage collections by origin (December 1997)

Origin	Medics	Vicia	Pisum	Lath	Trif	Alfa	Other forage	Total
WANA	**6427**	**3875**	**1129**	**1566**	**3723**	**322**	**3884**	**20945**
Afghanistan	15	25	148	20	82	24	6	320
Algeria	761	221	21	33	275	2	382	1695
Armenia	-	23	1	5	-	1	7	37
Azerbaijan	2	20	-	13	1	-	2	38
Bahrain	-	-	-	-	-	2	-	2
Cyprus	245	97	6	44	12	-	-	406
Egypt	54	15	6	2	22	10	71	180
Ethiopia	52	1	482	180	7	-	86	808

Iran	277	50	6	22	128	36	174	693
Iraq	147	16	3	10	77	5	18	277
Jordan	662	101	22	33	547	-	693	2058
Kazakhstan	-	-	20	-	-	-	1	21
Kyrgystan	-	-	8	-	-	-	-	8
Lebanon	217	42	2	-	3	17	3	284
Libya	247	1	1	-	-	-	-	249
Morocco	633	513	43	152	345	-	729	2416
Oman	-	-	-	-	-	84	21	105
Pakistan	15	38	20	91	43	2	17	226
Palestine	41	9	4	3	58	11	1	127
Saudi Arabia	-	1	-	-	-	7	-	8
Syria	1757	1013	86	519	1289	28	922	5615
Tadjikistan	1	36	40	8	1	-	3	89
Tunisia	586	108	6	39	230	1	580	1550
Turkey	709	1486	180	370	602	77	165	3599
Turkmenistan	5	21	2	10	-	-	3	45
Uzbekistan	1	38	21	12	1	-	-	73
Yemen	-	-	1	-	-	15	-	16
EUROPE	**985**	**1495**	**1763**	**232**	**623**	**198**	**559**	**5988**
Albania	-	12	7	-	-	-	-	19
Austria	-	1	1	-	-	-	-	2
Belarus	-	-	1	-	-	-	-	1
Belgium	1	18	2	-	2	1	1	25
Bulgaria	1	56	4	14	-	8	5	88
Croatia	-	-	-	-	-	1	-	1
Czechoslovakia	15	22	12	11	3	1	52	116
Denmark	2	2	14	1	2	-	2	23
Estonia	-	-	1	-	-	-	-	1
Finland	-	2	21	-	-	-	-	23
France	46	63	86	3	19	16	5	238
Georgia	1	17	9	10	-	-	1	38
Germany	6	91	251	13	6	4	10	473
Greece	192	128	81	110	95	5	1	612
Hungary	10	121	162	5	1	23	15	366
Italy	329	691	57	3	32	10	14	1136
Latvia	-	2	2	-	-	-	-	4
Lithuania	1	3	2	-	-	-	-	6
Malta	8	18	-	-	-	-	-	26
Moldova	-	-	-	1	-	-	2	3
Netherlands	-	2	120	-	-	-	2	124
Norway	-	-	1	-	-	-	2	3
Poland	1	16	53	1	1	8	6	86
Portugal	99	71	35	26	27	5	3	266
Romania	4	3	3	-	9	6	12	37
Russian Federation	5	34	43	6	18	4	5	125
Slovakia	-	-	-	1	-	-	-	1
Soviet Union	18	27	52	5	8	82	289	481
Spain	228	60	21	13	380	14	108	824
Sweden	2	13	401	1	-	2	1	420
Switzerland	2	-	-	1	1	-	3	7
Ukraine	-	11	12	5	2	-	2	32
United Kingdom	2	2	297	1	1	2	11	316

Yugoslavia	12	9	3	1	16	6	7	56
Europe	-	-	9	-	-	-	-	9
ASIA	**33**	**100**	**442**	**1215**	**28**	**11**	**15**	**1844**
Bangladesh	-	2	10	1115	-	-	-	1127
China	1	-	87	-	-	1	1	90
India	1	1	215	10	28	7	-	262
Japan	-	41	8	-	-	-	-	49
Mongolia	-	4	4	-	-	2	-	10
Nepal	31	52	117	90	-	1	14	305
Thailand	-	-	1	-	-	-	-	1
AFRICA	**1**	**2**	**34**	**-**	**18**	**7**	**5**	**67**
Gabon	-	1	-	-	-	-	-	1
Kenya	1	-	1	-	9	-	-	11
Nigeria	-	-	5	-	-	-	-	5
Senegal	-	-	3	-	-	-	-	3
South Africa	-	1	1	-	4	-	1	7
Sudan	-	-	19	-	5	7	-	31
Swaziland	-	-	-	-	-	-	4	4
Uganda	-	-	4	-	-	-	-	4
Zaire	-	-	1	-	-	-	-	1
AMERICA	**53**	**24**	**307**	**9**	**47**	**54**	**24**	**911**
Argentina	-	-	3	-	-	2	-	5
Bolivia	2	-	13	-	-	-	-	15
Brazil	3	-	1	-	2	-	-	6
Canada	2	5	30	5	-	30	13	85
Chile	20	-	9	-	1	-	-	30
Colombia	-	-	2	-	-	-	-	2
Costa Rica	-	-	1	-	-	-	-	1
Ecuador	1	9	24	2	-	-	-	36
Guatemala	-	-	1	-	-	-	-	1
Mexico	-	-	2	-	-	-	1	4
Netherlands Antilles	-	-	3	-	-	-	-	3
Paraguay	-	1	-	-	-	-	-	1
Peru	4	-	3	-	-	1	-	8
USA	12	9	213	1	43	20	10	700
Uruguay	9	-	-	1	1	1	-	12
Venezuela	-	-	2	-	-	-	-	2
OCEANIA	**106**	**34**	**27**	**10**	**79**	**8**	**5**	**269**
Australia	106	34	11	10	77	7	5	250
New Zealand	-	-	16	-	2	1	-	19
Unknown	148	28	569	7	68	51	39	910
TOTAL	**7753**	**5558**	**4271**	**3039**	**4586**	**651**	**4531**	**30934**

Table A11. Durum wheat collecting missions from 1983 to 1994

Country code	Mission code	Organizations cooperating	Samples collected
DZA	DZA89	ICARDA/ITGC/NARC-J	47
DZA	DZA90	ICARDA/ITGC	6
IRN	IRN93-1	ICARDA/SPII	2
IRN	IRN93-2	ICARDA/SPII	3
JOR	JOR88-1	ICARDA/JUST	1
JOR	JOR88-2	ICARDA/JUST	1
JOR	JOR91	ICARDA/NCARTT	7
JOR	TFREM31	ICARDA/IBPGR/ARCD	2
LBN	LBN93	ICARDA/ARI	5
LBY	LBY90	ICARDA/ARC	4
MAR	MAR84	ICARDA/IBPGR/GIBARI/INRA-M	6
MAR	MAR87-1	ICARDA/INRA-M/NARC-J	50
MAR	MAR90	ICARDA/INRA-M	6
SYR	SYR83-3	ICARDA	88
SYR	SYR87-1	ICARDA/ARCD	154
SYR	SYR88-1	ICARDA/ARCD	2
SYR	SYR88-2	ICARDA/ARCD	37
SYR	SYR88-4	ICARDA/ARCD	1
SYR	SYR89-4	ICARDA/ARCD	1
SYR	SYR90-1	ICARDA/VIR/ARCD	6
SYR	SYR90-2	ICARDA/VIR/ARCD	2
SYR	SYR92-3	ICARDA/ARCD	2
SYR	SYR93-1	ICARDA/ARC	1
SYR	SYR93-3	ICARDA/UKOY	1
SYR	TFREM31	ICARDA/IBPGR/ARCD	1
TUR	TUR89-1	ICARDA/PGRRI	2
TOTAL			**438**

Table A12. "Other cultivated wheats" collecting missions from 1983 to 1994

Country code	Mission code	Organizations cooperating	Samples collected
BGR	BGR89	ICARDA/IHAR/IIPGR	4
IRN	IRN93-1	ICARDA/SPII	1
IRN	IRN93-2	ICARDA/SPII	6
PAK	PAK86-2	ICARDA/PARC	3
RUS	SUN90	ICARDA/VIR	6
SYR	SYR87-1	ICARDA/ARCD	1
SYR	SYR88-2	ICARDA/ARCD	1
SYR	SYR92-3	ICARDA/ARCD	1
SYR	SYR94-3	ICARDA/ARCD	1
UZB	SUN91	ICARDA/VIR	2
TOTAL			**26**

Table A13. Wild *Triticum* collecting missions from 1983 to 1997

Country code	Mission code	Organizations cooperating	Samples collected
ARM	ARM92	ICARDA/AAI	7
BGR	BGR89	ICARDA/IHAR/IIPGR	4
BGR	BGR90	ICARDA/IIPGR/VIR	4
IRN	IRN93-1	ICARDA/SPII	1
IRN	IRN93-2	ICARDA/SPII	4
IRQ	IRQ93	ICARDA/ARCB	1
JOR	JOR85	ICARDA/USKW/JUST	162
JOR	JOR88-1	ICARDA/JUST	6
JOR	JOR88-2	ICARDA/JUST	6
JOR	JOR92	ICARDA/JUST/NCARTT	19
JOR	JOR95	ICARDA/NCARTT	63
LBN	LBN93	ICARDA/ARI	25
LBN	LBN94-1	ICARDA/ARI/UCR	17
SYR	ICARDA		1
SYR	SYR87-1	ICARDA/ARCD	2
SYR	SYR88-1	ICARDA/ARCD	11
SYR	SYR88-3	ICARDA/ICRISAT/ARCD	4
SYR	SYR88-4	ICARDA/ARCD	1
SYR	SYR91-3	ICARDA	23
SYR	SYR92-1	ICARDA	7
SYR	SYR92-2	ICARDA/ARCD	4
SYR	SYR92-3	ICARDA/ARCD	33
SYR	SYR92-4	ICARDA/AAI/ARCD	11
SYR	SYR93-1	ICARDA/ARC	9
SYR	SYR93-2	ICARDA	6
SYR	SYR93-3	ICARDA/UKOY	3
SYR	SYR94-2	ICARDA	6
SYR	SYR94-3	ICARDA/ARCD	10
SYR	SYR97-1	ICARDA/ARCD	15
SYR	TFREM31	ICARDA/IBPGR/ARCD	23
TUR	TUR89-1	ICARDA/PGRRI	15
TUR	TUR89-2	ICARDA/PGRRI	16
TUR	TUR95	ICARDA/AARI	75
TOTAL			**594**

Table A14. *Aegilops* spp. collecting missions from 1983 to 1997

Country code	Mission code	Organizations cooperating	Samples collected
ARM	ARM92	ICARDA/AAI	23
BGR	BGR89	ICARDA/IHAR/IIPGR	64
BGR	BGR90	ICARDA/IIPGR	16
BGR	BGR90	ICARDA/IIPGR/VIR	54
CYP	CYP89	ICARDA/IBPGR/ARIC	51
DZA	DZA89	ICARDA/ITGC/NARC-J	48
DZA	DZA90	ICARDA/ITGC	9
DZA	DZA91	ICARDA/ITGC	11
EGY	EGY89	ICARDA/ARCG	20
IRN	IRN93-1	ICARDA/SPII	38
IRN	IRN93-2	ICARDA/SPII	68
IRQ	ICARDA		1
IRQ	IRQ93	ICARDA/ARCB	33
JOR	JOR85	ICARDA/USKW/JUST	2
JOR	JOR88-1	ICARDA/JUST	74
JOR	JOR88-2	ICARDA/JUST	72
JOR	JOR91	ICARDA/NCARTT	6
JOR	TFREM31	ICARDA/IBPGR/ARCD	19
LBN	LBN88	ICARDA-Terbol	106
LBN	LBN92-2	ICARDA/ARI	32
LBN	LBN93	ICARDA/ARI	55
LBN	LBN94-1	ICARDA/ARI	7
LBY	LBY90	ICARDA/ARC	20
LBY	LBY91	ICARDA/ARC	12
MAR	MAR87-1	ICARDA/INRA-M/NARC-J	5
MAR	MAR90	ICARDA/INRA-M	57
PAK	ICARDA		5
PAK	PAK86-1	ICARDA/PARC	39
PAK	PAK93	ICARDA/PARC/PGRI/NARC	3

Table A14. (Cont'd)

Country code	Mission code	Organizations cooperating	Samples collected
RUS	SUN90	ICARDA/VIR	24
SYR	ICARDA		12
SYR	SYR88-1	ICARDA/ARCD	92
SYR	SYR88-2	ICARDA/ARCD	33
SYR	SYR88-3	ICARDA/ICRISAT/ARCD	8
SYR	SYR88-4	ICARDA/ARCD	32
SYR	SYR89-1	ICARDA	3
SYR	SYR89-4	ICARDA/ARCD	20
SYR	SYR90-1	ICARDA/VIR/ARCD	17
SYR	SYR90-2	ICARDA/VIR/ARCD	37
SYR	SYR91-1	ICARDA	9
SYR	SYR91-3	ICARDA	3
SYR	SYR91-4	ICARDA	4
SYR	SYR92-1	ICARDA	1
SYR	SYR92-2	ICARDA/ARCD	1
SYR	SYR92-3	ICARDA/ARCD	13
SYR	SYR92-4	ICARDA/AAI/ARCD	11
SYR	SYR93-2	ICARDA	4
SYR	SYR93-3	ICARDA/UKOY	5
SYR	SYR94-2	ICARDA	2
SYR	SYR94-3	ICARDA/ARCD	48
SYR	SYR96	ICARDA/ARCD	4
SYR	SYR97	ICARDA/ARCD	21
SYR	TFREM31	ICARDA/IBPGR	1
SYR	TFREM31	ICARDA/IBPGR/ARCD	74
TJK	SUN91	ICARDA/VIR	10
TKM	SUN91	ICARDA/VIR	47
UZB	SUN91	ICARDA/VIR	33
TUN	TUN90	ICARDA/INAT/ESAK	9
TUR	TUR89-1	ICARDA/PGRRI	125
TUR	TUR89-2	ICARDA/PGRRI	102
TUR	TUR95	ICARDA/AARI	43
TOTAL			**1798**

المركز الدولي للبحوث الزراعية في المناطق الجافة

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