

# Wild Lentils:

## *Treasure of Novel Diversity*

**Authors:**

**Mohar Singh, Ashutosh Sarker, Sandeep Kumar,  
Nikhil Malhotra, Ashok Kumar, Shiv Kumar  
and Kuldeep Singh**



**ICARDA**

**In collaboration of**

**ICAR-National Bureau of Plant Genetic Resources**

Pusa Campus, New Delhi-110 012, India

**and**

**International Center for Agricultural Research in the Dry Areas  
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# Contents

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Preface	v
Forewords	vii
<i>Chapter 1 : Wild Lentils: An Introduction</i>	1
<i>Chapter 2 : Domestication, Taxonomy and Diversity</i>	11
<i>Chapter 3 : Characterization and Evaluation of Wild Species</i>	31
<i>Chapter 4 : Utilization of Wild Lentils</i>	59
<i>Chapter 5 : Conclusions and Future Perspectives</i>	71
Annexures	73
About the Authors	131





# Preface

Most of the cultivated grain legume crop species including lentil have been exploited upto their maximum level of productivity. There is a projection that by 2050, the world population will be more than 9 billion, which require an astonishing increase in food production. To attain further breakthrough in enhancing yield and improving stability in future crop varieties, new sources of genes and alleles are required to be identified in the plant genetic resources (PGRs) including crop wild relatives (CWRs) followed by their incorporation into elite genetic backgrounds for generating novel germplasm. In the face of climate change, these ideal resources may prove instrumental for future food and nutritional security. Therefore, it is imperative to motivate crop breeders to search for new source of variations in untapped gene pool and identify target traits of interest using appropriate tools and techniques in order to make the selection more efficient and reliable. In this context, an effort has been made to bring together the rather scattered research work done in this useful area in the form of an authored collection, a compilation that should be of great value to the lentil researchers across the world. The monograph comprises a total of five chapters including appendices in which accession-wise original raw data has been presented. An introductory chapter describes some key issues linked to bottlenecks and potential of species/accession utilization on current trends of interspecific hybridization. Chapter 2 provides the origin, distribution, taxonomy, gene pool and diversity of global wild lentil collection. The most important chapter 3 contains some useful information on wild species characterization and screening against target traits of interest. Similarly, chapter 4 has been written on utilization of wild lentil accessions for enhancing genetic gains of cultivated gene pool. The last chapter describes the conclusions of this manuscript including some future projections on which wild lentil research could be initiated for breaking yield barriers. We are highly indebted to the Director General, Deputy Director General (Crop Sciences) and Assistant Director General (Seeds) of Indian Council of Agricultural Research for proving all necessary support and guidance from time to time in the completion of the ICAR-ICARDA collaborative research project on '*Pre-breeding and genetic enhancement of lentil and chickpea*'. The ICAR-NBPGR is highly obliged to ICARDA for supplying considerable number of global wild lentil accessions to Indian

National Gene Bank. Authors are also thankful to Directors of ICAR-NBPGR viz. Drs. SK Sharma, KC Bansal and Kuldeep Singh for providing all kind of technical and administrative support in the successful completion of pre-breeding project. Despite several rounds of proof-reading and our best efforts, the monograph may still have some scientific, technical and printing errors. We will appreciate if these omissions are brought to our notice, so that they may be addressed in future edition. Lastly, we hope that this work will serve as a reference for lentil researchers including students, who can take useful tips for genetic improvement of lentils.

***Authors***



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## Foreword

Crop improvement is facing various challenges including climate change, soil deterioration, use of limited genetic diversity in securing food and nutritional security of the country. In general, the production of grain legumes is lower than that of cereals, but their nutritional value makes them very valuable components towards achieving food and nutritional security. Nevertheless, limited by severe genetic bottlenecks during domestication and human selection, grain legumes, like other crops, have suffered from loss of genetic diversity, which is essential for providing genetic resources for crop improvement programs. Lentil, also known as “poor man’s meat” is one such crop which has major knowledge gaps that require a deeper understanding and characterization of genetic resources, including wild relatives for use in pre-breeding for future lentil improvement programs in India and abroad.

In this context, the multi-authored monograph entitled, “**Wild Lentils: Treasure of Novel Diversity**”, provides comprehensive coverage of important aspects related to key genetic resources developed for lentil and their main outcomes. The monograph also highlights characterization, evaluation, and utilization of genetic resources and future perspectives. I congratulate all the authors from ICAR-NBPGR and ICARDA, for their valuable contributions and hope the publication will be very useful for the scientists, teachers, students and other stakeholders.

  
(T. MOHAPATRA)

**Dated the 14<sup>th</sup> September, 2021**  
**New Delhi**







## Foreword

Food Legumes have been one of the major components of sustainable agriculture globally mainly because of their capacity to grow with N fertilizers, soil ameliorative properties and nutritional values for human and animal. Lentil is one of the staple food legumes in the drylands of South and West Asia, and East and North Africa for food, feed and in farming systems as a rotational crop with cereals. However, so far, its yield potential has not been exploited using the available genetic variability more specifically among wild species conserved at ICARDA gene-bank and elsewhere. Lentil germplasm from South Asia intrinsically have narrow genetic base with respect to yield contributing and climate resilient traits, which limits breeders' progress in generating new desirable genotypes. Besides, the lentil varieties developed in South Asia during last decades emanated from using few parents in cross-breeding programs.

To break the bottleneck of narrow genetic base, it is imperative to use diverse parents in genetic enhancement programs. Wild species and landraces offer unique opportunity that possess wealth of genes/alleles which can help to break yield barriers, enhance tolerance to biotic and abiotic stresses, and cope with climate change effects. Pre-breeding is one of the avenues to broaden the genetic base using wild relatives, which have not been extensively exploited. I am glad to communicate that a team of ICAR-National Bureau of Plant Genetic Resources and ICARDA scientists acted in this direction under funding support from the Government of India. ICARDA supplied considerable number of landraces and wild species, collected from the Center of Origin and areas of Primary Diversity in the Fertile Crescent of the Near-East.

The Monograph, **“Wild Lentils-Treasure of Novel Diversity”** is authored by Mohar Singh, Ashutosh Sarker, Sandeep Kumar, Nikhil Malhotra, Ashok Kumar, Shiv Kumar and Kuldeep Singh. It is based upon original research on comprehensive characterization of Lentil wild species, and their use in constructing new genetic variants to utilize in classical breeding programs. It is interesting to note that several accessions across crossable and distant wild species have been identified for yield contributing traits, biotic and abiotic stress resistance, phenological and quality traits, etc. Additionally, new genetic stocks have been constructed through aggregation of beneficial alleles/genes to develop desirable parents for use in breeding programs. This will certainly help breeders to develop climate-resilient lentil varieties with combination of multiple traits to realize higher and stable yield.

So far, I understand, this is the most extensive work performed by the researchers on characterization and use of wild relatives in lentil. I strongly believe that the information depicted in the Monograph will be of immense help to global lentil researchers as a ready reference.



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## Foreword

Lentil was considered as an orphan crop until recently with respect to availability of genetic resources in this crop. However, in the last decade, things have changed and new data and tools related to lentil improvement have been generated. Improving adaptation of cultivars is an ongoing process that frequently involves the introduction of novel variations from wild species and landraces. Despite the identification of target traits of interest in land races and wild *Lens* species, there is still great potential in terms of using genetic variation for improving genetic gain in the event of global climate change and for food and nutritional security.

The multi-authored monograph entitled, “**Wild Lentils: Treasure of Novel Diversity**”, presents an overview of the main genetic resources developed for broadening the lentil genetic-base. The significant findings along with suggested future projections can be used for continued efforts for Lentil improvement. Accumulated evidence suggests that the genetic variation retained in these lentil wild relatives can be used to improve yield, nutrient contents, and resistance/tolerance to environmental stresses by integration of phenomics, genetics, embryo rescue and modern genomics tools. This monograph is compiled by prominent scientists from ICAR-National Bureau of Plant Genetic Resources and International Centre for Agricultural Research in the Dry Areas, and I strongly believe that the information included in this publication will be of great help to the global lentil researchers as an organized reference.

  
(T.R. Sharma)



## Chapter 1

# Wild Lentils: An Introduction

### 1.1 Background

The cultivated lentil (*Lens culinaris* ssp. *culinaris*) is an annual herbaceous self-pollinating true diploid ( $2n=2x=14$ ) species with an estimated genome size of 4063 Mbp/C (Arumuganathan and Earle, 1991). The crop is one of the first domesticated species originated from the Near East center of origin (Zohary, 1999), and is most preferred grain legume of the old world (Smartt, 1990). It is an important winter season legume species grown in Mediterranean and semi-arid climates. It is a valuable source of protein (22-25%) and emerged as nutritious substitute for meat. Besides high protein, it also provides minerals (K, P, Fe and Zn), carbohydrates, crude fiber and vitamins (folic acid, pantothenic acid and vitamin B<sub>6</sub>) for human nutrition (Bhatty, 1988; Kumar et al., 2018). The lentil seeds are also rich in lysine and tryptophan amino acids (Erskine et al., 1990). Lentils high nutritional value with a low level of anti-nutritional factors and a shorter cooking time than most of other pulses, make it highly suitable for human consumption (Sahi et al., 2000).

The genus *Lens* belongs to family *Fabaceae* and a total of seven taxa have been recognized including domesticated species

as lentil gene pool. The other wild lentil taxa includes *L. culinaris* ssp. *odemensis* Ladizinsky; *L. culinaris* ssp. *orientalis* (Boiss) Ponert; *L. ervoides* (Brign) Granade; *L. lamottei* Czefer; *L. nigricans* (Bieb) Godron; and *L. tomentosus* Ladizinsky. As far as compatibility relationships of wild lentil taxa are concerned, *L. culinaris* subsp. *orientalis* is readily crossable with cultivated lentil (Robertson and Erskine, 1997) and considered as immediate progenitor of domesticated species (Barulina, 1930; Mayer and Soltis, 1994). Globally, lentil stands in sixth position in production among important pulses after common bean, pea, chickpea, faba bean and cowpea (FAO, 2018). However, the world lentil production contributed 6% of total dry pulse production during 2010-2015 with an average productivity of 926 kg/ha. India is the largest lentil producer in the world followed by Canada and Turkey, which collectively contributed to 66% of total world lentil production (FAO STAT, 2018). An average lentil grain yield in Asia is 817 kg/ha, which is far below the world average of 926 kg/ha. Lentil, despite its significant role in human food, animal feed and different cropping systems in the Indian sub-continent, West Asia, Ethiopia, North Africa and parts of Southern Europe,



Oceania and North America, has remained under-exploited and researched crop until recently. Further, modern lentil cultivars have some eliteness over traditional ones in terms of their good yielding ability, disease and pests' resistance, and high nutritional value. If we look into the contribution of top donors for developing high yielding varieties of lentil, a small number of genotypes have contributed significantly to the breeding of majority of improved cultivars through pure line and mass selection following hybridization between lines adapted to specific environmental conditions. Among different accounts across lentil growing regions of India, the pedigree analysis of 35 released lentil cultivars has been traced back to only 22 ancestors and the top ten contributed 30% to the genetic base of released cultivars (Kumar et al., 2003). This narrow gene flow situation could lead to the crop vulnerability to pest and disease epidemics and unpredictable climatic factors limiting progress towards enhancing lentil production. Furthermore, due to lentil cultivation on marginal lands in most of developing countries including India, its narrow genetic diversity makes it more vulnerable to several biotic and abiotic stresses leading to loss of yield and nutritionally contributing traits of interest. Being potential to be used as a staple crop in many regions of world and to meet the nutritious dietary requirements of growing human population through biofortification, it requires the consolidated efforts to enhance the gene pool of existing lentil varieties. Therefore, there is an immediate need to widen the genetic base of domesticated lentil cultivars by introgression of diverse gene sources, which are currently available in distantly related wild *Lens* taxa. To synthesize the new gene pool and maximize gains from

the selection, it is therefore imperative to accumulate favorable genes and alleles from unadapted germplasm into the backgrounds of cultivated germplasm.

## **1.2 Exploration, collection and on-farm *in-situ* conservation**

To broaden the crop gene pool, it is important that germplasm must be collected from the diversity rich regions across the globe. The establishment of *ex-situ* germplasm collections (genebanks) has been the result of rigorous global efforts of several decades to preserve genetic resources including crop wild relatives. As far as lentil genetic resources are concerned, the International Center for Agricultural Research in the Dry Areas (ICARDA) holds the largest collection of lentil germplasm including wild species collected from more than 46 countries of origin (Furman et al., 2009). The first *ex-situ* genebank of lentil collection including wild relatives was established in the Vavilov Institute for Plant Industry in Russia. The recent survey of global *ex-situ* collection of lentil germplasm lists more than 43,000 accessions including released cultivars, advanced breeding lines, mutants and wild species, which are stored in different genebanks around the world (GCDT, 2017). For wild lentil collection, ICARDA has undertaken more than 120 exploration trips and collected more than 400 wild accessions from diversity rich areas across the world (Redden et al., 2007). Turkey has the largest holdings of lentil land races (Atikyilmaz, 2010) followed by Nepal and Pakistan (Sultana and Ghafoor, 2008), Bangladesh, Spain, Syria, Ethiopia and China (Fikiru et al., 2007; Liu et al., 2008). However, an exact status of on-farm *in-situ* conservation of diverse germplasm is not

well documented (Furman et al., 2009). The important regions for *in-situ* on-farm conservation of wild *Lens* taxa comprise West Turkey for *L. nigricans*, Southeast Turkey, Southwest Syria and Jordan for *L. culinaris* ssp. *orientalis*, South Syria for *L. culinaris* ssp. *odemensis*, and the border areas of Turkey and Syria for *L. ervoides* (Ferguson et al., 1998).

### 1.3 Gene pool, characterization and evaluation

The wild lentil taxa are known for their distinct morphological characteristics and shows specific ecological affinities and typical geographic distribution. *L. culinaris* ssp. *orientalis* and *L. odemensis* are members of the primary gene pool, whereas *L. tomentosus*, *L. lamottei*, *L. nigricans* and *L. ervoides* belongs to the secondary gene pool. Recently, Genotyping by Sequencing (GBS) based study identified four gene pools, namely *L. culinaris*/*L. orientalis*/*L. tomentosus*, *L. lamottei*/*L. odemensis*, *L. ervoides* and *L. nigricans* which form primary, secondary, tertiary and quaternary gene pools, respectively (Wong et al., 2015). Further, germplasm enhancement approaches have also been demonstrated to study the variation among important traits of interests *viz.* early maturity, number of peduncles per plant, number of pods per plant, number of seeds per pod, number of clusters per plant, seed yield per plant, harvest index (%), biological yield (g), resistance against major biotic and abiotic stresses, and nutritional traits particularly mineral composition (Singh et al., 2014, 2020; Kumar et al., 2018). Sincere efforts have been made to characterize and evaluate various agro-morphological traits in large number of lentil germplasm including global wild accessions for which

remarkable variation was recorded (Singh et al., 2014). For utilization of available diversity in wild lentil into the background of cultivated gene pool, few attempts were made in the past to transfer some desirable traits from wild lentil species to cultigens using conventional and embryo rescue techniques. The present compilation entitled **“Wild Lentils: Treasure of Novel Diversity”** has been written on the phenotyping data of multilocation testing of all 405 accessions comprising global wild *Lens* collection. These studies were undertaken by ICAR-NBPGR in association with other NARS crop-based institutions. The results revealed a wide range of diversity against important agro-morphological traits and major biotic stresses. This testing led to the development of wild lentil core set comprising of 96 accessions which was further analysed for mineral composition. The study has also led to identification of various elite accessions carrying multiple traits of interest and these donors could be utilized for wide hybridization for enhancing genetic gains of cultivars.

### 1.4 Traits to be considered for base broadening

#### 1.4.1 Agro-morphological traits

##### Pod characteristics

Pod shattering is one of the major concerns for yield losses and would be of great significance to lentil production. Pod dehiscence was reported to be completely dominant over indehiscence (Singh et al., 2014). Erskine (1985) suggested selection to pod indehiscence controlled by quantitative variation and it was further confirmed by quantitative trait loci (QTL) studies, which determine that one major recessive and two minor dominant QTLs

accounted for 81% of assessed variation. Subsequently in mapping populations, the trait showed dehiscent and non-dehiscent pod variation.

### Seed characteristics

Seed size is also a very important trait of significance with focus on consumer preference and trade as well. Domesticated lentils are classified as *microsperma* (small seeded) and *macrosperma* (large seeded) and differ with seed weight and consumer's choice. The  $F_2$  segregating population of microsperma and macrosperma showed continuous variation, and two major and one minor QTLs have been reported to determine seed size in lentil. Further, immortal populations derived from wide crosses of *L. culinaris* ssp. *culinaris* x *L. ervoides* showed remarkable increase for the performance of important yield contributing traits (Tullu et al., 2011). In India, an international screening nursery resulted in the identification of germplasm lines (ILL 1005, ILL 4559, ILL 4637, ILL 4649, ILL 5488, ILL 5628, ILL 8072, ILL 8595, ILL 7946, ILL 7678, ILL 7943, ILL 9890, ILL 9894, ILL 10734, ILL 10736, ILL 10741, IPLS-09-17, IPLS-09-23, IPLS-0933, IPLS-09-35, ILL 45113 and ILL 45101) for large seed size in lentil (DAC-ICAR-ICARDA, Annual Progress Report, 2014).

### Flowering behaviour and plant architecture

Flowering behaviour is also very important trait of interest for crop adaptation and seed yield. Earliness is desirable character that ensures accomplishment of life cycle in a relatively short period of time and thereby avoid losses due to high temperature primarily at grain filling and maturity period. The genetics of flowering time has been reported as monogenic with earliness

being recessive and is represented by gene symbol '*Sn*' (Sarker et al., 1999). For the induction of earliness into the desired background of lentil, gene sources for earliness have been identified in India under collaborative research project (DAC-ICAR-ICARDA, Annual Progress Report, 2014). These sources include EC718431, ILL 6002, ILL 7663, ILL 2585, ILL 4605, ILL 10848, LIRL-21-50-1-1-1-0, LIRL-22-46-1-1-1-0, LIRL-22-46, ILL 45101, ILL 45107, IPLS-09-17 and IPLS-09-35 which can be promoted as useful donors in lentil enhancement program (Tyagi and Sharma, 1995; Toklu et al., 2009a and b).

### 1.4.2 Resistance to abiotic and biotic stresses

The cultivated lentil is vulnerable to prevailing major abiotic and biotic stresses and has less diversity for trait of higher productivity. Among important abiotic stresses, the most commonly distributed are cold, drought, heat, salinity, nutrient deficiency and toxicity (Yau and Erskine, 2000). Of these, drought and heat stresses are considered of serious concern globally (Turner et al., 2001). However, salinity is also an emerging issue in the Indian sub-continent and lentil is more sensitive to salt as compared to other legume crops (Katerji et al., 2003). Similarly, nutrient deficiencies and toxicities are endemic abiotic factors affecting production in various lentil growing regions of the World (Buddenhagen and Richards, 1998). Further, among biotic stresses, ascochyta blight is a global problem prevailing in majority of nations in general, and Canada and Australia in particular (Ahmed and Morrall, 1996; Ahmed et al., 1996; Johansen et al., 1994). In India, lentil rust, powdery mildew and Fusarium wilt are serious biotic stresses affecting lentil yield

(Robertson et al., 1992; Singh et al., 2014). Some rust resistant wild lentil accessions (EC718246, EC718247, EC718248, EC718600, EC718605, EC718522 and EC718526) have been identified for introgression purposes into the cultivated gene pool (Gupta and Sharma, 2006; Singh et al., 2014). Likewise for powdery mildew, cultivated germplasm has shown partial resistance against the pathogen. Some wild accessions (EC718313, EC718314, and EC718378) have also been identified as useful gene sources (Singh et al., 2014). The germplasm accessions which showed resistance to *Fusarium* wilt included EC718457, EC718460, EC718257, EC718486, EC718347, ILL 3492, ILL 4385, ILL 10956, ILL 6449, ILL 4649, ILL 3796, ILL 2502, ILL 2505, and ILL 5714 (Mohammadi et al., 2012; DAC-ICAR-ICARDA, Annual Progress Report, 2014). These gene sources can be exploited for the introgression of resistance into the elite genetic background of cultivated lentil varieties.

### 1.4.3 Nutritional traits

Crop Wild Species and Relatives have always been considered as a reservoir of important nutritional traits particularly high protein and essential micronutrients. Scarce information is available on the species-specific mineral composition of wild lentils. Further, as lentil has the potential to be used as a staple crop to eradicate the hidden hunger, there is need to identify essential micronutrient rich material and use them for biofortification of the cultivated varieties. So, core set developed in the present study was analysed for mineral composition. Some wild lentil accessions have been identified as useful gene sources including EC718235 and EC718529 for Ca content; EC718471,

EC718404 and EC718234 for Mg content; EC718519, EC718311, EC718692 and EC718297 for Fe content; EC718275 and EC718692 for Zn content; EC718316 for Cu content; EC718370 for Mn content, and EC718605 and EC718311 for Mo content (Kumar et al., 2018).

## 1.5 Progress towards wide hybridization

Rigorous efforts have been made so far to explore wild lentils for biotic and abiotic stresses and few for traits of economic significance. There are reports of very successful attempts of introgression of desirable genes from wild *Lens* taxa into cultivated varieties. Wide hybridization of cultivated lentil with species from different gene pools showed different success rates owing to readily crossable *Lens* species within the primary (*L. orientalis*) and secondary (*L. nigricans*) gene pools (Ladizinsky et al., 1984; Abbo and Ladizinsky, 1991; Abbo and Ladizinsky, 1994; Fratini et al., 2004; Fratini and Ruiz, 2006; Muehlbauer et al., 2006; Gupta and Sharma, 2007; Singh et al., 2013) in comparison to species from the secondary and tertiary gene pools, which are genetically distant from the cultivated lentil (Gupta et al., 2011). Apart from species variation, some researchers have reported genotypic differences within each species, which affects the success of wide hybridization. Among successful crosses between the cultivated and wild lentil, the fertility of hybrids is mainly dependent on compatible chromosomal arrangement of the wild parent (Ladizinsky et al., 1984). The failure of wide hybridization with few genotypes within readily crossable species or distant species is due to pre- and post-fertilization barriers (Abbo and Ladizinsky,

1991; Abbo and Ladizinsky, 1994; Gupta and Sharma, 2005). These barriers impeded the successful introgression of useful genes mostly from secondary and tertiary gene pools. Nevertheless, successful hybrids can be attempted by applying the post-fertilization growth hormones like GA3 (Ahmed et al., 1995) and by employing embryo/ovule rescue techniques (Cohen et al., 1984; Ladizinsky et al., 1985; Gupta and Sharma, 2005; Ahmed et al., 1995). Studies of Fratini et al. (2004) suggested that success of wide hybridization can be predicted based upon phenotypic similarity of taxa for pollen morphology and *in vitro* pollen length, pistil and style length.

## 1.6 Conclusions

It is concluded that wild lentil species are useful resources of untapped variation controlling desirable traits of interest for yield attributing characters, biotic and abiotic stresses, and nutritional traits to make substantial genetic improvement in productivity and quality, thereby broadening the base of cultivated varieties. Further, desirable traits belonging to different gene pools have been successfully transferred into cultivated lentil background using conventional and biotechnological approaches. However, to harness full potential of productivity genes from tertiary gene pools, efficient tissue culture protocols, advances in genetic engineering along with development of appropriate strategies to avoid linkage drag would ascertain the free flow of genes. Molecular markers would be valuable tools in lentil breeding program with their role in identification of donor parents, true to type  $F_1$  hybrids and backcrosses to efficient pre-breeding and phylogenetic studies. The marker assisted selection still has to

be employed in lentil breeding program, however, sequencing of lentil genome would break these barriers of successful utilization of genome based approaches alongwith conventional breeding.

## Abbreviations used

CWR, Crop Wild Relatives; FAO, Food and Agriculture Organization; ICARDA, International Center for Agricultural Research in the Dry Areas; GCDT, Global Crop Diversity Trust; GBS, Genotyping by Sequencing; FISH, Fluorescence *In-situ* Hybridization; GISH, Genomic *In-situ* Hybridization; ILWL, International Legume Wild Lentil; ILL, International Legume Lentil

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## Chapter 2

# Domestication, Taxonomy and Diversity

### 2.1 Introduction

The genus *Lens* Miller belongs to family Fabaceae (Leguminosae), subfamily Faboideae, tribe Fabeae, or alternatively to subfamily Papilionaceae, tribe Vicieae. *Lens* is one of the oldest crops domesticated at about the same time as wheat and barley in the Fertile Crescent of the Middle East. The genome size of lentil is 4.3 Gb. Genus *Lens* Miller includes seven species namely *L. culinaris*, *L. orientalis*, *L. tomentosus*, *L. odemensis*, *L. ervoides*, *L. lamottei* and *L. nigricans*, which are grouped into different groups or gene pools by different workers with developing understanding of their crossing behaviour, capability to produce fertile hybrids, taxonomy etc. All *Lens* species are self-pollinating annual diploids ( $2n=14$ ). On the basis of seed size, two main groups of domesticated lentils are recognized: i) microsperma and ii) macrosperma. Characterization and evaluation of these species based on agro-morphological traits, biochemical and molecular markers has led to the identification of trait specific accessions which can be used as donors in pre-breeding programs, level of inter- and intra-species genetic diversity and also contributed towards solving problems related to grouping of these species. In

this chapter, authors have tried to cover information related to domestication of *Lens* species, their genome size, karyotype, taxonomy, grouping in different gene pools and the available genetic diversity among and within the species.

### 2.2 Origin and domestication

The primary center of diversity for the domestic *Lens culinaris* as well as its wild progenitor *L. culinaris* ssp. *orientalis* is considered to be the Middle East (Zohary, 1972; Cubero, 1981). Lentil (*Lens culinaris* Medik), is one of the oldest crops domesticated at about the same time as wheat and barley in the Fertile Crescent of the Middle East, in what is present day Iraq, from today's Jordan northward to Turkey and southeast to Iran. Archaeological evidences confirmed the presence of lentil as far back as 8500-6000 BC in the Turkey/Syria/Iraq region (yadav et al., 2007) whereas the oldest known carbonized remains of lentil from Greece's Franchthi cave are dated to 11,000 BC (Sandhu and Singh, 2009). *L. orientalis* is the progenitor species (Ladizinsky et al., 1984). Given the coexistence of the wild and domesticated forms which is not found elsewhere, lentil diversity in the center of origin is still very high for both the cultivated primitive forms



and the wild relatives. Using molecular markers, Ferguson et al. (1998a, b) located areas alongside the border between Turkey and Syria as well as in areas of southern Syria and Jordan with high diversity for *ssp. orientalis* which along with archaeological evidences supports the Near East region as the most likely center of lentil domestication. Indicators of human activity suggest that some populations of *ssp. orientalis* were unconsciously subjected to selection (Harlan, 1992) which resulted in the cultivated lentil. Based on chromosome and DNA polymorphisms, the domestication event of lentil happened once or only a few times (Zohary, 1999). Cubero (1981) reported that lentil first spread to the Nile from the Near East, to Central Europe and then to the Indian subcontinent and the Mediterranean Basin by the end of the Bronze Age. It spread to South and Central America lately, presumably with the arrival of the Spanish. Subsequently, it was introduced into the United States before World War II and into Canada in 1969 (Cubero, 1981; Nene, 2006). Archaeological evidences substantiates the presence of lentil cultivation as far back as 8500-6000 BC in the present day region of Turkey, Syria and Iraq (Ford et al., 2007). Lentil domestication began in this region and spread to Nile Valley, Greece, Central Europe and eastwards to South Asia (Nene, 2006). It later dispersed to Ethiopia, Afghanistan, India, Pakistan, China and Latin America (Cubero, 1981; Ladizinsky, 1979a). Lev-Yadun et al. (2000) suggested a lentil domestication site close to or overlapping the area where einkorn and emmer wheats had been domesticated in the Fertile Crescent, concretely, the Karacadag/Diyarbakir region as the domestication center of lentil. Furthermore, Ferguson et al. (1998b) described two centers of diversity for *L.*

*culinaris ssp. orientalis* including Southeast Turkey and Northwest Syria, and West and North Jordan and southern Syria.

Ferguson and Robertson (1999) studied variation in selected phenological and agromorphological characters in 310 wild lentil accessions and reported that significant correlations exist between quantitative characters and latitude of origin. Phenological adaptation through sensitivity to photoperiod, temperature or both, appear to be a major evolutionary force in wild lentils. Variation was mapped according to geographical origin of accessions in order to identify geographical patterns or clines of variation e.g. accessions of *L. culinaris* subsp. *orientalis* from Uzbekistan, Turkmenistan and Tajikistan had among the largest biomass, the most peduncles per plant and many pods and seeds per plant. Similarly, lentil cultigens show a higher frequency of white flowers compared to the dominant purple-colored inflorescences of the wild relatives. This character is associated with better culinary quality and fixed by indirect selection of lighter-colored seed coats, showed a clear regional distribution pattern of cultivated lentil (Fratini et al., 2011).

Khazaei et al. (2016) estimated genetic diversity in cultivated lentil (*Lens culinaris* Medik.) collection consisting of 352 accessions originating from 54 diverse countries using 1194 SNP markers and categorized into three major groups that prominently reflected geographical origin (world's agro-ecological zones) including South Asia (sub-tropical savannah), Mediterranean, and northern temperate. These three clusters complemented the origins, pedigrees, and breeding histories of the germplasm. Lentil cultivars are often divided into two cultivar groups: Europe, North Africa and America are

known for cultivation of mostly large seeded *macrosperma* group, whereas the small seeded *microsperma* group is cultivated mainly in Asia, Egypt and Ethiopia (Khazaei et al., 2016). Western Asia and south-eastern Europe grow both cultivar groups (Ford et al., 2007). Stefano et al. (2019) used high-throughput genotyping by sequencing of the Mediterranean *ex-situ* lentil collection and found clustering pattern related to geographic patterns and phenotypic traits. They concluded that post-domestication routes introducing cultivation in Mediterranean countries and selection were major forces shaping lentil population structure.

## 2.3 Genome, karyotype and systematic taxonomic evolution

### 2.3.1 Genome size, ploidy, chromosomes, and karyotypes

Lentil genome C value (unreplicated haploid) was determined using flow cytometry to amount to 4.41pg, is equivalent to 4,063 Mbp (Arumuganathan and Earle, 1991). A draft genome assembly of Canadian variety CDC Redberry, consists of 7 pseudo molecules anchored through the use of 6 high-density genetic linkage maps, with the total assembled bases representing approximately half (2.6 Gbp) of the 4.3 Gb lentil genome is available (Bett, 2016; <http://knowpulse.usask.ca>). Kaur et al. (2016) sequenced nuclear genome of PBA Blitz using a whole-genome shotgun approach. A de novo assembly was generated comprised of 352,065 scaffolds and 444,011 singletons with N50 value of 94.4 kb, assembling a total of 2.3 Gbp. The assembly was then compared to the reference genome assembly from CDC Redberry v1.2.

The comparison indicated a c. 99% of similarity between the two assemblies. A total of 8,939,058 homozygous single nucleotide polymorphisms were identified between Blitz and Redberry across seven chromosomes of lentil with minimum coverage 5, maximum coverage 55 and minimum allele frequency of 80%. In comparison to other recently sequenced legumes including chickpea, pigeon pea and soybean, the genome size of lentil is relatively large (*L. culinaris* ssp. *culinaris*; genome size 4.3 Gb), it therefore requires more time and resources to generate a full reference (Kaur et al., 2016). But gene duplications, chromosomal rearrangements, and large amounts of repetitive elements make this large genome difficult to study, especially across the wild species. Based on the CDC Redberry draft genome, Ogutcen et al. (2018) developed an exome capture array from 16 wild lentils and 22 cultivar accessions of lentil, using multiple sources of transcript resources. Alignment rates were over 90%, and the genic regions were well represented in the capture array. After stringent filtering, 6.5 million high-quality variants were called, and the data set was used to assess the interspecific relationships within the genus *Lens*. The two samples of *L. nigricans*, which is the most distant relative of *L. culinaris*, had the lowest alignment rates (71.88%).

All *Lens* species are diploid (2n) and possess the same chromosome number (2n=14) and share similar karyotypes with three types of chromosomes: three pairs of metacentric and submetacentric chromosomes, three pairs of acrocentric chromosomes, and a pair of metacentric chromosomes with the nucleolar organizing region (NOR) secondary constriction site proximal to the centromere location, and formulated 3 m/

sm + 1m with sat + 3ac as their karyotypic formula (Ladizinsky, 1993). The number of SAT chromosomes in *L. culinaris*, the cultivated species, has been reported to vary between 0 and 3 (Bhattacharjee, 1951; Sharma and Mukhopadhyay, 1963; Sinha and Acharia, 1972; Gupta and Singh, 1981; Nandanwar and Narkede, 1991). In addition to the standard ssp. *culinaris* karyogram, Ladizinsky (1993) also described other karyotypes in ssp. *orientalis*, a single accession (No 113) showed a karyotype in which about three-quarters of the satellite had been translocated to another chromosome and the metacentric-satellited chromosome had become acrocentric. Accessions from Iran differed by a chromosomal rearrangement involving two metacentric chromosomes, and accessions from Turkey differed by a paracentric inversion and inclusive of two or even three chromosome rearrangements. Accordingly, ssp. *orientalis* appeared to be the most chromosomally variable *Lens* taxon. Balyan et al. (2002) studied karyotypes in five different species of genus *Lens* using Fluorescence *In-situ* Hybridization (FISH) and identified some karyotype variants viz. NOR region located in chromosome 3; chromosome 2 consisted of a submetacentric chromosome with a 5S locus distally located on the long arm (the major site of hybridization), whereas chromosome 6 comprised an acrocentric chromosome with the other 5S locus located proximal on the short arm (minor site). Namazi et al. (2007) studied karyotype and C-banding patterns of mitotic chromosomes in 10 cultivars and landraces of lentil and reported four pairs of metacentric and three pairs of submetacentric chromosomes. Chromosome 4 had a secondary constriction near centromeric

region of its long arm, whereas, arm ratio index of chromosomes ranged from 1.24 in chromosome 3 to 2.38 in chromosomes 6. They also observed that karyological characteristics and banding patterns of all materials studied were similar to each other, however, some polymorph C-bands were present on chromosome arms. Jha (2015) conducted detailed and comparative chromosomal analysis on two wild and 12 cultivated cultivars of *Lens* using enzymatic maceration and air drying (EMA) based Giemsa staining methods. Chromosomal analysis revealed chromosomal stability, uniform karyotype formula (3m + 1m (sat) + 2sm + 1st), one pair of interstitial sat in either chromosome number 3 or 4 and interesting variations in total chromatin length (53.6–121.2  $\mu$ m) in all the studied cultivars. Pal et al. (2016) analysed karyotype from root tip cells of 5 varieties of *L. culinaris* which showed gross uniformity in morphology. They concluded that karyotype analysis revealed minute differences in details and each lentil variety is thus characterized by its own karyotype, serving as one of the identifying criteria.

### 2.3.2 Taxonomy

Barulina (1930) and Davis and Plitmann (1970) considered that *Lens* Miller genus had four wild species: *L. orientalis* (Boiss.) Hand. Mazz., *L. nigricans* (M. Bieb.) Godr., *L. ervoides* (Brign.) Grande, and *L. montbretii* (Fish. & Mey.) Davis & Plit. The four taxa have the same chromosome number (2n=14) and share a similar karyotype of three metacentric or submetacentric chromosomes with a satellite (Ladizinsky, 1979a). Ladizinsky (1979b) based upon seed protein profile, observed that *L. culinaris*, *L. orientalis* and *L. nigricans* were similar and *L. ervoides* was distinct from these three species morphologically and

appears to be cross-incompatible with them. In 1982, Ladizinsky and Sakar found that *L. montbretii* was morphologically and cytogenetically different from other *Lens* species and given taxonomic status as *Vicia montbretii* Fisch. & Mey. Ladizinsky et al. (1984) based on crossability and fertility of hybrids, divided *Lens* genus into two biological species, *L. culinaris* and *L. nigricans*. Within species, considerable chromosome repatterning occurs, but as a rule, F<sub>1</sub> hybrids are easily obtained and are fertile or partially fertile. Three subspecies were defined in *L. culinaris*: ssp. *culinaris*, which encompasses the cultivated lentils; ssp. *orientalis*, which represents the wild lentils with lanceolate stipules (cytogenetically, some accessions of this subspecies are closely related to ssp. *culinaris*); and ssp. *odemensis*, characterized by semi-hastate stipules that form horizontal positions on the stem. In conventional taxonomic treatments of the genus, ssp. *odemensis* is considered as *L. nigricans*. *L. nigricans* is composed of two subspecies: ssp. *nigricans* has stipules that are considerably semi-hastate and dentate at their base and pointed upward in a parallel position to the stem; and *L. ervoides*, has semi-hastate or lanceolate stipules and is distinguished by its smaller leave, calyx teeth, pods, and seeds. These two subspecies rarely form mixed stands in nature, but their hybrids are partially fertile. Chloroplast DNA restriction fragment length polymorphisms (RFLP) showed a high degree of fragment length conservation among members of crossability group I, i.e., *L. c.* ssp. *culinaris*, *L. c.* ssp. *orientalis* and *L. c.* ssp. *odemensis* (Muench et al., 1991). In contrast to this, low level of similarity was observed in *L. nigricans* and *L. ervoides* based on isozyme polymorphism (Hoffman et al., 1986) and

chloroplast DNA-RFLP (Muench et al., 1991).

Czefranová (1971) and Ladizinsky (1997) described two new species of *Lens* (Leguminosae), *L. lamottei* and *L. tomentosus*, respectively. *L. lamottei* was identified among *L. nigricans* (M. Bieb.) Grand. herbarium material on the basis of horizontal and less dentate stipules. Two populations of *L. lamottei* belonging to France and Spain differs from *L. nigricans* populations by five chromosomal rearrangements (Ladizinsky et al., 1984). *L. tomentosus* resembles *L. culinaris* except in its tomentose pods. Karyotypically it differs from other *Lens* species by the satellite chromosome which is much smaller, extremely asymmetrical and bears a minute satellite. *Lens tomentosus* reproductively isolated from all other *Lens* species. Hybrids cannot be obtained because of embryo abortion, and irregular meiosis in hybrids raised via embryo culture. Currently, three populations of *L. tomentosus* are known in the Mardin area, south-east Turkey.

In 1997, Van Oss et al. were the first to state that genus *Lens* consisted of seven taxa including *L. culinaris* Medik. ssp. *culinaris*, its wild progenitor *L. culinaris* ssp. *orientalis* (Boiss.) Ponert, *L. odemensis* Ladiz., *L. nigricans* (M. Bieb.) Godr., *L. ervoides* (Brign.) Grande, and two newly recognized species *L. tomentosus* Ladiz. and *L. lamottei* Czeffr. On the basis of cpDNA divergence clustering pattern, they divided *Lens* species in three groups viz. *L. culinaris*, *L. tomentosus* and *L. odemensis*; *L. ervoides* and *L. lamottei*; and *L. nigricans*. But due to lack of distinguishable markers, taxa *L. lamottei*, *L. nigricans*, *L. odemensis* and *L. tomentosus* were always questioned. Ferguson et al. (2000) reassessed the

taxonomy of *Lens* species based on morphological characterization, isozymic electrophoresis and RAPD techniques with identification of markers that delimit taxa, with special reference to *L. lamottei*, *L. nigricans* and *L. odemensis* and proposed new classification which identified seven taxa grouped into four species: *L. culinaris* Medik. ssp. *culinaris*, ssp. *orientalis* (Boiss.) Ponert, ssp. *tomentosus* (Ladiz.) M.E. Ferguson et al., ssp. *odemensis* (Ladiz.) M.E. Ferguson et al.; *L. ervoides* (Brign.) Grande; *L. nigricans* (M. Bieb.) Godr.; *L. lamottei* Czeffr.. Some species specific traits useful in taxonomic identification of *Lens* species are listed in Table 2.1.

Despite the taxonomic re-organizations, all studies generally agreed that *L. culinaris* ssp. *orientalis* is the most closely related wild progenitor of *L. culinaris* ssp. *culinaris* while *L. nigricans* is the most distant relative. Alo et al. (2011) reported that *L. nigricans* and *L. ervoides* are well-defined species at the DNA sequence level and *L. culinaris* subsp. *odemensis*, *L. culinaris* subsp. *tomentosus*, and *L. lamottei* may constitute a single taxon. Therefore, further hybridization studies are needed to position *Lens tomentosus* and *L. lamottei* in the secondary or tertiary gene pool. On the basis of genotyping-by-sequencing of 60 wild lentil accessions, Wong et al. (2015) recently grouped the seven taxa into four gene pools, namely *L. culinaris*/*L. orientalis*/ *L. tomentosus*, *L. lamottei*/*L. odemensis*, *L. ervoides* and *L. nigricans* which form primary, secondary, tertiary and quaternary gene pools, respectively. Out of six species, five species can be used to make hybrids with cultivated lentil. Workers have reported discrepancies in this classification also. Koul et al. (2017) studied genetic structure and relationships of 130 lentil accessions belonging to

**Table 2.1: Some species-specific traits of *Lens* species useful for taxonomic studies**

Trait	<i>L. culinaris</i>	<i>L. tomentosus</i> *	<i>L. orientalis</i>	<i>L. odemensis</i>	<i>L. lamottei</i>	<i>L. ervoides</i>	<i>L. nigricans</i>
<b>Peduncle vs. Rachis</b>	Peduncle < Rachis	-	Peduncle > Rachis	-	-	Peduncle > Rachis	Peduncle > Rachis
<b>Stipule</b>	lanceolate stipules	lanceolate stipules	lanceolate stipules	semi-hastate stipules	semi-hastate stipules	semi-hastate or lanceolate stipules	semi-hastate stipules
<b>Stipule position</b>	-	-	-	horizontal positions	horizontal positions	-	upright (pointed upward in a parallel position to the stem)
<b>Degree of dentation</b>	absent	absent	absent	less dentate	dentate stipules intermediate between those of <i>L. nigricans</i> and <i>L. odemensis</i>	absent	dentate at their base

Trait	<i>L. culinaris</i>	<i>L. tomentosus*</i>	<i>L. orientalis</i>	<i>L. odemensis</i>	<i>L. lamottei</i>	<i>L. ervoides</i>	<i>L. nigricans</i>
<b>Length: width ratio of fully extended cotyledon leaf</b>	-	-	-	long, slender cotyledon leaves when fully expanded, particularly accentuated	long, slender cotyledon leaves when fully expanded	-	shorter, ovoidal cotyledon leaves
<b>Testa pattern</b>	-	-	-	distinctive V or W pattern	swirl	-	mottled
<b>Presence or absence of arista</b>	present	-	present or absent	-	present	absent	present
<b>Mean seed weight</b>	-	-	-	-	higher than any other taxa	-	-
<b>Leaflets</b>	upto 20 leaflets		upto 12 leaflets culinaris type	-	-	few and narrow leaflets	upto 10 leaflets <i>L. culinaris</i> type
<b>Calyx teeth to corolla</b>	calyx teeth smaller, subequal or greater than corolla	-	calyx teeth shorter than corolla	-	-	calyx teeth shorter than flowers	calyx teeth subequal or greater than corolla
<b>Pods</b>	pubescent pods	tomentose pods	-	-	-	short pods	-
<b>Satellite chromosome</b>	absent	Satellite chromosome which is much smaller, extremely asymmetrical and bears a minute satellite	absent	absent	absent	absent	absent

\* *L. tomentosus* is similar to *L. culinaris* for most of the traits and differs w.r.t. tomentose pods. It differs from other species by the presence of satellite chromosome. (Source: Ferguson et al., 2000 and Cubero, 1984)

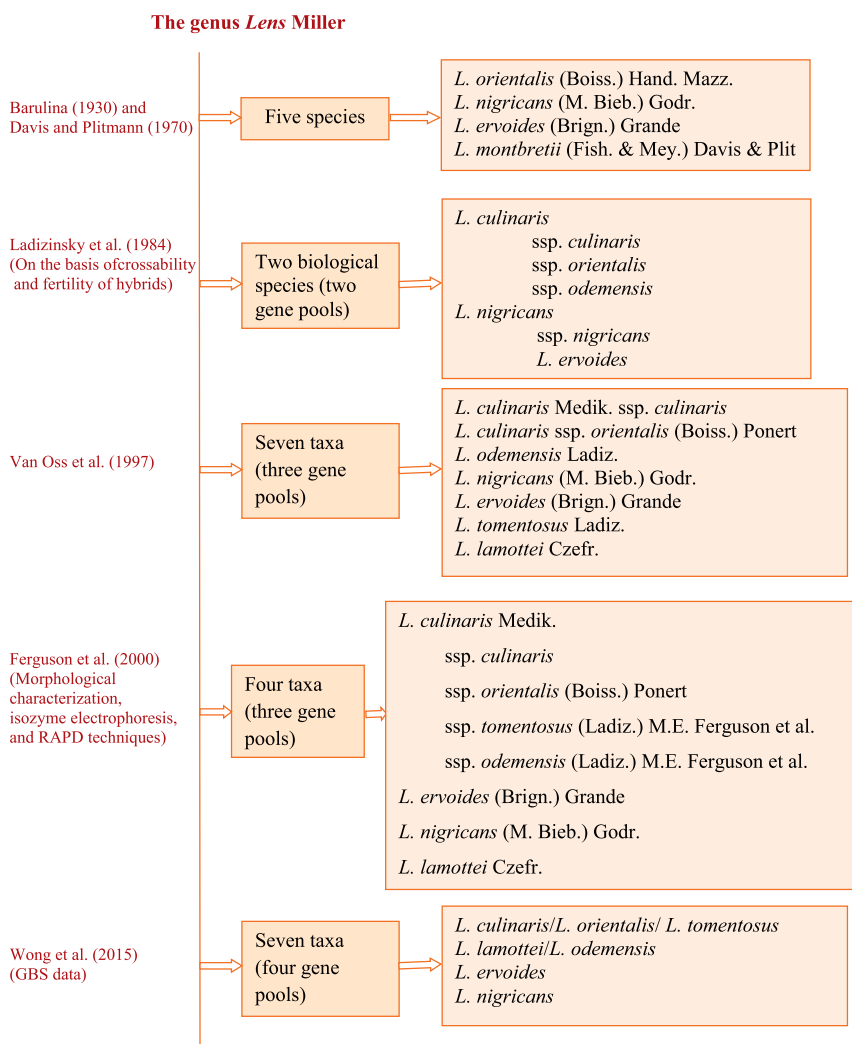


six taxa using seven morphological and 31 SSR primers. SSR primers grouped accessions broadly according to their taxonomic ranks, except *L. culinaris* ssp. *odemensis*. They concluded that *L. culinaris* ssp. *odemensis* seemed to have conserved genetic background and needs revision of its taxonomic status. On the other hand, recent work of Ogutcen et al. (2018) developed an exome capture array and used the data set to assess the interspecific relationships within the genus *Lens*, and found that *L. nigricans*, and *L. culinaris*, had the lowest alignment rates. Their results were in accordance with the results of Wang et al (2015). In a recent study, Dissanayake et al. (2020) identified a total of 422,101 high-confidence SNP markers in a lentil collection consisting of 467 wild and cultivated accessions against the reference lentil genome (cv. CDC Redberry). Phylogenetic analysis clustered the germplasm collection into four groups, namely, *L. culinaris*/*L. orientalis*, *L. lamottei*/*L. odemensis*, *L. ervoides*, and *L. nigricans*. Among all cultivated and wild lentil species, *L. nigricans* exhibited the greatest allelic differentiation across the genome compared to all other species/subspecies. These results indicate that *L. nigricans* is the most distantly related to *L. culinaris* and additional structural variations are likely to be identified from genome sequencing studies. A genome sequencing project is ongoing, to make available complete genomes for *L. culinaris* in version 1.X (<http://knowpulse.usask.ca>) and draft long read genomes for *L. lamottei*, *L. odemensis*, and *L. orientalis* (Bett et al., 2016). The outcomes of this project would further add to the taxonomy of the wild *Lens* species. Various developments related to taxonomic classification are shown in Fig. 2.1.

### 2.3.3 Gene pools

Relatedness, cross-compatibility, ability to produce fertile hybrids and cytogenetics evidences have been used as criteria to divide the wild lentil genus in different gene pools. Based upon Crossability potential, *L. culinaris* ssp. *culinaris* and the putative ancestor of the cultigen, *L. culinaris* ssp. *orientalis*, were grouped as a member of the crop's primary gene pool, whereas *L. odemensis*, *L. ervoides* and *L. nigricans* constitute the secondary gene pool (Ladizinsky et al., 1984; Ladizinsky and Muehlbauer, 1993; Muehlbauer et al., 1995). Based on clustering pattern according to cpDNA divergence, Van Oss et al. (1997) divided *Lens* species in three groups viz. *L. culinaris*, *L. tomentosus* and *L. odemensis*; *L. ervoides* and *L. lamottei*; and *L. nigricans*. However, the gene pool placement of two more lately identified species *L. lamottei* and *L. tomentosus* was found inconsistent among studies. On the basis of crossing only, Hancock (2004) grouped lentil species into three groups and placed intercrossable species *L. nigricans*, *L. ervoides*, and *L. lamottei* into group II or secondary pool. Crossing of Group I species with *L. nigricans* produces nonviable seeds in hybrids due to irregular meiosis (Ladizinsky et al., 1984, 1985). However, the use of embryo rescue can produce viable seed in hybrids derived from crossing between *L. culinaris* and *L. ervoides* (Ladizinsky et al., 1985). They also put *L. tomentosus* in group III or tertiary gene pool as a single species which does not produce viable seed in hybrids derived by crossing with other group of species. These two species *L. ervoides* and *L. tomentosus* were placed in the secondary gene pool by Muehlbauer and McPhee (2005). Fratini and Ruiz (2006) suggested that a hybrid between





**Fig. 2.1:** Developments related to taxonomic classification of genus *Lens* Miller

*L. culinaris* ssp. *culinaris* and *L. nigricans*, *L. ervoides*, and *L. odemensis* developed through embryo rescue can be viable with a rate of 3% -9%. Based on these observations, *L. odemensis* has been considered to be a member of secondary gene pool, and *L. nigricans* and *L. ervoides* were classified in the tertiary gene pool as per Ladizinsky (1993). In addition, Fratini and Ruiz (2006) developed an efficient protocol to recover lentil embryos, which yielded hybrids of cultivated *Lens* species

with *L. odemensis*, *L. ervoides*, and *L. nigricans* which suggested that *L. ervoides* and *L. nigricans* should be placed in the tertiary gene pool. Cubero et al (2009) suggested the placing of *L. odemensis* in the secondary gene pool, while *L. nigricans* and *L. ervoides* can also be part of secondary gene pool as their hybrids with cultivated species could be obtained by embryo rescue. The cultivated *L. culinaris* Medik. subsp. *culinaris* and wild subspecies *L. culinaris* subsp. *orientalis*

(Boiss.) Ponert, the progenitor *L. culinaris* subsp. *tomentosus* Ladiz. and *L. culinaris* subsp. *odemensis* Ladiz are in the primary gene pool, while *L. ervoides* (Brign.) Grande, *L. nigricans* (Bieb.) Godr. and *L. lamottei* Czefr. are in the secondary–tertiary gene pool (Ferguson et al., 2000). Alo et al. (2011) reported that *L. nigricans* and *L. ervoides* are well-defined species at the DNA sequence level while *L. culinaris* subsp. *odemensis*, *L. culinaris* subsp. *tomentosus*, and *L. lamottei* may constitute a single taxon. They also emphasized the need for further hybridization studies to position *L. tomentosus* and *L. lamottei* in the secondary or tertiary gene pool. Gupta et al. (2011) reported that the crossability of cultivated lentil with species of primary (*L. culinaris*, *L. orientalis*, and *L. tomentosus*) and secondary (*L. odemensis*, *L. lamottei*) gene pools was higher compared to the species from tertiary (*L. ervoides*) and quaternary (*L. nigricans*) gene pools. Wong et al. (2015) used next-generation sequencing-based genotyping of 60 lentil accessions and on the basis of phylogenetic tree and STRUCTURE analysis, they identified four gene pools, namely, *L. culinaris*/*L. orientalis*/*L. tomentosus*, *L. lamottei*/*L. odemensis*, *L. ervoides*, and *L. nigricans*, which form primary, secondary, tertiary and quaternary gene pools, respectively. Dissanayake et al. (2020) used SNP markers for analysis and clustered the germplasm collection into four groups, namely, *Lens culinaris*/*Lens orientalis*, *Lens lamottei*/*Lens odemensis*, *Lens ervoides*, and *Lens nigricans*. More recent work using an exome capture array is consistent with these results (Ogutcen, 2018). A genome sequencing project is ongoing, with a complete genomes available for *L. culinaris* in version 1.X (<http://knowpulse.usask.ca>) and draft longread genomes for *L. lamottei*, *L. odemensis*, and *L. orientalis* (Bett et al, 2016).

usask.ca) and draft longread genomes for *L. lamottei*, *L. odemensis*, and *L. orientalis* (Bett et al, 2016).

## 2.4 Characterization and evaluation: Diversity analysis, genetic structure and interrelationships in lentil species

Intensive breeding in cultivated lentil has led to a relatively narrow genetic base. Assessment of genetic diversity in the wild gene pool of lentil, as well as characterization of useful and novel alleles/genes that can be introgressed into elite germplasm, presents new opportunities and pathways for germplasm enhancement, followed by successful crop improvement.

### 2.4.1 Morphological markers

Maintaining and evaluating a large set of accessions of wild *Lens* species is often difficult due to various reasons like inadequate seed germination, high pod shattering and photoperiod sensitivity and certain wild *Lens* species do not flower under normal winter cropping season. These photoperiod sensitive accessions would require artificially lengthened days in the greenhouse or growing them under long days in summer season. Wild relatives of lentil are good sources of disease resistance as well as many useful agronomic characters like, high number of pods per plant, high number of pods per cluster, high number of branches per plant, and short internodes (Gupta and Sharma, 2006). The species-specific morphological traits which have been used to differentiate the species and for their classification have already been discussed in the taxonomy part of this chapter. Here,

we will discuss the available diversity in *Lens* genus based on morphological traits.

Cultivated lentil was initially studied in detail by Barulina (1930), a disciple and wife of N.I. Vavilov, and divided it into two subspecies, *microsperma* and *macrosperma*, according to seed size. Subspecies were defined by characters like pod and seed together with distinct differences in flower length and groups within the subspecies by characters like dehiscence, length of calyx teeth, and number of flowers per peduncle (Cubero et al. 2009). Erskine et al. (1989) studied quantitative agro- morphological variation in the germplasm of 13 major lentil-producing countries and identified three major regional groups. Germplasm from Afghanistan was found markedly different to the Indo-Ethiopian group and had a greater similarity to lentil germplasm from Iran and Turkey. Of all the accessions tested, the Afghan accessions were among the latest to mature. Germplasm from Pakistan was also of the *pilosae* group for qualitative characters, yet intermediate between Afghan and Indian material for quantitative traits. They observed that in cultivated lentil, environmental conditions were the major evolutionary driving force in the case of the cultivated lentil. Erskine et al. (1998) reported that countries with a much smaller area dedicated to lentil production (e.g., Lebanon and Chile) compared to South Asian countries (e.g., India and Pakistan) showed a higher mean coefficient of variation for the nine morpho-agronomic characters scored. Ferguson and Robertson (1999) studied variation in selected phenological and agro-morphological characters in 310 wild lentils accessions and reported that certain *L. culinaris* subsp. *orientalis* accessions had substantially more leaves

per plant, peduncles per plant, pods per plant and seeds per plant, and greater leaf area than two cultivated lentil checks, whereas, wild taxa *L. lamottei* had the highest average 100 seed weight. They also reported high broad-sense heritability for days to average flowering and days to average podding. Accessions of *L. culinaris* subsp. *orientalis* from Uzbekistan, Turkmenistan and Tajikistan had among the largest biomass, the most peduncles per plant and many pods and seeds per plant (Ferguson and Robertson, 1999). Pouresmael et al. (2012) characterized the 96 accessions of wild lentil collection from *L. nigricans*, *L. ervoides* and *L. odemensis* for 24 morphological traits and observed considerable variation among and between different accessions for traits like 100 seed weight (CV= 114%), rachis length (CV= 55%), rachis to peduncle length ratio (CV= 49.5%) and the number of pod per peduncle (CV= 33%), whereas, calyx length and leaflet width (CV= 25%) had the least variation in different species. Based on Shannon index, in qualitative traits, stipule shape (1.02) and pod pigmentation (0.92) showed high variation, whereas, pod dehiscence and shedding had lower variation. The multivariate analysis of quantitative and qualitative traits, morphological characters almost distinguished *L. ervoides* from two other species. Pratap et al. (2014) evaluated 88 accessions of lentil procured from ICARDA, Aleppo, Syria from *L. nigricans*, *L. culinaris* ssp. *odemensis*, *L. culinaris* ssp. *orientalis*, *L. culinaris* ssp. *tomentosus*, *L. ervoides*, *L. lamottei* and unknown *Lens* spp. and obtained significant genetic variation while for all characters except cotyledon colour. *L. ervoides* accessions had useful traits like plant height, internode length and pods/ cluster etc. Kumari et al. (2018) evaluated

96 elite, interspecific (*L. culinaris* × *L. orientalis*) and intraspecific advanced lentil genotypes and observed high heritability and genetic advance were recorded for number of seeds per pod, number of pods per plant, seed yield per plant and biomass per plant. Pouresmael et al. (2018) evaluated 138 genotypes received from ICARDA for 28 quantitative and qualitative traits and obtained high Shannon index belonged to ground colour of testa (1.33), testa pattern (0.85) and color of testa pattern (0.8). The traits seed weight per plant, grain yield, and pod weight per plant had highest variation. Agro-morphological evaluation of 405 diverse global wild annual *Lens* accessions comprising *L. culinaris* ssp. *culinaris*, *L. culinaris* ssp. *orientalis*, *L. culinaris* ssp. *odemensis*, *L. culinaris* ssp. *tomentosus*, *L. nigricans*, *L. ervoides* and *L. lamottei* was carried out by Singh et al. (2014). Based up on the data on various qualitative morphological traits viz. seedling stem pigmentation, leaf pubescence, leaflet size, tendril length, pod shedding, pod dehiscence, flower colour, ground colour of testa, pattern of testa and cotyledon colour and quantitative morphological traits viz. days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, 100 seed weight (g), seed yield per plant (g) and biological yield per plant (g), a core set of 96 accessions was developed. Singh et al. (2020) again characterized and evaluated this core set for agro-morphological traits and validated the wild lentil core set core.

#### 2.4.2 Evaluation for abiotic, biotic and nutritional traits

Gorim and Vandenberg (2017) evaluated root and shoot traits of genotypes of

cultivated lentil and five wild species grown under two water deficit regimes as well as fully watered conditions. They found that root distribution into different soil horizons varied among wild lentil genotypes. Genotypes employed diverse strategies such as delayed flowering, reduced transpiration rates, reduced plant height, and deep root systems to either escape, evade or tolerate drought conditions. Kumari et al. (2018) evaluated 96 elite, interspecific (*L. culinaris* × *L. orientalis*) and intraspecific advanced lentil genotypes and obtained promising results for creating new variation through wide hybridisation and identified lines L-354 and L-437-1 (rust-resistant) and HPLL-32 (moderately rust-resistant) superior for seed yield and related traits. Singh et al. (2020) evaluated wild *Lens* species against various disease pests and identified accessions resistant for rust, powdery mildew and Fusarium wilt.

Bhatty et al. (1976) analysed six genotypes of lentils (*L. culinaris* Medik.) for quality traits and found that on an average, lentil contains 28.6% protein and glutamic acid, aspartic acid, arginine, leucine and lysine as major amino acids. Alghamdi et al. (2014) analysed 35 introduced lentil genotypes (*L. culinaris* Medik.) for nutritional and proximate composition and found that some genotypes were excellent sources of proteins, essential amino acids, minerals, anti-oxidants, total phenolic contents (TPC) and total flavonoid contents (TFC). They reported that genotypes *FLIP2009-64L* and *FLIP2009-69L* could be used as a significant source of yield, total protein, essential amino acids, and antioxidant properties.

#### 2.4.3 Biochemical markers

Biochemical markers like seed storage proteins and isozymes were first used

in 1980s to differentiate the lentil wild species and to lay out geographical distribution (Ladizinsky, 1979b; Hoffman et al., 1986; Muehlbauer et al., 1989; Ferguson et al., 2000). Scippa et al. (2008) clearly differentiated the lentil populations of Conca Casale from the five commercial populations of Capracotta including the *macrosperma* based on protein level and then confirms at DNA level. They concluded that proteomic approach (protein markers, resolved by two-dimensional electrophoresis) can be considered a powerful tool in the phylogenetics and in the identification of the physiological and/or environmental markers that characterize different populations. El-Nahas et al. (2011) used SDS-PAGE of seed proteins to detect some biochemical markers associated with drought tolerance in six local and exotic genotypes of lentil but obtained low levels of genetic diversity. Ullah et al. (2016) evaluated forty four (44) germplasm of *L. culinaris* to explore genetic diversity based on seed storage protein profile. SDS-PAGE analysis showed a band "B6" was monomorphic while five (05) were polymorphic in lentil accessions. They revealed that seed proteins profile provide a powerful tool for estimating diversity existing in the *L. culinaris* genotypes, and can be successfully used to study the variation among the germplasm on geographic distribution. Kumar et al. (2018) studied the diversity among *Lens* wild species based on their elemental composition and found that grouping of accessions in clustering pattern was not in accordance with their geographical origins.

#### 2.4.4 Molecular markers

Introduction of DNA markers declined the use of protein profile and isoenzymatic electrophoresis procedures. Havey and

Muehlbauer (1989) used Restriction fragment length polymorphism (RFLP) markers as first molecular markers for lentil genetic and linkage analyses. Muench et al. (1991) used Chloroplast DNA restriction fragment length polymorphisms (RFLP) and obtained a high degree of fragment length conservation among members of crossability group I, i.e., *L. c. ssp. culinaris*, *L. c. ssp. orientalis* and *L. c. ssp. odemensis*. Randomly amplified polymorphic DNA (RAPD) markers were used to estimate intra- and interspecific variations in twenty cultivars of *L. culinaris* ssp. *culinaris*, including 11 *microsperma* (small-seeded) and nine *macrosperma* (large-seeded) types, and 16 wild relatives (four accessions each of *L. culinaris* ssp. *orientalis*, *L. odemensis*, *L. nigricans* and *L. ervoides*). The results revealed that *L. culinaris* ssp. *orientalis* is the most likely candidate for a progenitor of the cultivated species, and expect for *L. ervoides*, the level of intraspecific variation in cultivated lentil is lower than that in wild species (Abo-elwafa, 1995). The most extensive analysis of the genetic variation in cultivated lentil was carried out by Ferguson et al. (1998c) who analyzed isozyme and RAPD variation in accessions derived from 16 different countries. Ferguson et al. (1998a) mapped the geographical distribution of genetic variation by using randomly amplified polymorphic DNA (RAPDs), in four wild relatives of the cultivated lentil, namely *Lens culinaris* ssp. *orientalis*, *L. odemensis*, *L. ervoides* and *L. nigricans*. They identified centres of diversity for *L. culinaris* ssp. *orientalis* in southeast Turkey and northwest Syria, and in south Syria and Jordan; a centre of diversity in Sweida province, south Syria, for *L. odemensis*, and for *L. ervoides* along the coastal border region between Syria and Turkey

stretching down along the Syrian coast; and a centre of diversity for *L. nigricans* in west Turkey.

Many molecular studies after 1998 were limited to local lentil germplasm genetic diversity analysis with an overview that genetic diversity is higher in or near the area where the domestication of lentil occurred in the Fertile Crescent (Durán and Pérez de la Vega 2004; Hamwieh et al. 2009; Toklu et al. 2009). Duran and Pérez de la Vega (2004) used RAPD and ISSR markers, and observed that continental Spanish *macrosperma* and *microsperma* were more similar between lentils than with *microsperma* from different origins. Reddy et al. (2010) used cross-genera SSRs for diversity analysis of *Lens* species.

Wong et al. (2015) carried out GBS of 60 accessions of different species developed an automated GBS pipeline and they constructed a phylogenetic tree using 5,389 SNPs and grouped the germplasm collection into their respective taxa with strong support. Khazaei et al. (2016) assessed genetic diversity and population structure of cultivated lentil (*L. culinaris* Medik.) collection consisting of 352 accessions originating from 54 diverse countries using 1194 polymorphic single nucleotide polymorphism (SNP) markers. The three clusters obtained complemented the origins, pedigrees, and breeding histories of the germplasm. The three groups included South Asia (sub-tropical savannah), Mediterranean, and northern temperate. Koul et al. (2017) studied genetic structure and relationships of 130 lentil accessions belonging to six taxa using seven morphological and 31 SSR primers. SSR primers grouped accessions broadly according to their

taxonomic ranks, except *L. culinaris* ssp. *odemensis* and they concluded that *L. culinaris* ssp. *odemensis* seemed to have conserved genetic background and needs revision of its taxonomic status. Khazaei et al. (2018) used SNP markers for association mapping analysis to study the seed dimensions of 138 diverse cultivated lentil accessions and identified three marker–seed thickness associations and validated two SNP markers closely associated with seed diameter. Ates et al. (2019) identified genetic diversity of 94 Turkish lentil landraces utilizing 16,383 SNPs based on DArT technology and obtained large genetic variation among Turkish lentil landraces. Highest genetic variation was between geno34 and geno76 (0.9126) while the lowest genetic variation was between geno7 and geno1 (0.0104) and the average genetic variation among 94 lentil landraces was 0.63. Stefano et al. (2019) used high-throughput genotyping by sequencing to resolve the genetic structure of the Mediterranean *ex-situ* lentil collection and observed clustering pattern to be related to geographic patterns and phenotypic traits, indicating that post-domestication routes introducing cultivation in Mediterranean countries and selection were major forces shaping lentil population structure. Dissanayake et al. (2020) assessed genetic relationships in a lentil collection consisting of 467 wild and cultivated accessions that originated from 10 diverse geographical regions. They identified a total of 422,101 high-confidence SNP markers from reference lentil genome (cv. CDC Redberry) and used for phylogenetic analysis which clustered the germplasm collection into four groups, namely, *L. culinaris*/*L. orientalis*, *L. lamottei*/*L. odemensis*, *L. ervoides*, and *L. nigricans*. Genetic distance matrices



revealed a comparable level of variation within the gene pools of *L. culinaris* (Nei's coefficient 0.01468–0.71163), *L. ervoides* (Nei's coefficient 0.01807–0.71877), and *L. nigricans* (Nei's coefficient 0.02188–1.2219). Among all cultivated and wild lentil species, *L. nigricans* exhibited the greatest allelic differentiation across the genome compared to all other species/subspecies

## 2.5 Conclusions

The genus *Lens* Miller is one of the oldest crops domesticated at about the same time as wheat and barley in the Fertile Crescent of the Middle East. The classification of seven species of the genus namely *L. culinaris*, *L. orientalis*, *L. tomentosus*, *L. odemensis*, *L. ervoides*, *L. lamottei* and *L. nigricans*, have been classified into different groups and gene pools. The classification of *L. odemensis*, *L. ervoides*, *L. lamottei* and *L. nigricans* as well as their placement into secondary/tertiary or quaternary gene pool has been doubted by many workers. Recently, based on GBS analysis, Wong et al. (2015) grouped *Lens* species into four groups. The ongoing genome sequencing project on *Lens culinaris* would further add to more accurate classification of the *Lens* species. Further, huge variability is available within wild lentil germplasm as highlighted by the characterization and evaluation studies based on morphological, biochemical and molecular studies. So, there is need to tap this untapped potential of wild species to transfer the trait of interest to the modern cultivars.

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## Chapter 3

# Characterization and Evaluation of Wild Species

### 3.1 Introduction

Introduction, characterization, evaluation and utilization of wild species for distinct morphological and agronomic characteristics, tolerance to major biotic and abiotic stresses, and nutritional traits are prerequisites for conducting successful and effective breeding programmes in annual crop plants (Duvick, 1984; Lazaro et al., 2001; Naghavi and Johansouz, 2005; Singh et al., 2019). The results of the present study revealed that global wild lentil accessions of different origin had a significant variation with respect to morphological and agronomic characters, response to biotic stresses and mineral composition. Characterization refers to the study of gene pool classification which determines the expression of highly heritable traits generally expressed in all environments, whereas evaluation is prerequisite for use of germplasm in crop improvement (Chang, 1985). Characterization and evaluation of germplasm is the key to know the potential and actual value of these genetic resources. The major difference between characterization and evaluation data lies in that characterization is based primarily on plant descriptors of highly

heritable and easily observable traits, whereas, evaluation data is based on characters related to survival, adaptation, productivity, quality and response to various biotic and abiotic stresses. Characters for germplasm evaluation can often be grouped into both qualitative and quantitative nature. Thus, the whole activity of characterization and evaluation facilitates the utilization of germplasm in crop improvement programmes. For effective utilization of genetic resources, it is important that germplasm should be characterized and evaluated for important agro-morphological traits, major biotic and abiotic stresses and nutritional traits, which in turn will help in the identification of superior genetic stocks and subsequently their utilization in breeding programme. Evaluation of genetic resources before their utilization as parents in crossing programme is essentially required to identify the desirable traits for developing the improved plant type through breeding. Lack of evaluation data for characters of economic importance is a major constraint to their use in breeding programme. Domesticated lentil has low amount of variability (Muench et al., 1991; Wong et al., 2015). Like other pulses, it needs substantial improvement

for higher economic returns. The genetic gain is only possible by introgressing useful traits from wild lentils for diversification of cultivated gene pool. It can be accomplished through precise germplasm characterization, which refers to the classification of entire gene pool into distinct morphological traits. These traits can help to distinguish distinct phenotypic groups. A narrow genetic base of the crop and loss of genes for higher productivity, as well as biotic and abiotic stresses were identified as an underlying cause for limited genetic advances in yield of lentil (Ferguson et al., 1998; Ford et al., 1999; Gupta and Sharma, 2006). The biotic stresses are numerous and include: susceptibility to *Ascochyta* blight caused by *Ascochyta lentis*; Anthracnose caused by *Colletotrichum truncatum*; Fusarium wilt caused by *Fusarium oxysporum*; Sclerotinia white mold caused by *Sclerotinia sclerotiorum*; rust caused by *Uromyces fabae* and numerous aphids transmitted viruses. Beside this, pod dehiscence, lodging and suboptimal crop management are some agronomic problems which limit the crop production and also affects seed nutritional value. Heat and drought are major abiotic stresses which lentil encounters in dry areas affecting its yield potential (Kumar et al., 2016). Many economically important traits, such as resistance to biotic and abiotic stresses, are not currently represented in *L. culinaris* ssp. *culinaris*, but have been identified in wild relatives (Tullu et al., 2006; Fiala et al., 2009; Podder et al., 2013; Vail et al., 2012). Therefore, the genetic diversity present in wild lentil are potentially important source of genetic variation for the improvement of cultivated lentil, particularly in such stress environments.

Introgression of these useful genes will greatly enhance the genetic base of cultivated lentil and have great value for future genetic improvement.

Wild relatives have earned great focus in crop research for their better tolerance to abiotic and biotic stresses and constitute an important source of donor genes. For instance *L. nigricans* provided the maximum number of resistant accessions for biotic (wilt, powdery mildew and rust) and tolerance to abiotic stresses (Gupta and Sharma, 2006). A set of 405 global wild annual *Lens* collection of ICARDA genebank was characterized and evaluated for agro-morphological traits under two agro-ecological regions of north-western India and a core set was developed by Singh et al. (2014). This diverse collection comprising 4 accessions of cultivated *L. culinaris* ssp. *culinaris*, 171 of *L. culinaris* ssp. *orientalis*, 42 *L. culinaris* ssp. *odemensis*, 20 of *L. culinaris* ssp. *tomentosus*, 35 of *L. nigricans*, 124 of *L. ervoides* and 9 of *L. lamottei*. This core set was further evaluated for mineral profile.

### 3.2 Trait-specific characterization and evaluation

The present study of characterization and evaluation of wild lentil species carried out at ICAR-NBPGR, New Delhi and different partner centres revealed that *Lens* taxa have a wide range of intraspecific and interspecific variation for majority of the morphological plant characteristics. It further revealed that the character seedling stem pigmentation exhibited variations in all the *Lens* taxa except *L. culinaris* ssp. *culinaris*. Other characters viz. leaf pubescence, leaflet size and tendril length also revealed remarkable variations in all *Lens* taxa.

Substantial variations for pod shedding and dehiscence in majority of the *Lens* species except, *L. culinaris* ssp. *culinaris* were observed. Flower colour was white and purple in majority of wild species, except *L. ervoides*, where it was purple only. The ground colour of testa was mostly grey and brown in all the species except, *L. culinaris* ssp. *culinaris*, where it was all brown. Substantial variations were also found for the pattern of testa in all the wild species. Majority of wild accessions had orange and yellow cotyledon colour except, *L. culinaris* ssp. *tomentosus*, where it was all orange. Evaluation revealed significant variations in the range for the morphological traits as shown in Table 3.1. In general, coefficient of variation ranged from low to high for important agro-morphological traits. However, the mean performance for days to flowering and maturity was lowest in *L. culinaris* ssp. *culinaris*, followed by *L. culinaris* ssp. *orientalis*. Likewise, mean performance for plant height was recorded

maximum in *L. lamottei* and *L. nigricans* and lowest in *L. culinaris* ssp. *culinaris*. The mean number of branches plant<sup>-1</sup> was highest in *L. ervoides* followed by *L. culinaris* ssp. *tomentosus*, *L. culinaris* ssp. *odemensis*, *L. lamottei* and *L. culinaris* ssp. *orientalis*, and lowest in *L. culinaris* ssp. *culinaris*. There was also substantial variation in the range for number of pods plant<sup>-1</sup> with maximum number of pods plant<sup>-1</sup> recorded in *L. ervoides* followed by *L. culinaris* ssp. *culinaris*, *L. culinaris* ssp. *odemensis*, *L. culinaris* ssp. *tomentosus* and *L. culinaris* ssp. *orientalis*. Further, quantitative data revealed maximum diversity among the species *L. ervoides* accessions from Turkey and Syria. Similarly, a set of 310 accessions of wild annual *Lens* species was characterized by Ferguson and Robertson (1999) for morphological and phonological variation and found wide range of variation for high leaves plant<sup>-1</sup>, high peduncle plant<sup>-1</sup>, and high pods plant<sup>-1</sup>. Toklu et al. (2009) also characterized Turkish lentil landraces

**Table 3.1: Wild lentil accessions showing significant variations in range for different traits along with their species**

Trait	Accessions with minimum value	Species	Accessions with highest value	Species
Days to 50% flowering	EC718543 (42)	<i>L. orientalis</i>	EC718304 (143)	<i>L. odemensis</i>
Days to 80% maturity	EC718543 (81)	<i>L. orientalis</i>	EC718251 (176)	<i>L. nigricans</i>
Plant height (cm)	EC718566 (20.2)	<i>L. orientalis</i>	EC718268 (95.5)	<i>L. nigricans</i>
No. of branches/plant	EC718644 (2)	<i>L. orientalis</i>	EC718413 (52)	<i>L. ervoides</i>
No. of pods/ plant	EC718600 (3)	<i>L. orientalis</i>	EC718413 (1002)	<i>L. ervoides</i>
No. of seeds/ plant	EC718374 (3)	<i>L. ervoides</i>	EC718413 (1425)	<i>L. ervoides</i>
No. of seeds/pod	EC718607 (0.7)	<i>L. orientalis</i>	EC718560 (2.3)	<i>L. orientalis</i>
100 seed weight (g)	EC718498 (0.1)	<i>L. orientalis</i>	EC718600 (4)	<i>L. orientalis</i>
Seed yield/ plant (g)	EC718459 (0.01)	<i>L. orientalis</i>	EC718413 (5.7)	<i>L. ervoides</i>
Biological yield/plant (g)	EC718462 (0.2)	<i>L. orientalis</i>	EC718378 (29.5)	<i>L. ervoides</i>

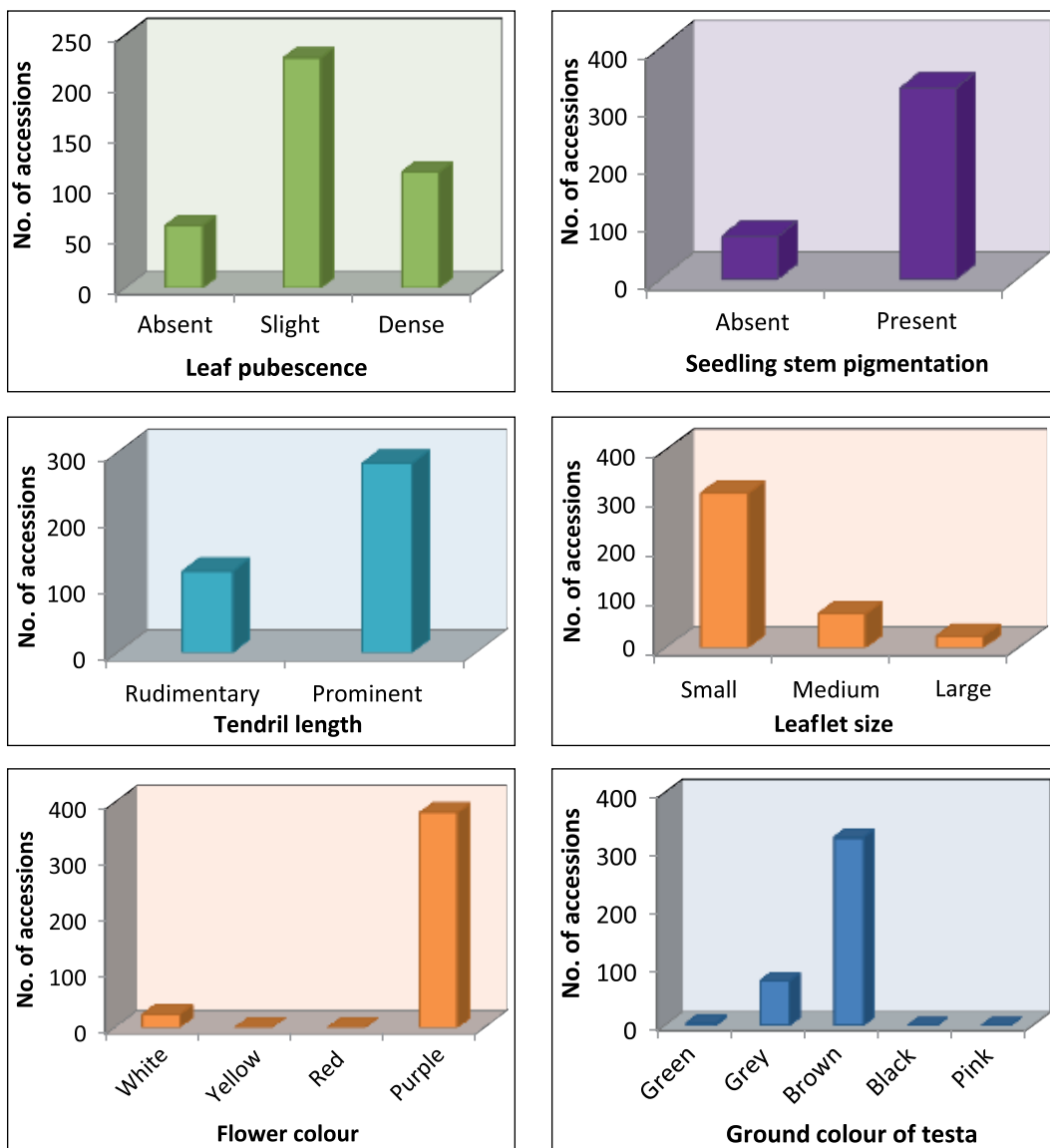


for important agro-morphological traits and observed wide range of diversity with respect to plant height, internode length and 100 seed weight. The data was pooled to work out range and mean, and based on which a dendrogram was created to find out the clustering pattern of wild lentil accessions. The frequency

distribution of distinct morphological traits (Fig. 3.1-3.3) showed wide range of inter- as well as intra-specific variation.

### Leaf pubescence

Pubescence development has been considered an important attribute in lentil taxonomy and is a major criterion



**Fig. 3.1:** Frequency distribution of distinct qualitative traits: a) Leaf pubescence, b) seedling stem pigmentation, c) tendril length, d) leaflet size, e) flower colour, and f) ground colour of testa



to differentiate inter and intra-specific variation. The development of pubescence of the leaves, stems and pods of the plant is a unique wild type trait of *microsperma* lentils, which are probably more primitive in evolution. The presence of pubescence provides protection against water loss and insect attack. Intensity of pubescence varies across plant to plant. In this study, it was observed before maturity. Maximum expression of pubescence was seen on the growing tips at the vegetative stage and also on the inflorescence. Leaf pubescence was found absent in 62 accessions, dense in 115 accessions, whereas, 228 accessions showed slight leaf pubescence (Fig. 3.1).

### Seedling stem pigmentation

Presence or absence of anthocyanin pigmentation on the epicotyl was observed visually in the experimental field. Seedling stem pigmentation was recorded at seedling stage as purple epicotyl pigmentation. A total of 74 accessions showed pigmentation whereas it was absent in rest of 331 accessions (Fig. 3.1).

### Tendrill length

Tendrill type was another important character observed with sufficient variability in wild lentil accessions. Tendrill length was recorded during pod filling stage. Prominent tendrill length was seen in 283 accessions and rudimentary in 122 accessions (Fig. 3.1).

### Leaflet size

Remarkable diversity was observed for leaflet size. Leaflet size was observed on fully expanded leaves on lower flowering nodes. It was assessed as small, medium and large. Out of 405 accessions screened for the trait, 313 accessions showed small leaflet size, medium was observed in

69 accessions and large leaflet size was observed in 23 genotypes (Fig. 3.1).

### Flower colour

This trait was extremely variable in wild lentil gene pool and was categorized as white, yellow, red and purple. Colour of fully developed freshly open flowers was observed visually in the morning time. Flower colour was observed as white in 23 accessions, purple in 382 accessions, whereas, no accession was observed with yellow or red flower colour (Fig. 3.1).

### Ground colour of testa

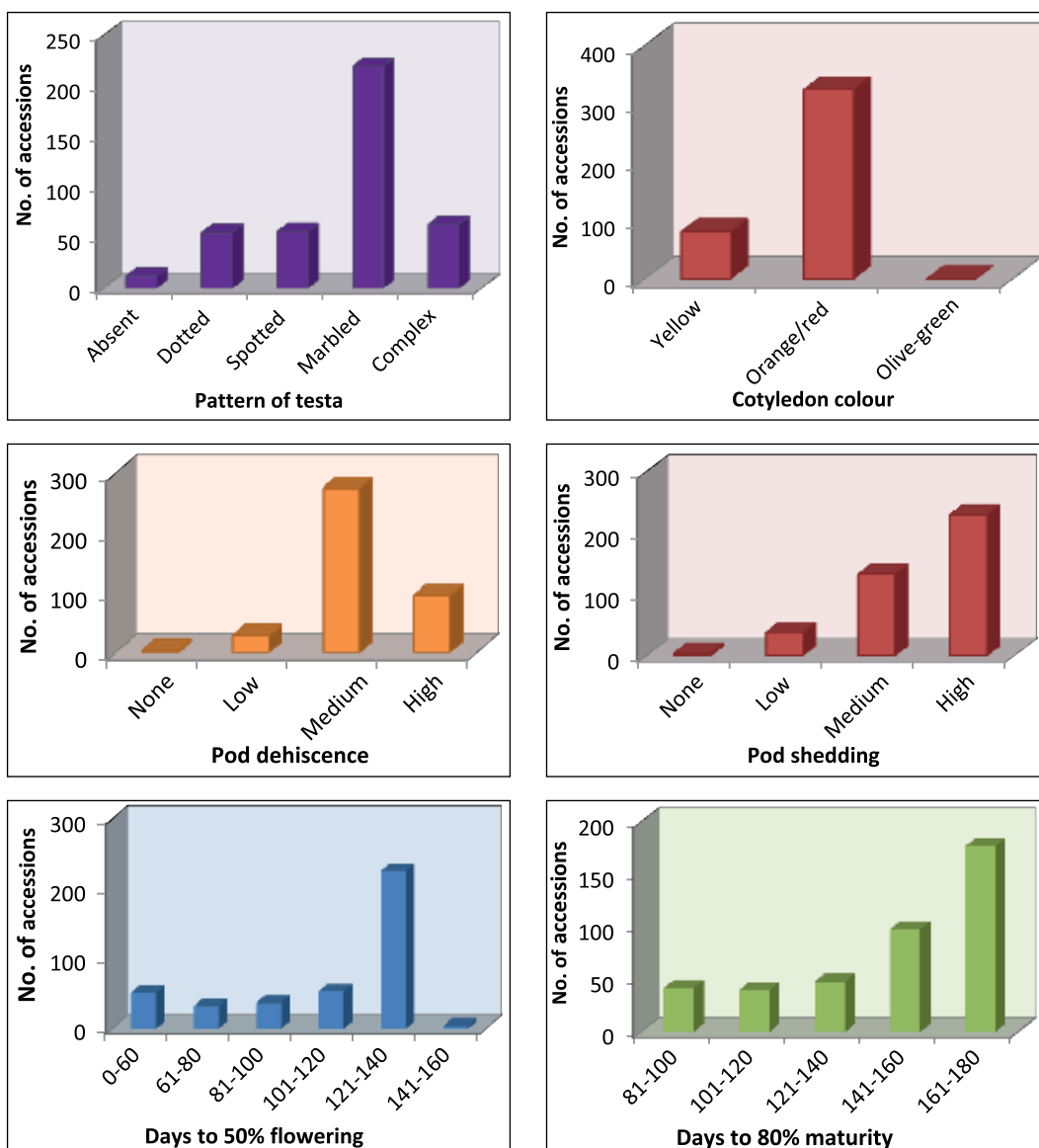
It was observed on seeds less than three months old. Ground colour of testa was observed in all 405 wild lentil accessions which were screened and green testa colour was seen in 4 accessions, grey in 78 and brown in 323 accessions, while no accession with black and pink testa colour was observed (Fig. 3.1).

### Pattern of testa

Spotting pattern on seed coat was recorded after harvesting the seeds and observed on seeds less than three months old as dotted, spotted, marbled and complex in pattern. It was observed as dotted in 55 accessions, spotted in 56 accessions, marbled in 219 and complex in 63 accessions, whereas rest accessions (12) did not exhibit this trait (Fig. 3.2).

### Cotyledon colour

Cotyledon colour of lentil has been reported as yellow, orange/red and olive green. It was recorded after harvesting and colour of cotyledons of 20 randomly selected seeds of each accession was observed visually after removal of seed coat with the help of a sharp blade. It was observed as yellow



**Fig. 3.2:** Frequency distribution of distinct qualitative and quantitative traits: a) Pattern of testa, b) cotyledon colour, c) pod dehiscence, d) pod shedding, e) days to 50% flowering, and f) days to 80% maturity

in 81 accessions and orange /red in 324 accessions while no accession exhibited olive green cotyledon colour (Fig. 3.2).

### Pod dehiscence

Pod dehiscence is a trait of great economic value as it sometimes causes significant

loss before or during harvesting time. It is a typical feature of wild lentils. It was scored after one week of maturity on scale 1- 9. Total 405 accessions of wild lentil were screened and high pod dehiscence was observed in 96 accessions and 276 accessions showed

medium pod dehiscence, 29 accessions showed low pod dehiscence whereas pod dehiscence was absent in four accessions (Fig. 3.2).

### Pod shedding

Pod shedding was scored during harvesting, a week after maturity of seed. It was recorded as none, low, medium and high. Out of total 405 accessions screened, no pod shedding was recorded only in 4 accessions, low pod shedding in 38 accessions, medium pod shedding in 133 accessions and high pod shedding in 230 genotypes (Fig. 3.2).

### Days to 50% flowering

Flowering time is very important for crop adaptation and yield, which determines the length of the vegetative phase and conditions of crop exposure during reproductive growth to climatic settings. Flowering time is highly influenced by temperature and showed considerable variation. It is number of days taken from seed sowing to attain 50% flowering. Flowering time ranged from 42 days to 143 days as shown in Fig. 3.2. Earliest flowering was seen in *L. orientalis* accession EC718543 (42 days) and late flowering was observed in *L. odemensis* accession EC718304 (143 days).

### Days to maturity

Days to 80% maturity is the number of days taken from seed sowing to attain 80% maturity of pods. Days to 80% maturity ranged from 81 to 176 days among wild lentil accessions (Fig. 3.2). An earliest maturity was observed in the accession EC718543 (*L. culinaris* ssp. *orientalis*) and longest maturity in accession EC718251 (*L. nigricans*).

### Plant height (cm)

Plant height was measured at the time of 80% maturity of five representative plants of each accession. It was recorded in centimeters from ground level to the extended foliage of the plant. The plant height showed extreme variation and a very good amount of variability was observed ranging from 20.2 cm to 95.5 cm (Fig. 3.3). *L. nigricans* accession EC718268 was recorded with tallest plant height whereas *L. orientalis* accession EC718566 was the shortest among the lentil germplasm evaluated.

### Number of branches per plant

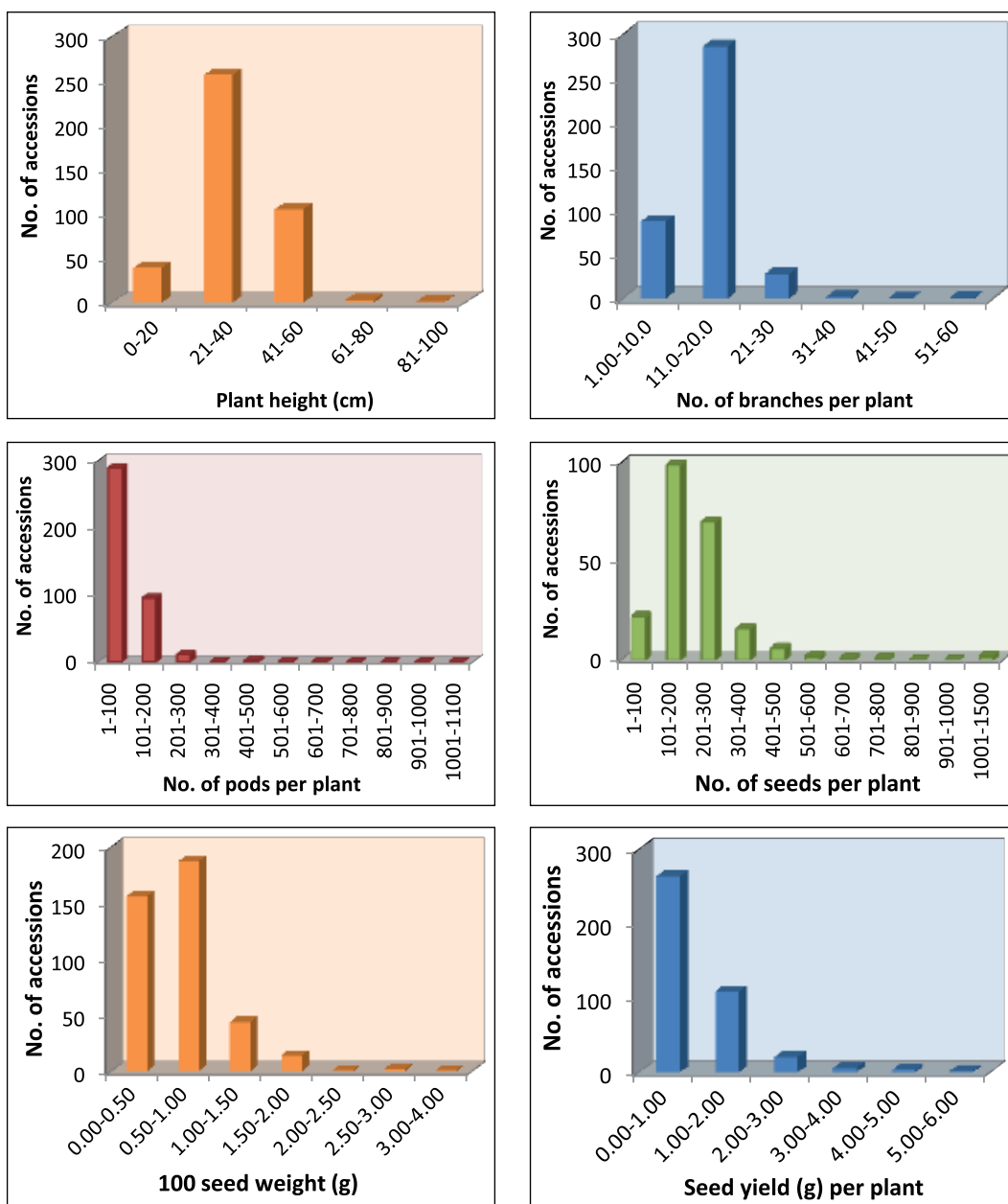
The number of branches per plant was observed on main stem at late flowering stage. It varied between 2 to 52 (Fig. 3.3). *L. ervoides* accession EC718413 had the highest number of branches. This trait is very significant as it contributes directly to seed yield. Therefore, increasing branches per plant may be an ideal trait for enhancing seed yield.

### Number of pods per plant

This is the average number of fully developed pods per plant from each accession counted at maturity stage. Some accessions produced two or three pods per leaf axil in contrast to usual one. Mature and effective pods on the main shoots, primary and secondary branches were counted and averaged. Highest number of pods were present in *L. ervoides* accession EC718413 (1002 pods plant<sup>-1</sup>) and the minimum number in *L. culinaris* ssp. *orientalis* accession EC718600 (3 pods plant<sup>-1</sup>). The frequency distribution for the trait is shown in Fig. 3.3.

### Number of seeds per plant

Number of seeds per plant was recorded which ranged from 3 to 1425 seeds per plant



**Fig. 3.3:** Frequency distribution of distinct quantitative traits: a) Plant height, b) number of branches per plant, c) number of pods per plant, d) number of seeds per plant, e) 100 seed weight, and f) seed yield per plant

as depicted in the frequency distribution figure (Fig. 3.3). Maximum number of seeds was observed in accession EC718413 and minimum number in accession EC718374,

both belonging to *L. ervoides* species. Therefore, *L. ervoides* accession could be utilized for genetic improvement of cultivated lentil for enhancing pod number trait.

### 100 seed weight (g)

After harvesting, seeds were sun dried and then weight of 100 seeds selected at random was recorded in grams. Based on average, 100 seed weight of 405 wild lentil accessions which were scored ranged from 0.1 to 4.0 g. Accession EC718600 (*L. culinaris* ssp. *orientalis*) had highest seed weight (Fig. 3.3).

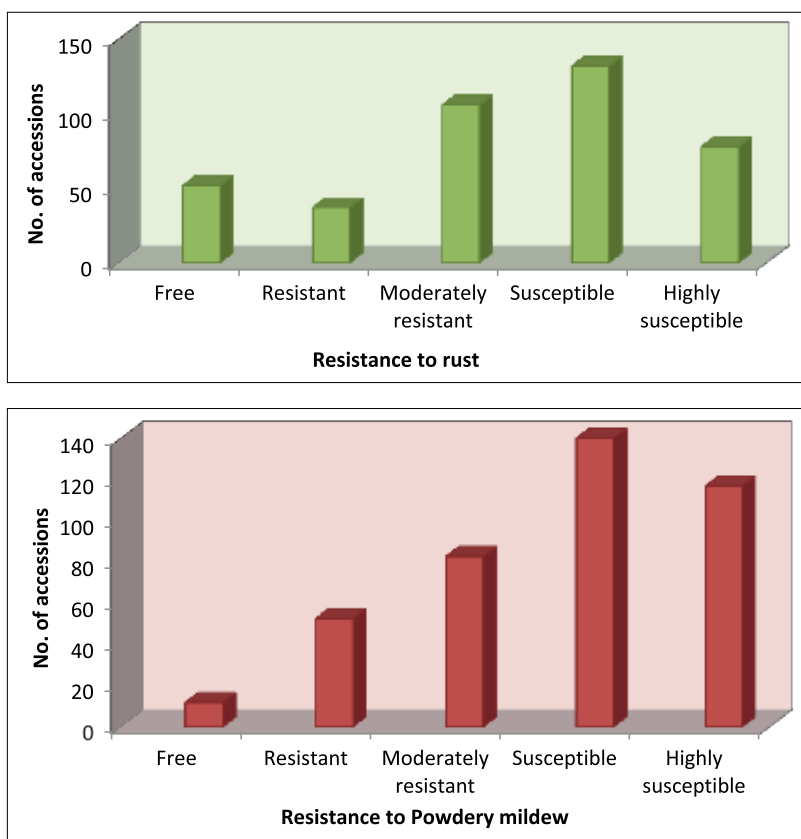
### Seed yield per plant (g)

Seed yield per plant was recorded from all wild lentil accessions. The highest seed yield per plant was observed in *L. ervoides* accession EC718413 (*L. ervoides*) with 5.7 g. The frequency distribution for the seed yield per plant (g) is shown in Fig. 3.3.

## 3.3 Screening against foliar biotic stresses

Evaluation of genetic resources in any crop against diseases and identification of trait-specific accessions is very crucial as variability of their degree of expression not only depends upon the germplasm but also upon virulence of pathogen and the environmental conditions. Domesticated lentil suffers from important yield attributing traits, and major biotic and abiotic stresses. Among important abiotic stresses, cold, drought, heat, salinity, nutrient deficiency and toxicity are most prevailing ones whereas among biotic stresses, lentil rust, powdery mildew, ascochyta blight and fusarium wilt are major diseases in lentil growing regions. Lentil rust is the most prevalent fungal disease affecting lentil productivity in Indian sub-continent and Ethiopia. It is a major constraint in those areas where mild temperature and humid conditions favor the occurrence of this fungus (Muehlbauer et al., 1995). In cultivated lentil, partial resistance to

*Uromyces fabae* has been reported (Gupta and Sharma, 2006) but wild annual *Lens* taxa showed complete resistant reaction against this pathogen and some resistant wild accessions have been identified for introgression into the background of cultivated varieties. Likewise, powdery mildew is another prevailing biotic stress in India and cultivated germplasm has also shown partial resistance against the pathogen. Singh et al. (2014) screened a global collection of 405 wild lentil accessions against two major foliar diseases i.e. rust caused by *Uromyces fabae* and powdery mildew caused by *Erysiphe polygoni* under two agro climate regions in the north western Indian conditions. The study revealed some wild accessions resistant against powdery mildew (EC718317, EC718314 and EC718378), and rust (EC718600, EC718605, EC718522, EC718526, EC718246, EC718247 and EC718248). These rust and powdery mildew resistant gene sources could be of great significance for utilization purposes into the cultivated background and for exploiting in breeding resistant varieties especially for the epidemiologically important regions in the lentil growing areas of India or elsewhere. The data was recorded on terminal diseases reaction at vegetative and reproductive plant stage using 1-9 rating scale. Based on diseases score, the accessions were categorized for their reaction to rust and powdery mildew infection as: 1= asymptomatic (Free), 3= resistant (R), 5= moderately resistant (MR), 7= susceptible (S) and 9= highly susceptible. The study revealed that many of the wild lentil accessions were resistant and moderately resistant to rust and powdery mildew. Out of 405 accessions which were screened for rust resistance, 52 accessions were found asymptomatic, 37 accessions were resistant, 106 were



**Fig. 3.4:** Frequency distribution of resistance against biotic stresses: a) Resistance to rust, and b) resistance to powdery mildew

moderately resistant, 132 were susceptible and 78 accessions were highly susceptible to rust (Fig. 3.4). Likewise, in screening of powdery mildew, only 12 accessions were reported asymptomatic or free, 53 were resistant, 83 accessions were moderately resistant, 140 accessions were susceptible and 117 accessions were highly susceptible (Fig. 3.4). These resistant gene sources can be exploited for the induction of resistance into the elite genetic background of lentil varieties. The wild lentil accessions, which showed resistant disease reaction to *Fusarium* wilt included EC718234, EC718476, EC718488, EC718513, EC718521, EC718555 and EC718566 (*L. orientalis*); EC718277 (*L.*

*odemensis*); EC718686 and EC718782 (*L. tomentosus*). Accessions EC718329, EC718401, EC718411 and IG136626 (*L. ervoides*); EC718238, EC718242, EC718246, EC718256, EC718258 and EC718263 (*L. nigricans*) and EC718687 (*L. lamottei*) were found resistant against the wilt.

### 3.4 Development of core set

A core collection is a limited set of accessions of any crop gene pool. Concept of core collection was originally developed in 1980 (Frankel and Brown, 1984). It represents about 10% of the entire collection that captures most of

the available genetic diversity of species (Brown, 1989). But depending upon the diversity and size of collection, number of accessions in a core set may vary from 5% to 20%. While mini core collection represents about 1% but capture most of the useful variation of the crop (Upadhyaya and Oritz, 2001). The core and mini core should be designed with a minimum repetition and maximum representation of entire genetic diversity. The core collection should serve as a working collection and should be extensively screened and the accessions which are not included in the core collection would be designated as reserve collection. The core collection being smaller in size in comparison to the whole collection, can be used very effectively as a starting point for basic and strategic research involving screening of the germplasm against desirable traits. Development of regional core sets of the germplasm has been suggested for harnessing the wider adaptability and genetic enhancement of the yield. The

core collection of wild lentil gene pool could serve as a working collection for the users to be extensively evaluated and validated for lentil genetic improvement. Based on phenotypic characterization data, the core has been developed in wild lentil which provides useful sources of new traits (Singh et al., 2014). Three different core sets were derived from entire wild lentil collection based on combined data on both qualitative and quantitative variables, data only on qualitative variables and data on quantitative variables. A total of 86 accessions (21%) were selected, when data only on quantitative variables was used, whereas, 36 accessions (about 9%) could be selected, when data only on qualitative characters was used for analysis. Using qualitative variables alone, a smaller core size of about 9% was achieved (Table 3.2). Representation of proportionately greater number of desired accessions in the core set derived from qualitative morphological data could be the existence of good polymorphism with different descriptor

**Table 3.2: Species-wise representation of entire *Lens* collection and representation of accessions in core sets derived from different data sets**

Lens species	Accessions in entire collection	Accessions in core sets		
		I	II	III
<i>L. culinaris</i> ssp. <i>culinaris</i>	4	4	4	3
<i>L. culinaris</i> ssp. <i>orientalis</i>	171	21	19	7
<i>L. culinaris</i> ssp. <i>odemensis</i>	42	15	12	4
<i>L. culinaris</i> ssp. <i>tomentosus</i>	20	12	9	6
<i>L. nigricans</i>	35	18	17	7
<i>L. ervoides</i>	124	20	19	5
<i>L. lamottei</i>	9	6	6	4
<b>Total</b>	<b>405</b>	<b>96 (23.7%)</b>	<b>86 (21%)</b>	<b>36 (8.9%)</b>

Core sets based on I = combined data on both quantitative and qualitative variables; II = data only on quantitative variables, and III = data only on qualitative variables, respectively.

states for qualitative traits with major gene effect. A total of 66 and 25 accessions were common between the core set developed using combined data on qualitative and quantitative variables and that obtained from quantitative and qualitative variables alone, respectively. Only 15 accessions were common between the core sets obtained using both quantitative and qualitative variables separately. The wild lentil accessions comprising core set along with

their country of origin are listed in Table 3.3. Among core set accessions, qualitative data analysis revealed maximum interspecific as well as intraspecific variability between *L. ervoides* and *L. culinaris* ssp. *orientalis*, and among *L. culinaris* ssp. *orientalis*, accessions, respectively. A few promising accessions found across all the core sets are listed in Table 3.4 based on agronomic traits and major biotic stresses. The pictures of promising wild lentil accessions identified

**Table 3.3: List of wild lentil core set accessions along with their country origin**

S. No.	Species/ accessions	Origin
<b><i>L. culinaris</i> ssp. <i>orientalis</i></b>		
1	EC718234	Turkey
2	EC718617	Turkey
3	EC718456	Israel
4	EC718470	Turkey
5	EC718475	Turkey
6	EC718476	Turkey
7	EC718479	Turkey
8	EC718488	Syria
9	EC718490	Syria
10	EC718505	Syria
11	EC718513	Syria
12	EC718515	Syria
13	EC718519	Syria
14	EC718521	Syria
15	EC718529	Turkey
16	EC718548	Syria
17	EC718554	Syria
18	EC718555	Syria
19	EC718560	Syria
20	EC718566	Syria
<b><i>L. nigricans</i></b>		
21	EC718585	Tajikistan
22	EC718596	Turkey
23	EC718605	Turkey
24	EC718607	Syria
25	EC718235	Syria
26	EC718236	Syria
27	EC718238	France
28	EC718239	Alpes-Cote d'Azur
29	EC718241	France
30	EC718242	Spain
31	EC718245	Italy
32	EC718254	Spain
33	EC718256	Ukraine
34	EC718257	Turkey
35	EC718258	Turkey
36	EC718682	Croatia
37	EC718262	Turkey
38	EC718266	Italy
39	EC718270	Croatia
40	EC718273	Spain



S. No.	Species/ accessions	Origin
41	EC718275	Turkey
<b><i>L. culinaris ssp. tomentosus</i></b>		
42	EC718471	Turkey
43	EC718473	Syria
44	EC718658	Syria
45	EC718659	Syria
46	EC718660	Turkey
47	EC718661	Turkey
48	EC718662	Syria
49	EC718673	Syria
<b><i>L. lamottei</i></b>		
50	EC718252	France
51	EC718685	France
52	EC718252	Spain
53	EC718686	Spain
54	EC718692	France
<b><i>L. culinaris ssp. odemensis</i></b>		
55	EC718243	Palestine
56	EC718276	Turkey
57	ILWL 56	Palestine
58	EC718281	Syria
59	EC718282	Syria
60	EC718283	Syria
61	ILWL 196	Not known
62	EC718291	Syria
63	EC718295	Turkey
64	EC718297	Syria
65	EC718298	Syria
66	EC718301	Syria
67	EC718302	Turkey

S. No.	Species/ accessions	Origin
68	EC718303	Turkey
69	EC718311	Israel
70	EC718694	Syria
<b><i>L. ervoides</i></b>		
71	EC718318	Spain
72	EC718316	Croatia
73	EC718321	Croatia
74	EC718322	Montenegro
75	EC718329	Turkey
76	EC718331	Turkey
77	EC718332	Turkey
78	EC718333	Turkey
79	EC718335	Turkey
80	EC718432	Turkey
81	EC718451	Turkey
82	EC718362	Syria
83	EC718370	Turkey
84	EC718374	Turkey
85	EC718378	Turkey
86	EC718383	Turkey
87	EC718401	Lebanon
88	EC718404	Lebanon
89	EC718407	Syria
90	EC718411	Syria
91	EC718413	Syria
92	EC718417	Turkey
93	EC718418	Turkey
94	EC718439	Israel
<b><i>L. culinaris ssp. culinaris</i></b>		
95	ILL 8006	Syria
96	ILL 10829	Syria

**Table 3.4: Identification of some promising accessions for few agronomic and major biotic traits for their introgression in lentil enhancement selected from the entire *Lens* collection**

S. No.	Accessions	Species	Gene pool	Trait of Interest	Origin
1	EC718461	<i>L. culinaris</i> ssp. <i>orientalis</i>	Primary	Resistant to powdery mildew	Turkey
2	EC718580	<i>L. culinaris</i> ssp. <i>orientalis</i>	Primary	High number of pods plant <sup>-1</sup> , resistant to powdery mildew	Turkmenistan
3	EC718287	<i>L. culinaris</i> ssp. <i>odemensis</i>	Primary	High number of pods plant <sup>-1</sup> , resistant to rust	Syria
4	EC718446	<i>L. culinaris</i> ssp. <i>tomentosus</i>	Primary	High number of pods plant <sup>-1</sup>	Syria
5	EC718257	<i>L. nigricans</i>	Secondary/ Tertiary	High number of pods plant <sup>-1</sup> , resistant to rust and powdery mildew	Turkey
6	EC718682	<i>L. nigricans</i>	Secondary/ Tertiary	High number of pods plant <sup>-1</sup> , resistant to rust and powdery mildew	Turkey
7	EC718647	<i>L. ervoides</i>	Secondary/ Tertiary	Resistant to powdery mildew	Turkey
8	EC718370	<i>L. ervoides</i>	Secondary/ Tertiary	High number of pods plant <sup>-1</sup> , resistant to rust and powdery mildew	Turkey

(Source: Singh et al., 2014)

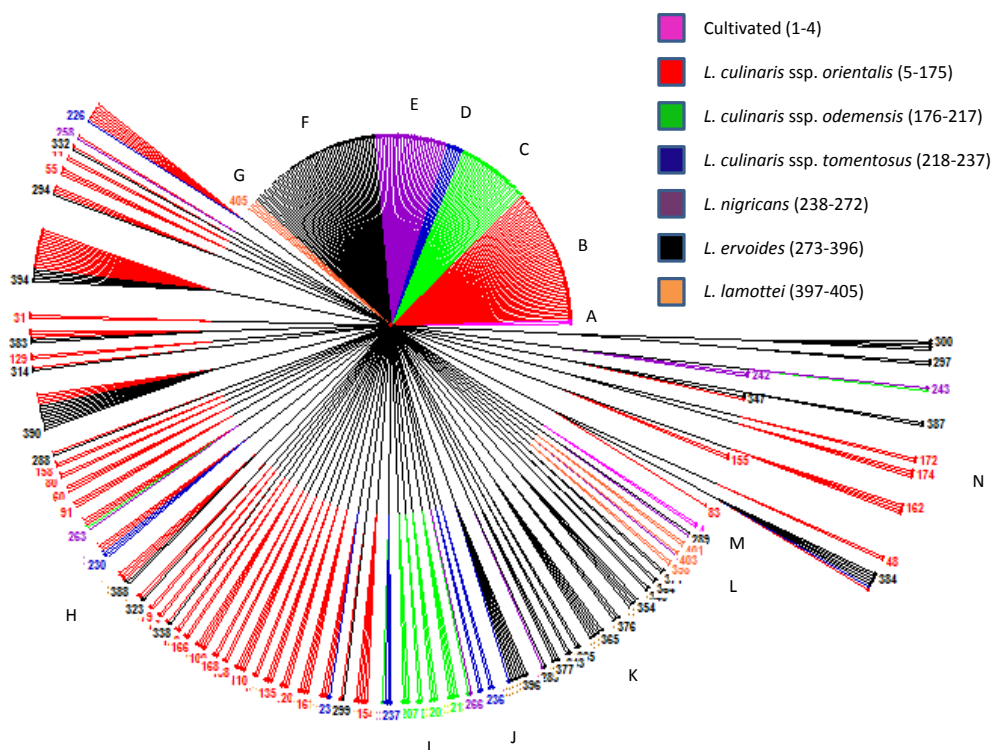
for target traits of interest are presented in Fig. 3.5.

Besides possessing resistance against diseases, these accessions were also found promising for yield related trait like high number of pod plant<sup>-1</sup> which has significant breeding potential for yield enhancement. Maximum representation of accessions in core collections, derived from all data sets was from Turkey, followed by Syria, indicating rich diversity for many of the wild relatives of cultivated lentil. Further, the study revealed that the Shannon Diversity Indices (SDIs) were always higher in the core sets derived from different data sets which indicates better representation of existing diversity in each core set.

Diversity analysis was also carried out using both qualitative and quantitative phenotypic data of complete collection of 405 wild accessions and then compared with core set developed. Based on qualitative data, the hierarchical clustering pattern of complete collection (Fig. 3.6 and 3.7) revealed that maximum variability was interspecific and not limited to a particular country. Accessions belonging to species *L. ervoides* from Turkey and Syria presented maximum diversity based on quantitative data. Qualitative data analysis of core set accessions showed maximum interspecific as well as intraspecific variability between *L. ervoides* and *L. culinaris* ssp. *orientalis*, and among *L. culinaris* ssp. *orientalis*, accessions, respectively. On the basis of



**Fig. 3.5:** Promising accessions identified for target traits in different wild lentil species



**Fig. 3.6:** Hierarchical clustering of *Lens* accessions based on qualitative phenotypic data

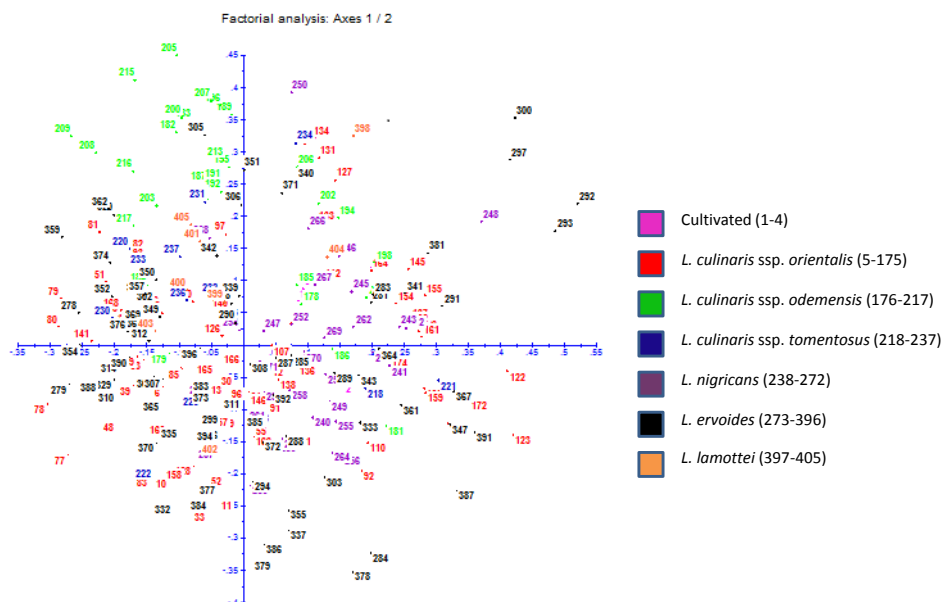
(Source: Singh et al., 2014)

quantitative data of core set accessions, maximum diversity was observed in *L. ervoides* accessions from Turkey. Core set included representative accessions from each group categorised based on entire set of qualitative data excluding two to three accessions from *L. nigricans* and *L. culinaris* ssp. *tomentosus*, each (Fig. 3.8). So, core set accessions revealed substantial diversity based on qualitative data analysis as available in the entire wild lentil germplasm.

### 3.5 Validation of wild lentil core accessions

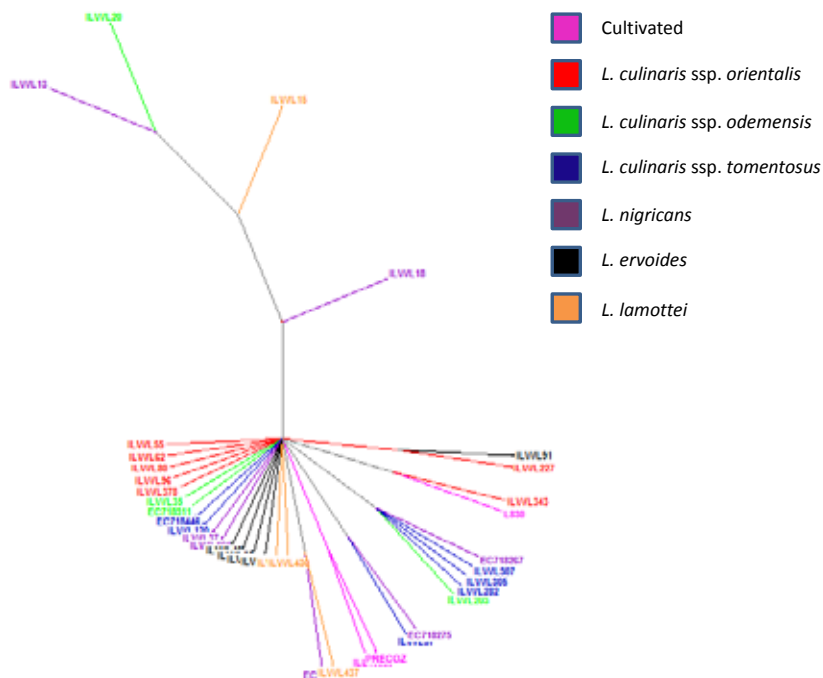
The primary objective of this study was to evaluate and validate wild lentil core

accessions for identification of economically useful agro-morphological traits and resistance against major biotic stresses (rust, powdery mildew and Fusarium wilt). The study revealed substantial variations in seed yield and its important attributes. Further, the diversity analysis of wild lentil core accessions exhibited two major clusters which were bifurcated into sub-clusters, thereby suggesting their broader genetic base. The principal component analysis also manifested that seed yield plant<sup>-1</sup>, number of seeds plant<sup>-1</sup>, number of pods plant<sup>-1</sup>, harvest index and biological yield plant<sup>-1</sup> contributed significantly to the total genetic variation assessed in wild lentil core accessions. Moreover, some of the wild core accessions collected from Syria



**Fig. 3.7:** Factorial analysis of *Lens* accessions based on qualitative phenotypic data

(Source: Singh et al., 2014)



**Fig. 3.8:** Hierarchical clustering of *Lens* core set accessions based on qualitative phenotypic data

(Source: Singh et al., 2014)



and Turkey regions showed resistance against more than one disease indicating rich diversity of lentil genetic resources. The identification of most promising genotypes carrying resistance against major biotic stresses could be utilized in the cultivated or susceptible varieties of lentil for enhancing genetic gains (Singh et al., 2020). The study has identified some trait specific accessions, which could also be taken into the consideration while planning distant hybridization in lentil. Further, the study has assisted in identifying the confirmed and stable gene sources (donors) across intra and interspecific accessions viz. EC789113 of *L. odemensis* for rust and high pod number; EC718515, EC718605 of *L. orientalis* for rust and powdery mildew; EC718682, EC718235 and EC718257 of *L. nigricans* for rust and powdery mildew, EC718266 of *L. nigricans* for powdery mildew and Fusarium wilt and EC728782 of *L. tomentosus* for rust and Fusarium wilt. These gene sources could be taken in lentil wide hybridization program for enhancing genetic gains of cultivated varieties and could also be shared among lentil breeders/researchers in the country or elsewhere under Standard Material Transfer Agreement (SMTA) for strengthening the on-going lentil genetic improvement programs.

### 3.6 Biochemical evaluation of wild lentil core set for mineral profile/composition

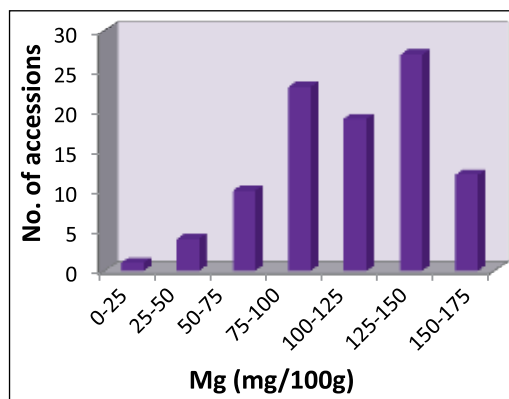
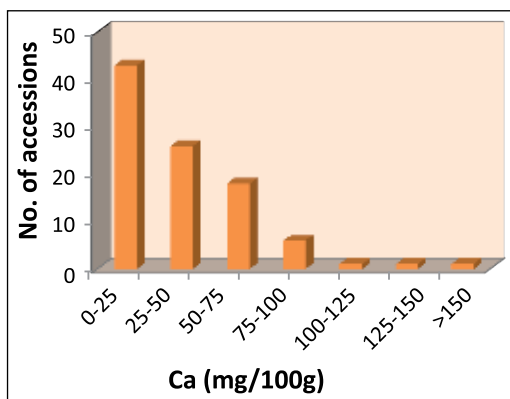
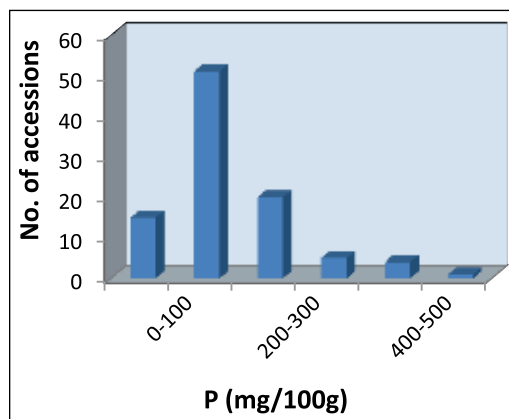
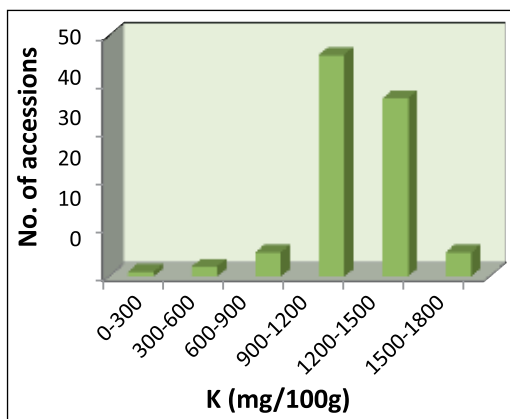
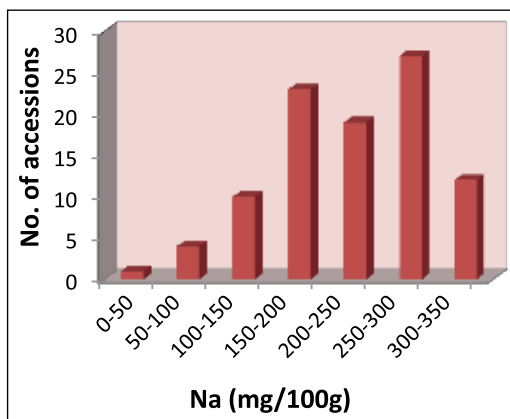
Globally, billions of people are not receiving the required daily dose of minerals particularly essential micronutrients. Human beings require these minerals for maintaining physiological activities and so the general health. Inadequate intake of food over prolonged periods of time results in energy malnutrition/undernutrition

due to deficiency of macronutrients like carbohydrates, proteins, fats, water, and minerals like Ca, Mg and K etc. Nine elements namely iron, zinc, copper, manganese, molybdenum, chromium, fluoride, iodine and selenium perform atleast one physiological function in human metabolism, are ranked as essential micronutrients and should be consumed regularly in food or as supplements (Pogatschnik, 2014; Stehle et al., 2016). Globally, among children under 5 year age, 150.8 million (22.2%) are stunted and 50.5 million are wasted. Meanwhile 20 million babies are born of low birth weight each year. Women have a higher burden than men when it comes to certain forms of malnutrition: one third of all women of reproductive age have anaemia. Millions of women are still underweight (Global Nutrition Report, 2018). Other than macro- and micro-minerals, some heavy metals also enter into the body through food chain. Some of these elements are required in trace amounts in the body such as Co is an essential component of vitamin B<sub>12</sub> and Ni has a role in metabolic activities (Cundeva et al., 2007).

Crop wild relatives (CWRs) have always been considered as a source of traits like resistance to biotic and abiotic stresses and nutritional parameters. In literature, scarce information is available on elemental composition of wild lentil species. So, there is an urgent need to identify or develop value added material for the essential micronutrients through fortification/bio-fortification particularly in crops that can be used as staple food, to eradicate the problem of hidden hunger. As lentil can be used as staple crop and makes a candidate crop for biofortification, wild lentil core set was analyzed to determine variations in mineral composition with an aim to find out its bio-fortification potential.

The accessions comprising wild lentil core collection were analysed for different minerals including Na, K, P, Ca, Mg, Fe, Zn, Cu, Mn, Mo, Ni, Pb, Cd, Co and As (Kumar et al., 2018). Sodium (Na) and potassium (K)

were determined using flame photometer 128 (Systronics), phosphorus (P) by using spectrophotometer DR5000 (HACH). Calcium (Ca) and magnesium (Mg) were determined by using Atomic Absorption Spectrophotometer (AnalytikJena ZEE nit 700, Germany). Other mineral elements namely, iron, copper, zinc, manganese, molybdenum, nickel, lead, cadmium, cobalt and arsenic were determined using ICP-Mass Spectrophotometer (Nexlon® 300X Series, Perkin-Elmer). The physiological and biological activity, range, promising accessions and frequency distribution of important minerals are discussed here. The frequency distribution of different minerals showed wide range of variation (Fig. 3.9 and 3.10).



**Fig. 3.9:** Frequency distribution of macro-minerals: a) Na, b) K, c) P, d) Ca and e) Mg



### 3.6.1 Macro-nutrients

#### Sodium

Na is mainly required in maintaining the electrolyte balance (Kaplan, 2002).

Na content in seed of wild lentil core set accessions ranged from 30-318 mg/100g. *L. culinaris* ssp. *tomentosus* accession ILWL90 from Turkey had highest Na content. Maximum variability for the Na content found in *L. ervoides* accessions which ranged from 72.50 to 316.67 mg/100g. Maximum number of accessions (27) had Na content in the range 250-300 mg/100g followed by 23 accessions in the range of 150-200 mg/100g.

#### Potassium

Potassium has many biological functions. Along with Na, K is also required in maintaining the electrolyte balance

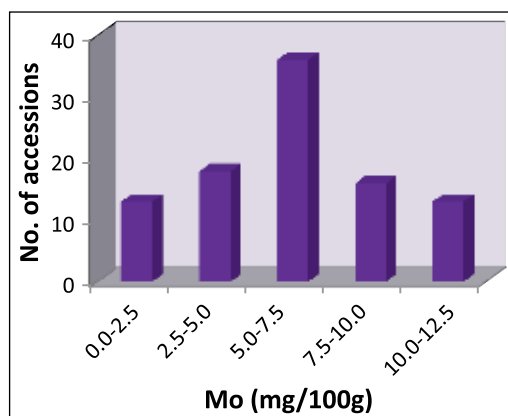
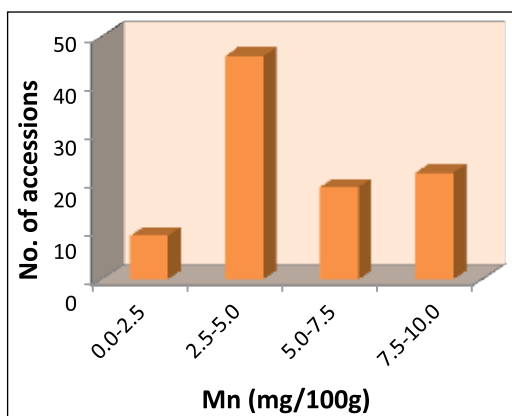
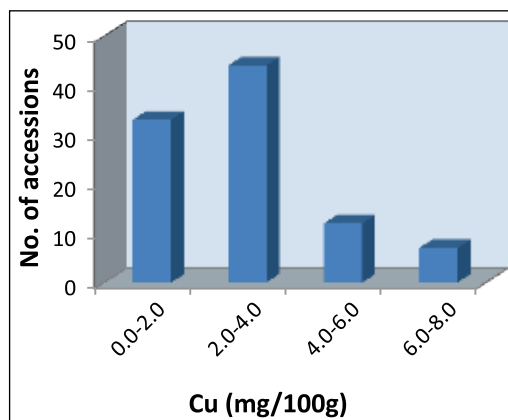
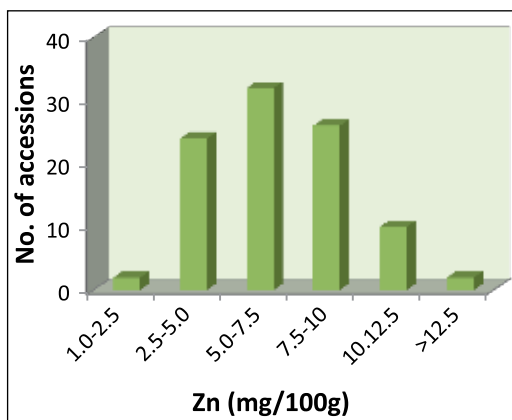
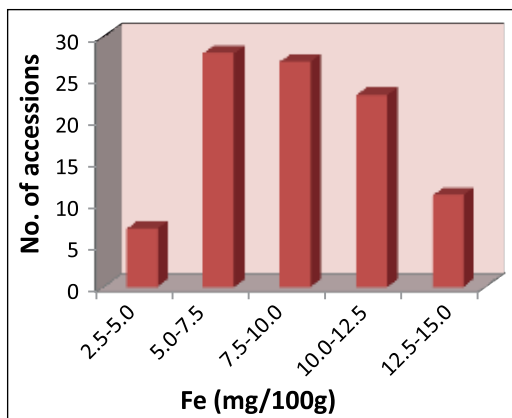


Fig. 3.10: Frequency distribution of micro-minerals: a) Fe, b) Zn, c) Cu, d) Mn and e) Mo

(Kaplan, 2002). It acts as a co-factor for many enzymes and is required for insulin secretion, creatine phosphorylation, carbohydrate metabolism and protein synthesis. The ratio of intracellular to extracellular potassium is the major determinant of muscular and neuronal excitability and if this balance is disturbed, various pathological states can develop (Ringer and Bartlett, 2007). Potassium content ranged from 138.29-1578 mg/100g among the wild lentil core set accessions. *L. culinaris* ssp. *tomentosus* accession EC718659 from Syria had highest K content followed by *L. ervoides* accession EC718404 (1563.33 mg/100g). Maximum accessions i.e. 46 had K content in the range of 900-1200 mg/100g followed by 37 accessions in the range of 1200-1500 mg/100g. Five accessions had K content greater than 1500 mg/100g.

### Phosphorus

Among the core set accessions, phosphorus content ranged from 37.50-593.75 mg/100g. Among the species, P content was highest in *L. ervoides* accessions with 172.5 mg/100g (EC718318) to 593.75 mg/100g (EC718374) followed by *L. culinaris* ssp. *culinaris* with 365 mg/100g (ILL10829) to 392.50 mg/100g (ILL8006). Five accessions had P content higher than 400 mg/100g. Phosphorus is involved in metabolic regulation through and in conserving the cellular energy in form of mono-, di- and tri-phosphates (Calvo and Park, 1996).

### Calcium

Ca content was present in core set accessions in the range of 4.74-188.75 mg/100 g. *L. nigricans* accession EC718235 had the highest Ca content followed by *L. culinaris* ssp. *orientalis*

accession EC718529 (136.63 mg/100 g). Accessions from Syria and Turkey were found promising for Ca content. Among species, maximum variability for Ca content was observed in *L. nigricans*. Nine accessions had Ca content >75 mg/100g and three accessions had >100 mg/100g. Ca is essential for healthy skeleton and intermediary metabolism (Abramov et al., 2004).

### Magnesium

Our body requires Mg for protein synthesis, membrane integrity, nervous tissue conduction and intermediary metabolism (Laires et al., 2004). In mineral analysis, Mg content ranged from 15-159 mg/100 g. *L. culinaris* ssp. *tomentosus* accession EC718471 had highest Mg content. Among the species *L. ervoides* and *L. culinaris* ssp. *orientalis* showed substantial variability for the Mg content. Maximum number of accessions (27) had Mg content in the range of 125-150 followed by 23 and 19 accessions in the range of 75-100 and 100-125 mg/100g, respectively. Twelve accessions had Mg content higher than 150 mg/100g.

## 3.6.2 Micro-nutrients

### Iron

Fe requiring physiological and biological activities includes oxygen transport and metabolism (Yang et al., 2007). Among the evaluated core set accessions, Fe content ranged from 2.82-14.12 mg/100 g. *L. culinaris* ssp. *orientalis* accessions EC718519 had highest Fe content. Among the species, accessions of *L. culinaris* ssp. *odemensis* and *L. culinaris* ssp. *orientalis* had high variability for Fe content. Under frequency distribution, 34 accessions had Fe content higher than 10 mg/100g.

## Zinc

Among the core set accessions, Zn content varied from 1.29-12.62 mg/100 g. *L. nigricans* accession EC718275 had highest Zn content. Among the species, accessions belonging to *L. culinaris* ssp. *orientalis* and *L. culinaris* ssp. *odemensis* had high variability. Maximum number of accessions i.e. 32 had Zn content in the range of 5.0-7.5 mg/100g. Zn is essentially required for genetic material transcription and stabilizing plasma membranes (Shils et al., 1994).

## Copper

Cu is required as a key component of redox enzymes (Cundeva et al., 2007). In the present study, Cu content ranged from 0.5-7.12 mg/100 g with highest in accession EC718316. Among the species, *L. ervoides* showed maximum variability followed by *L. culinaris* ssp. *odemensis*. In case of frequency distribution, maximum number of wild lentil accessions (44) had Cu content in the range of 2.0-4.0 mg/100g followed by 33 accessions between 0-2.0 mg/100g. Seven accessions had >6.0 mg/100g Cu content.

## Manganese

In our body, Mn is required as a component and activator of a number of enzymes (Pogatschnik, 2014; Stehle et al., 2016). Among core set accessions, Mn content ranged from 1.22-9.99 mg/100 g. High variability for Mn content was observed in *L. Culinaris* ssp. *orientalis* followed by *L. culinaris* ssp. *odemensis*. Promising accessions includes EC718370, ILWL 56 and EC718548. In maximum number of accessions (46), the Mn content lied in the range 2.5-5.0 mg/100g. 22 wild lentil accessions had >7.5 mg/100g Mn content.

## Molybdenum

Mo is required as a component and activator of a number of enzymes (Cundeva et al., 2007). Mo content ranged from 1.02-11.89 mg/100 g in the present study. Accessions EC718605 had highest Mo content followed by EC718311 (11.85). In maximum number of accessions (36), Mo content ranged between 5.0-7.5 mg/100g. 13 accessions had >10.0 mg/100g Mo content.

### 3.6.3 Accessions with multiple traits

Some accessions namely EC718685 of *L. lamottei* found promising for Mg, Fe, Zn, Mn and Mo; and EC718662 of *L. culinaris* ssp. *tomentosus* for Ca, Mg, Cu, Mn, Mo; and EC718404 of *L. ervoides* for Ca, Mg, Fe and Zn. Promising accessions from different species rich in various minerals identified are listed in Table 3.5.

## 3.7 Diversity analysis

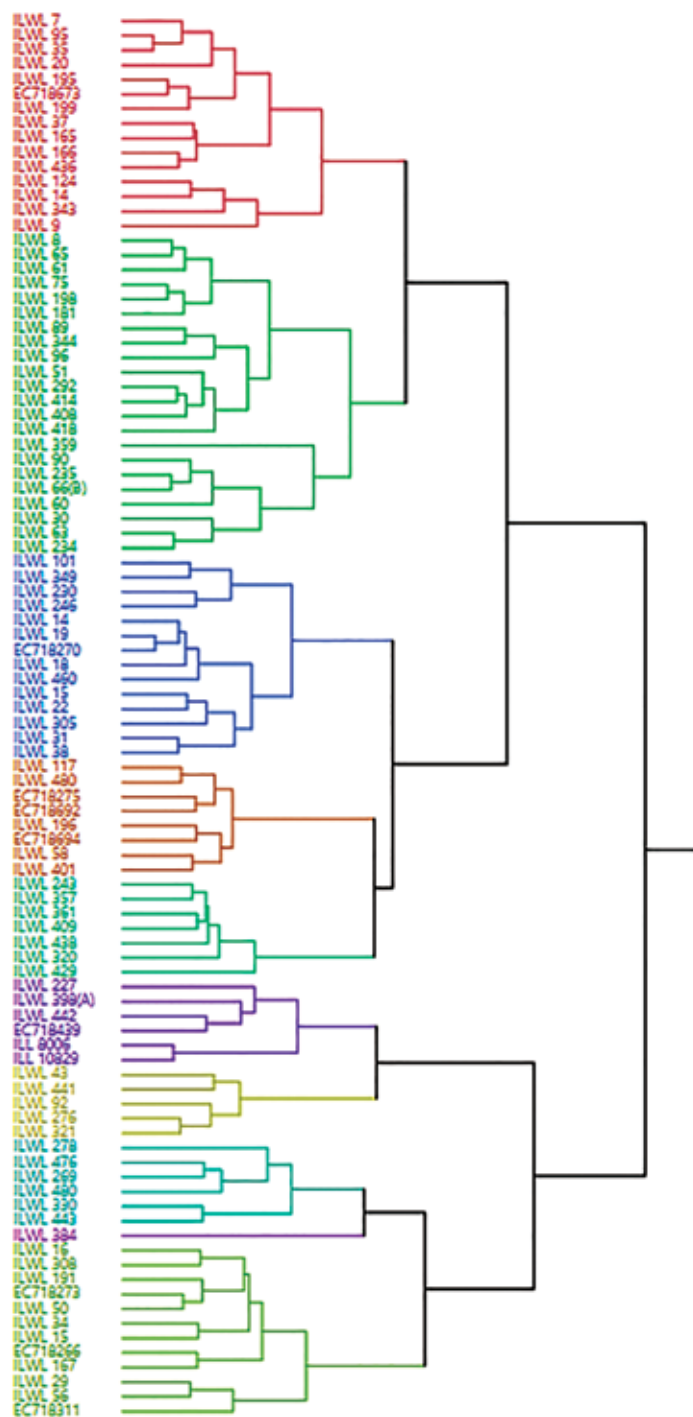
Diversity analysis was done using mineral data including Na, K, P, Ca, Mg, Fe, Zn, Cu, Mn, Mo, Ni, Pb, Cd, Co and As (Kumar et al., 2018). The maximum distance was observed between *L. Culinaris* ssp. *orientalis* accessions belonging to Turkey and Syria. The hierarchical clustering of accessions resulted into different clusters A-J as shown in different colors in Fig. 3.11. All the clusters occupied by the accessions of different species, but in some clusters majority of the accessions were observed species specific. Cluster C was mainly occupied by *L. nigricans*, E by *L. culinaris* ssp. *odemensis*, F by *L. ervoides* and *L. culinaris* ssp. *culinaris*, G by *L. ervoides*, H by *L. culinaris* ssp. *orientalis*. EC718585 forms a separate cluster I. The clustering pattern indicates

**Table 3.5: Promising accessions identified for some important minerals for their use in lentil improvement programme**

Species	Ca*	Mg*	Fe*	Zn*	Cu*	Mn*	Mo*
<b><i>L. culinaris</i> ssp. <i>orientalis</i></b>	EC718529 (136.63)	EC718234 (158.00)	EC718519 (14.12)	EC718488 (12.46)	EC718605 (5.02)	EC718548 (9.57)	EC718605 (11.90)
	EC718554 (113.37)	EC718488 (157.00)	EC718488 (12.62)	EC718607 (11.03)	EC718596 (4.81)	EC718596 (9.20)	EC718560 (10.74)
	EC718490 (99.43)	EC718607 (155.00)		EC718560 (10.61)			
		EC718475 (146.00)		EC718515 (9.14)			
<b><i>L. nigricans</i></b>		EC718554 (145.65)					
	EC718235 (188.75)	EC718257 (156.00)	EC718275 (13.56)	EC718275 (12.62)	EC718273 (5.24)	EC718256 (8.35)	EC718239 (11.77)
	EC718238 (99.0)	EC718235 (148.75)	EC718238 (12.97)	EC718238 (12.36)		EC718239 (8.33)	EC718256 (11.77)
	EC718236 (95.62)	EC718254 (146.25)	EC718245 (12.16)				
<b><i>L. culinaris</i> ssp. <i>tomentosus</i></b>	EC718660 (83.97)	EC718471 (159.00)	EC718660 (10.18)	EC718660 (9.11)	EC718662 (6.20)	EC718662 (9.28)	EC718661 (11.27)
	EC718662 (64.83)	EC718662 (155.50)					EC718662 (11.23)
		EC718659 (148.00)					
		EC718673 (147.00)					
<b><i>L. lamottei</i></b>	EC718252 (72.74)	EC718252 (149.00)	EC718692 (13.95)	EC718692 (12.60)	EC718252 (4.68)	EC718685 (8.84)	EC718685 (11.12)

Species	Ca*	Mg*	Fe*	Zn*	Cu*	Mn*	Mo*
		EC718685 (141.00)	EC718685 (13.32)	EC718685 (12.48)		EC718252 (7.70)	
<b><i>L. culinaris</i> ssp. <i>odemensis</i></b>	EC718276 (37.34)	EC718311 (155.00)	EC718311 (14.12)	EC718694 (12.41)	ILWL 56 (7.03)	ILWL 56 (9.77)	EC718311 (11.85)
		EC718276 (152.50)	EC718297 (13.62)	EC718297 (12.37)			
		ILWL56 (151.00)	EC718301 (13.32)				
		EC718282 (150.00)					
<b><i>L. ervoides</i></b>	EC718322 (71.38)	EC718404 (158.33)	EC718329 (12.64)	EC718417 (9.84)	EC718316 (7.13)	EC718370 (9.99)	EC718370 (11.31)
	EC718404 (51.73)	EC718432 (156.00)	EC718417 (11.90)	EC718404 (9.24)	EC718451 (6.93)		
		EC718329 (153.00)	EC718318 (11.66)	EC718374 (9.23)	EC718417 (6.79)		
			EC718404 (11.58)		EC718374 (6.57)		
					EC718321 (6.32)		

\*Data in parenthesis is in mg/100 g. (Source: Kumar et al., 2018)



**Fig 3.11.** Hierarchical clustering of 96 wild lentil accessions comprising core set based on mineral composition data

(Source: Kumar et al., 2018)

that grouping of accessions was not according to their geographical origins.

## Conclusions

Characterization and evaluation of germplasm and identification of trait-specific germplasm is essential for their effective utilization in any crop improvement program. So, global wild lentil collection was characterized and evaluated, and trait-specific accessions were identified for: various agro-morphological traits like seed yield, number of pods per plant, number of seeds per plant, number of branches per plant, days to maturity, 100 seed weight; resistant to biotic stresses including rust and powdery mildew; and essential minerals. The identified trait-specific wild accessions provide starting material for pre-breeding and used for broadening the genetic base of cultivated lentil as described in next chapter.

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## Chapter 4

# Utilization of Wild Lentils

### 4.1 Introduction

Lentil is a self-pollinated diploid species ( $2n=2x=14$ ) with a genome size of approximately 4 Gbp (Kumar et al., 2015; Singh et al., 2018). The cultivated lentils are divided into two subspecies, the large-seeded macrosperma and small-seeded microsperma (Barulina, 1930; Cubero, 1981; Ferguson et al., 2000). Taxonomic classification of the genus *Lens* Mill. has gone through several modifications, initially with five species, *L. culinaris*, *L. orientalis*, *L. ervoides*, *L. nigricans* and *L. montbretii* (Cubero, 1981), to the present seven species, *L. culinaris* ssp. *culinaris*, *L. culinaris* ssp. *orientalis*, *L. culinaris* ssp. *tomentosus*, *L. culinaris* ssp. *odemensis*, *L. ervoides*, *L. lamottei* and *L. nigricans* (Ferguson et al., 2000). Alo et al. (2011) detected the divergence, following domestication, of the domesticated gene pool into overlapping macrosperma and microsperma groups. The cultivated lentil is reported to have two centers of origin, India and the Middle East (Ladizinsky, 1993), whereas wild lentil species have multiple centers of origin which overlaps in Turkey and then differ geographically (Pratap et al., 2014; Singh et al., 2014a, b). Within the cultivated lentils, the extreme specificity of adaptation to ecogeographies

limits the scope of the direct introduction of exotic landraces. South Asian landraces are generally early maturing small-seeded red lentils, and the West Asian landraces are late maturing large-seeded mostly yellow lentils. The major lentil-growing countries in the world are India, Turkey, Canada, Australia, United States of America, Nepal, China, and Ethiopia. The production and productivity of lentil has increased from an average yield of 565 kg ha<sup>-1</sup> in 1961-1963 to 1153 kg ha<sup>-1</sup> during 2016-2017 globally (FAO, 2017). Despite the tremendous improvement, the current lentil yield is much below as compared to other pulses. In cultivated lentil varieties, the yield limiting factors are lack of seedling vigour, high flower drop rate, low pod setting and lack of lodging resistance along with exposure to major biotic and abiotic stresses (Erskine et al., 2009; Sharpe et al., 2013; Kumar et al., 2015). Therefore, to attain further breakthrough for enhancing genetic gains, new target traits are needed to be identified and introgressed into cultivated gene pool for widening the genetic base of cultigens. Hence, utilization of lentil genetic resources including the crop wild relatives (CWRs) could set up tone for future lentil breeding programs to meet the food security needs of the new world.

## 4.2 Production-related problems

Domesticated lentil is vulnerable to major abiotic and biotic stresses and has less variation than CWRs for genes of higher productivity (Singh et al., 2014a, b). The severity of these stresses is unpredictable in field experiments, hence, field trials are increasingly being supplemented with controlled environment testing and physiological screening.

### 4.2.1 Abiotic stresses

Among important abiotic stresses, the most widely distributed are cold, drought, heat, salinity, nutrient deficiency and toxicity (Yau and Erskine, 2000). Of these, drought and heat stresses are considered of serious concern globally (Turner et al., 2001). Salinity is also an emerging problem in the Indian subcontinent and lentil is more salt sensitive as compared to other pulse crops such as faba bean and soybean (Katerji et al., 2003). Similarly, nutrient deficiencies and toxicities are endemic abiotic constraints affecting lentil production in many regions of the World (Buddenhagen and Richards, 1998).

#### 4.2.1.1 Cold hardiness

Susceptibility to cold has resulted in limited production of lentil in the high land regions worldwide. The effect of extreme winters on lentil plant included flower and pod abortion, damage to seed and injury to vegetative tissues. Therefore, cold stress is major constraint of international lentil breeding programmes (Eujayl et al., 1999). However, germplasm is available that has desirable degree of resistance to cold, which makes it possible to breed winter hardy varieties, which can be grown in highlands with a reasonable expectation of survival during winters (Erskine et al.,

1981). There are several released cultivars having winter hardiness such as Kofkas, Cifci and Uzbek and now being cultivated by farming community in Turkey highlands (Hamdi et al., 1996). However, some other breeding lines of *L. culinaris* ssp. *culinaris* have been identified as cold tolerant under on-farm evaluation and these can be utilized as gene sources for developing winter-tolerant cultivars (Ali et al., 1999). Kahraman et al. (2004) pointed out that winter hardiness is controlled by many genes and suggested that combined effects of several quantitative trait loci (QTLs) accounted for 42% variation in winter survival and seven QTLs were identified for winter hardiness with one common QTL across all environments.

#### 4.2.1.2 Drought tolerance

Drought is another most important abiotic stress in many countries of the world including India (Johansen et al., 1994). Sarker et al. (2001) suggested that lentil crops suffer from terminal drought condition in the Mediterranean regions of West Asia and North Africa, whereas in South Asia, generally the crop is grown in residual soil moisture and faces intermittent drought stresses. Malhotra et al. (2004) suggested the identification of drought-tolerant genotypes an important researchable issue in view of climate changes. Among the wild *Lens* taxa, *L. nigricans* appeared to be drought tolerant species under North-Western Indian hills (Gupta and Sharma, 2006). The resulting drought-tolerant lines are now available with the National Agricultural Research System (NARS) in India through the lentil nursery screening programme in collaboration with the International Center for Agricultural Research in the Dry Areas (ICARDA) under National Food Security Mission funded by the Ministry of Agriculture and Farmer's

Welfare (MAFW), Government of India. Under this programme, some promising accessions of *L. culinaris* ssp. *culinaris* and advanced breeding lines have been identified from the screening nursery which can be used in drought tolerance breeding programme for developing suitable cultivars. Other traits such as early seedling growth and vigour, rapid ground coverage, high biomass, early flowering and maturity were also considered useful for selecting drought-tolerant germplasm (Hamdi and Erskine, 1996). Singh et al. (2016) studied genetic analysis and molecular mapping of seedling survival drought-tolerance genes in lentil and also suggested introgression of drought tolerance into high yielding cultivars (Hamdi and Erskine, 1996; Singh et al., 2017; Singh et al., 2017; Singh et al., 2017). Some researchers have also identified tolerant sources against drought like Eston in *L. culinaris* ssp. *culinaris*, EC718658 in *L. culinaris* ssp. *tomenstosus*, EC718689 in *L. lamottei* and EC718422 in *L. ervoides* (Gorim and Vanderberg 2017; Hamdi and Erskine, 1996; Malhotra et al., 2004; Singh et al., 2017; Singh et al., 2017; Singh et al., 2017).

CWRs have wide variations within and between species in drought tolerance mechanisms. Omar et al. (2019) examined drought tolerance in crosses of elite lentil varieties with CWRs. Tolerance was associated with pubescent leaves, cell membrane stability, relative leaf water content, increased root/shoot ratio and reduced wilting along with transpiration and canopy temperature. Tolerant segregants are being advanced for trait fixation. Sanderson et al. (2019), with a focus on drought tolerance and disease resistance, studied RILs of crosses of lentil cultivars with *L. orientalis*, *L. odemensis* and *L. ervoides* in the ICARDA lentil pre-breeding

project. It was aimed to develop genetic maps and markers for lentil and CWRs for the transfer of key drought traits into breeding programs for drought tolerance.

#### 4.2.1.3 Heat tolerance

Lentil CWRs are yet to be screened for heat tolerance. Heat stress tolerance has been only been reported in cultivated lentils (Sita et al., 2017). Singh et al. (2019) used genome-wide transcription to identify heat responsive genes in the regulatory system of lentil cultivars. However, more analysis of heat tolerance mechanisms is required to elucidate heat tolerance. With the assumption that CWRs are adapted to their environment of collection (Baute et al., 2015) and the reproductive period occurs in May-June every year, sources of heat tolerance in *L. orientalis* may occur in Turkmenistan specifically along with Tajikistan and Northern Syria.

#### 4.2.1.4 Salinity tolerance

Salinity adversely affects nodulation and nitrogen fixation by restricting growth of root hairs (Rai et al., 1985; Rai and Singh, 1999). Genetic resources with substantial amount of variation towards salt tolerance have been recorded (Asraf and Waheed, 1993, 1999). Problems associated with salinity are not widespread, but these can be severe in certain regions of South Asia including India, parts of Egypt and in some regions of Turkey. In India, under the Indian Council of Agricultural Research (ICAR) and ICARDA collaborative research project, some wild lentil accessions (EC718536, EC718574, EC718590 and EC718640) of *L. culinaris* ssp. *orientalis* were identified as salinity tolerant and prospective sources for breeding resistance against salinity (DAC-ICAR-ICARDA Annual Progress Report, 2014). Kumawat et al. (2017) have also identified salinity-tolerant genotypes

based on their stress-tolerant experiments of lentils. Further, the screening of 100 accessions of *L. culinaris* subsp. *orientalis* under hydroponic culture at 120-mM NaCl concentration resulted in the identification of several donors for salinity tolerance (Singh et al., 2017). Importantly, flowering and growth responses of wild *Lens* to light quality have also been studied (Yuan et al., 2017).

### 4.2.2 Biotic stresses

Among biotic stresses, Ascochyta blight is a widespread problem in all the lentil growing countries of the world in general, while Canada and Australia in particular (Ahmed and Morrall, 1996; Ahmed et al., 1996; Johansen et al., 1994). Moreover, rust, powdery mildew and Fusarium wilt are also prevailing biotic stresses in most lentil growing regions of India (Robertson et al., 1992; Singh et al., 2014a, b; Singh et al., 2018). Lentil rust caused by *Uromyces fabae* Pers. is a serious constraint in areas where mild temperature and humid weather conditions favors the occurrence of fungus (Muehlbauer et al., 1995). In cultivated lentil germplasm, partial resistance to *U. fabae* has been reported, however, wild annual *Lens* taxa have shown complete resistant against the pathogen (Singh et al., 2014a, b). The germplasm accessions which showed resistance to Fusarium wilt included some accessions of *L. culinaris* ssp. *culinaris*, EC718457, EC718460 and EC718486 of *L. culinaris* ssp. *orientalis*, EC718257 of *L. nigricans* and EC718347 of *L. ervoides* (Mohammadi et al., 2012; DAC-ICAR-ICARDA Annual Progress Report, 2014). Some other potential rust resistant wild accessions viz. EC718522, EC718600, EC718605 and EC718526 of *L. culinaris* ssp. *orientalis* along with EC718246, EC718247 and EC718248 of *L. nigricans* have been identified for introgression

into the cultivated gene pool (Gupta and Sharma, 2006; Singh et al., 2013). Likewise, for powdery mildew disease, cultivated germplasm has also shown partial resistance against the pathogen. But some wild accessions such as EC718313, EC718314 and EC718378 of *L. ervoides* have been identified as resistant sources against *Erysiphe polygoni* DC (Singh et al., 2014a, b). A recent study by Singh et al. (2020) identified the confirmed and stable donors across intra and interspecific accessions viz. EC789113 of *L. odemensis* for rust, EC718515 and EC718605 of *L. orientalis* for rust and powdery mildew, EC718682, EC718235 and EC718257 of *L. nigricans* for rust and powdery mildew, EC718266 of *L. nigricans* for powdery mildew and Fusarium wilt and EC728782 of *L. tomentosus* for rust and Fusarium wilt. These promising sources can be exploited for the introgression of resistance into elite genetic background of cultivated lentil varieties. Moreover, the development of lentil cultivars with combined resistance against major biotic stresses may lead to the development of suitable management strategies to identify novel genes for resistance breeding of lentil in future.

### 4.3 Progress in wide hybridization

Considerable efforts have been made to introgress desirable characters from wild lentils into the cultivated varieties. Based on genotyping-by-sequencing (GBS), the *Lens* taxa have been classified into four gene pools viz. primary (*L. culinaris* ssp. *culinaris*, *L. culinaris* ssp. *orientalis* and *L. tomentosus*), secondary (*L. lamottei* and *L. odemensis*), tertiary (*L. ervoides*) and quaternary (*L. nigricans*) gene pools (Wong et al., 2015). Most of the success to broaden the genetic base of cultivated lentil



has been achieved through interspecific crossing of genotypes from primary and secondary gene pools with cultivated lentils. Ladizinsky (1979) was pioneer to start inclusion of wild traits into cultivated lentils background. He had successfully crossed cultivated lentil with *L. orientalis* to obtain normal F<sub>1</sub> hybrids, and suggested that cultivated lentil and *L. orientalis* share the same karyotype with some exceptions.

As evident from the previous works, *L. orientalis* and *L. odemensis* are crossable with cultivated lentil (Ladizinsky et al., 1984; Abbo and Ladizinsky, 1991, 1994; Fratini et al., 2004; Fratini and Ruiz, 2006; Muehlbauer et al., 2006; Gupta and Sharma, 2007; Singh et al., 2013), although the fertility of the hybrids depends on the chromosome arrangement of the wild parent. Crosses are possible between *L. culinaris* and the remaining species, but they are characterized by a high frequency of hybrid embryo abortion, albino seedlings and hybrid sterility. *L. nigricans* and *L. ervoides* are not readily crossable with *L. culinaris* because of hybrid embryo breakdown (Abbo and Ladizinsky, 1991, 1994; Gupta and Sharma, 2005). However, embryo rescue allowed for the transfer of anthracnose resistance from *L. ervoides* to *L. culinaris* (Fiala et al., 2009) and recombinant inbred lines (RILs) have been developed (Tullu et al., 2013). Only four crosses have not resulted in hybrids to date, namely *L. orientalis* × *L. ervoides*, *L. orientalis* × *L. nigricans* (Ladizinsky et al., 1984), *L. tomentosus* × *L. lamottei* (Van Oss et al., 1997) and *L. odemensis* × *L. ervoides* (Ladizinsky et al., 1984), though viable hybrids have been reported between cultivated species and *L. ervoides*, *L. odemensis* and *L. nigricans* with the use of gibberellic acid (GA<sub>3</sub>) (Ahmad et al., 1995). Fratini and Ruiz (2006)

developed an efficient protocol to recover lentil embryos, which yielded hybrids of cultivated species with *L. odemensis*, *L. ervoides* and *L. nigricans*. Moreover, Tullu et al. (2011) have successfully crossed *L. culinaris* with *L. tomentosus*.

The success of wide hybridization can be predicted by studying phenotypic similarity of species for pollen morphology and in vitro pollen length, pistil and style length (Fratini et al., 2004). Among few studies, comparative agronomic performance of lentil interspecific derivatives revealed high level of fruitful heterosis for seed yield and its important component traits, which signifies the importance of inclusion of useful and unexplored gene reservoir from wild to cultivated species (Singh et al., 2017; Singh et al., 2017; Singh et al., 2017; Fig. 4.1). Overall, attempts have been made to introgress desirable characters of wild lentil taxa into cultivated varieties (Singh et al., 2018). However, the cross-compatibilities and taxonomic relationships between crops and their wild relatives influenced the fertility of the final progeny (Singh et al., 2018).

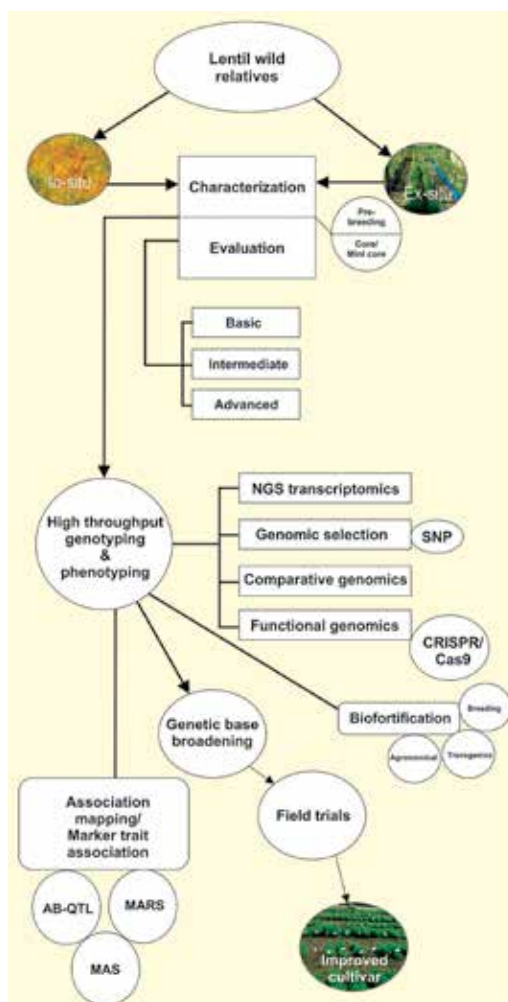
Further, genotypic characterization studies of lentil genetic resources have clearly shown distinct clusters of cultivated and wild germplasm (Ferguson et al., 1998; Hamwieh et al., 2009; Alo et al., 2011). Among polymerase chain reaction (PCR)-based markers, lentil-specific simple sequence repeat (SSR) markers are limited (Hamwieh et al., 2005; Hamwieh et al., 2009; Verma et al., 2014). Kumar et al. (2015) reviewed DNA markers in lentil and reported development of single nucleotide polymorphism (SNP) markers consisting of 44879 SNPs (Sharpe et al., 2013), 50960 SNPs (Temel et al., 2014), expressed sequence tags (ESTs) (Vijayan et al., 2009)





**Fig. 4.1:** Growing lentil interspecific derivatives under multi-location evaluation experimental fields at a) ICARDA, Bhopal b) PAU, Ludhiana

and EST-SSRs along with SNPs (Kaur et al., 2011) as most useful markers for future marker assisted selection (MAS) in lentil breeding. Another study using SNPs showed that lentil landraces clustered primarily on the basis of ecogeographical origin into three distinct clusters viz. South Asia, Mediterranean and Northern Temperate (Khazaei et al., 2016). Moreover, genomic maps have been developed for the identification of linked markers to QTLs governing the trait of interest in lentil taxa (Eujayl et al., 1998; Tullu et al., 2003; Kahraman et al., 2004; Saha et al., 2010a, b; Bhadauria, et al. 2017; Rodda et al., 2017). Singh et al. (2017), Singh et al. (2017) and Singh et al. (2017) have reported successful use of markers associated with QTLs under heat stress conditions for genotyping the intraspecific  $F_2$  mapping population for dissecting the candidate genes to develop heat tolerant molecular markers for improving lentil cultivars. Further, exome capture methodology was developed and applied to a panel of cultivated and wild lentils, in order to reduce the large genome size of the lentil genome (Ogutcen et al., 2018). High-density interspecific maps have been developed for a cross between *L. culinaris* and *L. odemensis* (Polanco et al., 2019).



**Fig. 4.2:** Integrated approaches for achieving higher genetic gains from lentil wild relatives

Breeders have used CWRs in their breeding schemes typically as sources of resistance to various biotic and abiotic stresses (Hajjar and Hodgkin, 2007). However, this inevitably led to the occurrence of undesired wild type traits, which have been removed or altered through the domestication process (Meyer and Purugganan, 2013). Thus, these undesired traits should be removed via repeated backcrosses of elite crop genotypes accompanied by trait testing. The wild lentil taxa are potential resource of various untapped genes controlling desirable traits for high yield, biotic and abiotic stresses to make substantial improvement in productivity, thereby widening the base of cultivated lentil. Fig. 4.2 depicts a plan of integrating multidisciplinary approaches for enhancing higher genetic gains in lentils. Lastly, marker-assisted selection has to be employed in breeding programme, although sequencing of lentil genome would lead to the successful utilization of genome based approaches with conventional breeding methods.

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## Chapter 5

# Conclusions and Future Perspectives

The genetic and phenotypic characterization of crops allows us to elucidate their evolutionary and domestication history, the genetic basis of important traits, and the use of variation present in their wild relatives to enhance resilience. Wild species are valuable sources of novel variation for yield traits, resistance to biotic and abiotic stresses and nutritional traits. However, these climate smart adaptations inevitably led to the occurrence of undesired wild type traits, which have been removed or altered through the domestication process. Thus, these undesired traits need to be removed via repeated backcrosses of elite crop genotypes accompanied by trait testing, a process that can be facilitated by the use of molecular markers either for the trait or background selection.

The wild lentil taxa are potential resource of various untapped genes controlling desirable traits for high yield, biotic and abiotic stresses and essential minerals to make substantial improvement in productivity and quality, thereby widening the base of cultivated lentil. Some efforts have been made on characterization and evaluation of 405 diverse global wild lentil germplasm against the target traits of interest under diverse agro-ecological

conditions. The studies have helped in identifying the useful gene sources *viz.* earliness, high number of branches plant<sup>-1</sup>, high number of pods plant<sup>-1</sup>, high number of seeds plant<sup>-1</sup>, multiple disease resistance and essential minerals in different *Lens* taxa across gene pools. This has led to the identification of confirmed and stable gene sources (donors) across intra and interspecific accessions *viz.* EC718287 of *L. odemensis* for rust and high pod number; EC718515, EC718605 of *L. orientalis* for rust and powdery mildew; EC718329, EC718365, EC718383, EC718404, EC718405, EC718413 and EC718428 of *L. ervoides* for high number of seeds plant<sup>-1</sup>; EC718682 and EC718257 of *L. nigricans* for rust and powdery mildew; EC718266 of *L. nigricans* for powdery mildew and Fusarium wilt; and EC728782 of *L. tomentosus* for rust and Fusarium wilt. These gene sources could be taken in lentil wide hybridization programme for enhancing genetic gains of cultivated varieties and could also be shared among lentil breeders/researchers in the country or elsewhere under Standard Material Transfer Agreement (SMTA) for strengthening the on-going lentil genetic improvement programmes.

Desired genes from wild lentils belonging to different gene pools have been successfully transferred into cultivated lentil background using conventional and biotechnological approaches. However, to harness full potential of useful genes from distantly related CWR gene pools, efficient tissue culture protocols, advances in genetic engineering along with development of strategies to avoid linkage drag would ascertain the free flow of genes. Molecular markers would be valuable tools in every breeding programme and their role in identification of donor parents, true  $F_1$  hybrids and backcrosses to efficient pre-breeding and phylogenetic analysis. Marker-assisted selection still has to be employed in breeding programme; however, sequencing of lentil genome would break these barriers of successful utilization of genome based approaches with conventional breeding.

Further, improving adaptation of cultivars is an ongoing process that frequently involves the introduction of alleles from close wild species. Despite the identification of loci associated with traits of interest in wild *Lens*, there is still great potential in terms of genetic variation that can be exploited to maintain and expand yield gains and to face agricultural challenges such as climate change and food security. Also, elucidating the adaptation of *Lens* taxa to different environments is needed to assist breeders in increasing diversity through

introduction of germplasm from diverse regions. Lastly, for effective conservation, both local leadership and international partnerships are required. Recent works on *in-situ* and *ex-situ* conservation have led to the establishment of a range of principles and also renewed the interest of some organizations in PGR management. Ideas such as preserving locations with high overlap of lentil CWRs, as well as sites with unique characteristics, are important. Setting up preserves to allow migration in response to climate change will also be necessary. However, the social aspects of *in-situ* preservation will likely be more challenging. Funding is an essential requirement for carrying out large scale characterization of CWRs and prebreeding activities, where international collaborations can play a major role. However, with the availability of limited support particularly for conservation science, we need to create new opportunities and upgrade existing infrastructure to effectively utilize CWRs for genetic enhancement of latest cultivars. Local communities should come forward to preserve natural niches harbouring such treasure of novel diversity for future nutritional security. We hope that this monograph has illustrated the utilization of *Lens* taxa through prebreeding and genetic enhancement for breaking the yield barriers by promoting sustainable conservation of CWRs which can also be followed in other crops.



# *Annexures*



S. No.	Accession	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of Branches/ plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Resistance to rust	Resistance to powdery mildew
1	L830	42	86	24.1	7.0	208	316.5	1.5	1.2	4.2	13.9	9	9
2	ILL10829	43	82	22.8	6.5	27	48.5	1.8	2.0	0.2	6.3	5	3
3	ILL8006	43	98	23.9	9.5	117	196	1.6	0.7	0.7	8.3	3	3
4	PRECOZ	42	81	21.3	9.5	19	28.5	1.5	2.5	2.1	7.1	1	9
5	EC718231	132	164	31.0	19	33	56.5	1.7	0.5	0.3	1.8	5	7
6	EC718232	130	164	23.0	7.5	24	37.5	1.5	0.2	0.1	0.9	5	7
7	EC718233	133	165	26.0	6.0	19	25.0	1.3	0.4	0.1	1.0	5	7
8	EC718234	51	96	20.6	7.0	25	31.5	1.2	0.8	0.3	2.1	5	5
9	EC718268	95	132	95.5	4.0	86	92.5	1.0	0.8	0.9	3.4	7	7
10	EC718326	91	122	44.5	5.5	88	91.5	1.1	0.4	1.1	3.1	7	5
11	EC718269	91	120	40.5	4.8	44	50.0	1.3	2.0	0.6	2.3	7	7
12	EC718250	132	164	49.0	14.0	49	95.0	1.9	0.7	0.6	2.4	3	7
13	EC718451	132	166	26.0	12.0	56	60.0	1.0	0.5	0.3	2.4	3	7
14	EC718452	129	168	28.0	10.0	62	68.0	1.0	0.9	0.8	2.5	5	7
15	EC718453	95	148	22.0	12.0	88	97.0	1.1	1.0	1.4	3.1	1	7
16	EC718454	97	156	26.0	13.5	110	119.0	1.0	1.3	1.8	3.9	5	9
17	EC718455	90	132	22.0	15.0	88	96.0	1.0	1.4	1.1	2.9	3	9
18	EC718456	130	164	24.0	4.0	8	10.0	1.2	2.0	0.2	0.5	7	9
19	EC718457	98	133	20.8	9.0	76	88.0	1.1	0.8	0.9	2.1	5	9
20	EC718458	121	132	20.9	8.0	56	67.0	1.1	0.8	0.9	2.3	5	9
21	EC718459	130	164	27.7	15.0	8	13.5	1.6	0.2	0.01	1.2	5	9
22	EC718460	132	164	28.0	6.0	22	35.0	1.5	0.4	0.1	0.7	5	9
23	EC718461	130	162	26.0	5.0	12	12.0	1.0	2.0	0.2	0.6	5	3
24	EC718462	129	154	23.0	9.0	54	95.0	1.7	0.3	0.4	1.9	1	5
25	EC718463	122	153	24.0	11.0	88	92.0	1.7	1.0	1.4	3.8	5	7
26	EC718465	100	136	22.0	12.0	89	99.0	1.0	1.1	1.5	2.9	5	7
27	EC718466	98	127	26.0	14.0	99	112.0	1.1	1.6	1.7	4.1	3	7
28	EC718467	123	156	36.5	18.0	39	73.4	1.9	0.6	0.3	2.4	3	7
29	EC718468	122	146	36.5	20.0	16	27.5	1.7	0.6	0.1	1.9	7	7



S. No.	Accession	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of Branches/ plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Resistance to rust	Resistance to powdery mildew
30	EC718469	111	137	28.5	16.7	37	66.5	1.8	0.7	0.4	1.4	7	7
31	EC718470	103	135	30.0	19.0	56	107.7	1.9	0.7	0.7	1.8	7	9
32	EC718472	122	155	29.0	16.0	112	119.0	1.0	1.1	1.9	4.1	7	9
33	EC718473	101	138	35.0	13.2	7	6.5	1.2	2.0	0.3	2.0	7	5
34	EC718474	112	136	39.3	18.5	49	90.0	1.8	0.8	0.7	3.5	7	7
35	EC718475	113	132	38.4	12.2	40	72.5	1.8	1.2	0.8	2.9	7	7
36	EC718476	100	129	33.5	13.7	86	166.2	1.3	0.4	0.6	6.4	9	7
37	EC718477	129	155	26.0	14.0	90	111.0	1.2	0.9	1.7	3.9	9	7
38	EC718478	112	134	31.0	10.7	42	78.7	1.8	0.8	0.5	4.0	9	7
39	EC718479	111	142	44.0	12.5	39	64.0	1.6	1.3	0.8	5.6	9	7
40	EC718480	100	132	26.5	15.7	59	112.7	1.8	0.7	0.7	4.6	9	7
41	EC718481	100	134	34.0	14.2	16	26.2	1.7	0.5	0.1	3.8	3	7
42	EC718482	104	142	26.6	16.3	72	75.0	1.0	0.4	0.4	4.4	5	9
43	EC718483	122	155	28.0	16.0	79	87.0	1.0	0.9	1.1	2.9	5	9
44	EC718484	112	147	25.0	14.0	88	101.0	1.1	1.0	1.3	4.1	5	9
45	EC718485	111	134	41.2	12.8	27	48.0	1.8	0.5	0.2	3.5	5	9
46	EC718486	105	138	25.5	13.5	12	15.0	1.2	0.4	0.01	4.8	5	5
47	EC718487	100	134	30.6	8.0	33	35.0	1.0	0.6	0.2	3.2	5	5
48	EC718488	105	136	27.2	16.7	133	140.0	1.0	1.1	1.4	3.8	1	3
49	EC718489	111	142	33.0	20.5	13	13.0	1.0	0.8	0.07	3.8	5	7
50	EC718490	100	147	20.6	13.5	94	94.0	1.0	1.1	0.7	4.0	5	7
51	EC718491	100	133	31.7	16.0	55	55.0	1.0	0.4	0.2	4.3	5	9
52	EC718492	77	102	20.5	7.5	7	10.5	1.0	0.5	0.1	2.8	1	5
53	EC718493	109	141	23.0	14.7	34	34.0	1.0	0.4	0.2	3.1	7	7
54	EC718494	65	101	24.0	8.5	32	43.5	1.3	1.0	0.6	2.6	9	3
55	EC718495	53	98	25.0	14.0	21	30.0	1.4	0.8	0.3	2.6	1	3
56	EC718496	64	105	21.0	11.0	9	11.0	1.0	0.5	0.05	1.8	5	7
57	EC718497	67	100	21.4	4.0	10	15.6	1.9	0.4	0.1	2.3	1	5
58	EC718498	70	105	27.0	7.5	24	29.0	1.3	0.1	0.2	2.4	1	5

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59	EC718619	61	92	26.5	8.0	35	35.0	1.0	3.0	1.2	2.9	9	3
60	EC718620	63	92	24.5	8.5	88	137.0	1.5	3.0	1.5	3.5	9	9
61	EC718500	78	122	29.0	13.0	112	130.0	1.1	1.1	1.4	3.0	7	7
62	EC718501	55	86	20.8	8.5	6	10.0	1.6	0.4	0.2	3.5	1	3
63	EC718502	89	123	22.0	12.0	78	88.0	1.1	0.9	1.1	2.9	7	5
64	EC718503	67	105	26.0	7.0	8	8.0	1.0	1.0	0.05	1.1	1	5
65	EC718504	112	135	43.0	17.0	82	82.0	1.0	0.4	0.4	3.8	7	5
66	EC718505	123	148	23.7	9.7	82	82.0	1.0	0.8	0.7	4.0	7	5
67	EC718506	111	144	21.0	10.2	58	58.0	1.0	0.8	0.5	3.4	5	5
68	EC718507	100	134	23.2	15.2	40	40.0	1.0	0.7	0.2	3.3	7	9
69	EC718508	102	137	31.7	19.7	60	60.0	1.0	0.7	0.6	4.3	7	9
70	EC718509	111	143	32.2	13.5	71	135.0	1.9	0.7	0.9	4.7	7	9
71	EC718510	122	149	31.0	14.5	88	91.0	1.0	0.9	1.0	4.6	7	9
72	EC718511	100	138	31.6	16.0	96	96.0	1.0	0.8	0.7	4.1	9	9
73	EC718512	102	136	32.0	15.0	102	109.	1.0	1.1	1.1	4.8	9	9
74	EC718513	130	160	34.3	11.6	42	77.6	1.8	0.8	0.5	4.0	9	7
75	EC718514	127	157	21.0	18.0	65	129.6	1.9	0.5	1.2	6.8	9	7
76	EC718515	128	160	41.6	20.3	116	224.6	1.9	1.4	3.2	7.5	1	1
77	EC718516	127	159	23.7	16.7	82	157.0	1.9	1.1	1.5	5.2	3	7
78	EC718517	130	154	29.0	11.0	35	61.6	1.7	1.1	0.6	3.9	3	7
79	EC718518	112	143	22.0	12.0	56	68.0	1.2	0.8	1.1	3.1	7	7
80	EC718519	124	153	23.6	14.3	88	167.0	1.8	1.0	1.6	5.9	7	5
81	EC718520	111	137	23.0	13.0	67	74.0	1.1	0.9	1.1	2.9	7	5
82	EC718521	124	153	26.0	25.0	192	341.0	1.7	0.8	3.1	6.9	7	5
83	EC718522	123	154	41.2	16.2	110	214.0	1.9	0.7	1.8	6.2	1	9
84	EC718523	135	166	31.3	13.6	46	90.0	1.9	0.8	0.7	5.8	1	5
85	EC718524	121	150	24.0	20.0	108	190.0	1.7	0.6	1.4	5.5	5	7
86	EC718525	122	157	30.3	17.6	36	68.3	1.8	0.7	0.4	4.5	5	5
87	EC718526	112	153	23.0	19.0	250	250.0	1.0	0.6	1.6	5.3	3	7



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88	EC718527	123	153	21.3	22.0	75	144.3	1.9	0.7	1.0	6.0	7	7
89	EC718528	58	101	26.5	8.5	38	54.0	1.4	0.7	0.3	2.9	9	5
90	EC718529	53	101	26.3	13.5	14	20.0	1.4	0.8	0.3	3.4	7	9
91	EC718530	52	102	25.5	7.0	16	21.7	1.4	0.6	0.1	2.8	7	3
92	EC718531	52	94	25.5	8.5	125	154.5	1.2	0.7	1.2	3.7	7	3
93	EC718533	77	102	23.0	10.0	77	89.0	1.1	0.8	1.1	2.5	7	3
94	EC718534	67	106	21.0	15.3	4	4.0	1.0	1.0	0.01	1.0	1	5
95	EC718535	61	105	20.9	16.0	6	6.0	1.0	2.0	0.3	1.1	7	5
96	EC718536	58	100	22.0	6.0	5	5.0	1.0	2.0	0.1	0.8	1	5
97	EC718537	61	89	23.0	11.0	55	72.0	1.3	0.8	1.1	3.2	7	9
98	EC718538	61	97	28.0	9.0	77	89.0	1.1	1.0	1.1	2.7	7	7
99	EC718539	53	100	21.0	13.0	5	5.0	1.0	2.0	0.1	1.7	9	3
100	EC718540	52	102	23.0	8.5	24	42.5	1.8	0.6	0.2	3.3	7	3
101	EC718541	52	102	21.6	8.6	36	61.5	1.7	1.1	1.3	2.9	7	3
102	EC718542	54	98	22.0	8.0	28	40.0	1.4	0.4	1.0	3.6	1	3
103	EC718543	42	81	21.3	7.0	79	137.6	1.7	1.0	1.3	3.5	7	7
104	EC718544	66	99	23.0	8.0	77	89.0	1.1	1.2	1.3	3.1	9	9
105	EC718545	118	150	21.0	16.0	59	114.7	1.9	0.7	0.7	4.1	9	1
106	EC718546	56	92	21.5	8.5	69	99.0	1.4	0.9	0.8	3.7	7	3
107	EC718547	57	105	24.5	11.5	4	7.0	1.7	0.2	0.01	2.0	5	5
108	EC718548	57	101	26.0	8.0	90	130.0	1.4	1.2	1.7	10.7	5	3
109	EC718549	128	162	40.0	15.6	26	39.3	1.4	0.4	0.7	3.5	7	7
110	EC718550	57	101	24.0	9.0	52	65.0	1.2	0.8	0.5	5.9	1	7
111	EC718551	51	102	21.0	4.3	8	11.3	1.4	1.6	0.6	2.6	7	3
112	EC718552	57	98	23.0	11.5	6	9.0	1.5	2.0	0.4	1.6	1	5
113	EC718553	56	100	24.0	8.0	9	12.0	1.3	2.0	0.4	2.7	1	5
114	EC718554	128	157	22.5	10.0	9	10.0	1.1	1.0	0.1	4.8	7	5
115	EC718555	53	86	21.5	8.5	44	72.0	1.6	0.6	0.7	4.6	1	7
116	EC718556	67	104	21.6	8.2	25	42.5	1.7	1.2	0.4	2.7	1	7

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117	EC718557	117	150	20.3	17.3	125	234.0	1.8	0.6	1.5	5.8	7	3
118	EC718558	102	134	33.0	14.0	89	112.0	1.2	1.1	1.7	4.8	7	9
119	EC718559	103	135	35.0	16.0	102	116.0	1.1	1.4	1.9	4.6	7	9
120	EC718560	57	108	22.0	9.0	6	14.0	2.3	1.5	0.1	2.2	1	5
121	EC718561	115	150	21.5	18.0	122	232.0	1.9	1.1	2.0	5.7	7	3
122	EC718562	56	105	22.3	12.6	4	5.6	1.5	1.0	0.06	1.4	3	3
123	EC718563	57	105	21.5	18.0	7	9.5	1.4	1.0	0.2	1.4	1	5
124	EC718564	67	102	24.0	8.0	54	68.0	1.2	0.7	1.1	3.6	7	9
125	EC718565	112	150	23.6	21.0	61	118.0	1.9	0.8	1.8	5.4	7	9
126	EC718566	112	150	20.2	13.7	57	113.2	1.9	0.6	0.7	3.8	7	3
127	EC718567	88	113	30.0	15.5	77	96.0	1.2	1.1	1.6	3.7	7	7
128	EC718568	118	153	20.8	19.0	76	149.0	1.9	0.6	1.0	4.2	7	7
129	EC718569	123	153	29.0	21.5	41	76.5	1.8	0.8	0.6	3.9	7	7
130	EC718570	115	150	27.0	19.0	230	230.0	1.0	0.9	2.0	5.8	1	7
131	EC718571	100	132	28.0	17.0	112	134.0	1.1	1.0	2.1	4.8	3	7
132	EC718572	119	154	24.2	7.7	103	152.5	1.4	0.5	0.8	2.1	5	3
133	EC718573	118	153	26.0	18.0	215	215.0	1.0	0.6	1.3	2.5	5	7
134	EC718574	102	140	34.0	16.0	113	167.0	1.4	1.4	1.9	4.3	5	9
135	EC718575	56	96	23.2	18.0	132	197.0	1.4	0.8	1.8	8.4	1	3
136	EC718576	121	156	30.0	18.0	26	42.0	1.6	0.4	0.2	5.1	5	7
137	EC718577	67	89	28.0	10.0	78	113.0	1.4	0.8	0.9	3.4	3	3
138	EC718578	129	161	30.7	23.7	47	87.5	1.8	0.6	0.4	3.6	5	9
139	EC718579	128	164	36.3	13.0	31	53.6	1.7	0.9	0.5	4.2	5	9
140	EC718580	57	102	27.0	18.0	106	179.0	1.6	0.2	1.1	4.8	5	3
141	EC718582	128	162	40.0	19.0	40	72.6	1.8	0.6	0.4	5.3	5	3
142	EC718583	121	156	31.5	21.0	56	107.5	1.9	0.7	0.7	6.7	3	3
143	EC718584	127	163	30.0	18.0	9	12.6	1.4	0.8	0.1	4.1	5	3
144	EC718585	58	102	28.0	30.0	249	409.0	1.6	0.9	2.8	18.5	3	5
145	EC718586	105	136	21.3	13.0	47	75.0	1.5	0.3	0.4	10.6	1	7

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146	EC718587	128	164	37.0	13.5	90	90.0	1.0	0.4	0.8	3.1	5	5
147	EC718588	57	105	22.0	12.3	5	7.3	1.3	1.0	0.2	2.8	1	5
148	EC718589	58	101	25.2	8.33	9	12.3	1.4	0.4	0.2	1.1	5	9
149	EC718590	53	100	22.0	16.0	53	84.0	1.5	0.8	0.9	5.3	3	5
150	EC718591	57	105	22.1	9.5	6	8.0	1.3	1.0	0.1	1.4	5	5
151	EC718592	56	100	22.0	12.0	33	48.0	1.4	0.8	0.4	1.5	5	5
152	EC718593	56	100	23.0	14.5	36	52.5	1.4	1.1	0.6	2.9	5	7
153	EC718594	56	105	26.0	17.0	29	46.0	1.5	1.2	0.6	2.0	1	5
154	EC718595	56	103	26.1	16.0	15	22.0	1.4	1.0	0.2	1.9	5	7
155	EC718596	56	100	25.0	7.5	20	33.5	1.6	1.1	0.9	2.6	7	7
156	EC718597	130	166	50.6	22.2	12	12.0	1.0	0.8	0.08	4.0	1	5
157	EC718598	128	164	29.0	21.0	79	79.0	1.0	0.5	0.4	6.7	5	7
158	EC718599	128	164	27.0	21.3	19	19.0	1.0	0.6	0.1	3.7	5	9
159	EC718600	66	100	24.1	16.0	3	5.0	1.6	4.0	0.2	2.5	1	5
160	EC718601	125	160	22.3	9.5	180	184.0	1.0	0.6	0.9	5.8	5	9
161	EC718602	57	100	22.1	15.5	47	81.0	1.7	0.9	0.7	2.4	3	5
162	EC718603	56	100	21.5	13.0	66	112.0	1.6	1.3	1.0	3.2	3	7
163	EC718604	56	93	23.0	5.0	21	31.2	1.5	0.9	0.3	2.8	5	9
164	EC718605	57	100	28.0	35.0	176	224.0	1.2	1.0	2.4	7.5	1	1
165	EC718606	128	164	40.7	18.0	47	42.5	0.9	0.8	0.3	3.4	5	7
166	EC718607	129	166	36.5	21.0	24	17.5	0.7	0.8	0.1	5.9	5	1
167	EC718609	51	105	25.0	11.5	6	8.7	1.5	0.8	0.07	1.6	5	3
168	EC718610	130	164	30.7	18.5	139	139.0	1.0	0.9	1.2	5.4	5	9
169	EC718611	123	156	20.7	13.5	68	68.0	1.0	1.0	0.6	4.2	5	9
170	EC718612	59	103	24.0	19.5	21	32.0	1.5	1.2	0.4	1.9	9	7
171	EC718613	62	103	21.0	8.7	17	23.7	1.3	1.4	0.3	2.3	9	5
172	EC718614	58	100	27.0	12.0	43	60.0	1.3	0.6	0.4	3.8	9	3
173	EC718615	121	156	24.2	13.0	141	145.5	1.0	0.8	1.2	4.4	7	7
174	EC718616	48	98	20.9	18.0	109	185.0	1.6	0.6	2.2	5.0	7	3

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175	EC718617	121	156	23.0	12.6	117	225.6	1.9	0.3	1.3	5.7	7	9
176	EC718236	129	164	36.0	17.0	123	229.0	1.8	0.8	2.1	6.7	5	9
177	EC718243	92	131	56.0	4.2	81	134.5	1.6	0.8	1.1	2.9	5	5
178	EC718274	129	153	46.5	13.5	69	76.5	1.2	0.6	1.0	3.1	3	5
179	EC718246	115	150	50.2	4.7	79	142.0	1.8	0.4	0.7	4.3	7	3
180	EC718276	132	164	35.6	18.0	31	55.0	1.7	0.4	0.2	6.4	7	9
181	EC718277	101	132	59.9	3.5	64	86.5	1.3	0.8	0.6	2.4	1	3
182	EC718462	88	124	51.5	4.6	6	6.0	1.3	1.0	0.1	0.2	5	5
183	EC718464	132	160	30.3	16.0	162	308.6	1.9	0.7	2.0	10.0	5	5
184	EC718675	132	164	41.2	17.0	47	88.4	1.8	1.1	0.8	4.2	5	9
185	EC718676	141	164	44.0	20.0	6	11.4	1.7	0.4	0.06	4.1	5	9
186	EC718677	132	164	24.2	18.0	42	75.0	1.7	0.6	0.5	5.3	7	9
187	EC718279	136	156	35.5	18.7	68	127.7	1.8	0.7	0.9	5.7	7	9
188	EC718281	129	156	26.0	15.0	174	340.6	1.9	0.7	2.5	8.2	3	9
189	EC718282	129	156	27.2	22.0	127	245.5	1.9	0.6	1.8	6.5	7	9
190	EC718283	126	154	25.7	17.0	87	168.5	1.9	0.9	1.6	6.0	3	9
191	EC718287	126	154	25.2	14.2	113	221.0	1.9	1.0	1.4	7.3	1	9
192	EC718288	132	156	36.7	17.0	41	76.7	1.8	0.9	0.6	5.0	7	7
193	EC718289	141	174	35.5	19.0	16	27.5	1.7	0.4	0.2	4.3	7	7
194	EC718291	139	163	34.0	12.0	94	94.0	1.0	1.0	0.9	3.3	5	7
195	EC718292	127	156	25.5	14.0	134	258.7	1.9	0.8	2.2	6.8	3	7
196	EC718293	127	156	22.3	15.0	80	151.6	1.9	0.8	1.2	6.0	3	7
197	EC718294	127	156	25.6	12.6	26	45.0	1.7	0.9	0.4	3.8	7	7
198	EC718664	140	164	47.5	17.0	37	68.7	1.8	0.7	0.5	5.4	7	7
199	EC718295	139	170	40.5	13.0	76	136.0	1.7	0.7	1.0	8.2	7	7
200	EC718297	120	151	22.0	14.0	105	203.0	1.9	0.7	1.4	4.8	7	7
201	EC718298	120	156	27.0	9.0	48	91.6	1.9	0.9	0.7	4.4	7	9
202	EC718299	120	151	25.6	17.0	49	92.6	1.9	0.6	0.5	4.8	9	9
203	EC718301	120	151	40.7	15.0	62	120.2	1.9	1.0	0.9	5.7	9	9

S. No.	Accession	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of Branches/ plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Resistance to rust	Resistance to powdery mildew
204	EC718302	110	145	31.0	19.0	32	56.0	1.7	0.9	0.5	7.2	9	5
205	EC718303	112	146	53.2	15.0	30	51.2	1.7	0.5	0.3	6.4	9	5
206	EC718304	143	170	31.2	15.5	33	58.7	1.7	0.5	0.3	5.1	9	9
207	EC718305	129	150	27.0	15.5	76	141.0	1.8	0.6	0.8	5.8	9	9
208	EC718691	128	156	26.3	15.0	127	248.3	1.9	0.7	2.0	6.2	9	9
209	EC718306	129	150	22.7	15.7	109	210.5	1.9	0.5	1.4	5.4	9	7
210	EC718307	129	150	20.3	8.3	35	39.0	1.1	0.6	0.2	3.0	5	7
211	EC718308	129	150	27.3	13.6	59	105.0	1.7	0.8	0.9	4.6	5	7
212	EC718309	129	156	24.2	16.0	106	203.0	1.9	0.9	1.6	6.8	5	5
213	EC718310	132	156	31.0	18.0	35	63.7	1.8	0.7	0.5	4.4	7	5
214	EC718311	129	156	24.7	17.0	60	108.2	1.8	0.9	0.8	4.1	7	9
215	EC718312	129	156	27.2	17.0	69	134.5	1.9	0.8	1.1	5.4	7	9
216	EC718693	132	164	25.2	16.0	141	263.7	1.8	0.6	1.6	7.3	9	7
217	EC718694	129	156	32.0	17.0	186	357.5	1.9	0.8	3.3	10.55	9	7
218	EC718446	132	173	24.0	16.0	107	200.1	1.8	0.3	0.6	4.8	7	5
219	EC718471	130	163	41.6	18.3	129	240.0	1.8	1.1	2.5	8.8	7	5
220	EC718473	132	163	41.2	19.0	84	161.2	1.9	1.0	1.1	6.5	7	5
221	EC718477	120	158	50.0	12.2	5	6.0	1.3	0.1	0.01	1.9	7	3
222	EC718658	131	163	41.0	18.0	9	12.0	1.3	0.1	0.01	5.4	7	9
223	EC718659	131	163	41.7	17.0	129	253.7	1.9	0.6	1.1	6.5	7	9
224	EC718443	129	163	33.2	14.0	58	108.7	1.8	0.8	0.9	5.5	7	9
225	EC718444	127	156	25.5	10.5	27	47.5	1.7	0.8	0.4	6.6	7	9
226	EC718445	127	162	31.5	13.0	60	113.0	1.8	0.8	1.1	4.5	9	7
227	EC718447	129	163	30.3	15.0	103	103.0	1.0	1.1	1.1	6.0	9	7
228	EC718695	128	165	27.2	15.0	78	150.5	1.9	1.1	1.6	6.0	9	7
229	EC718656	129	163	31.0	17.3	80	150.0	1.8	0.9	1.4	6.9	9	7
230	EC718657	127	156	30.5	10.5	9	11.5	1.2	1.0	0.1	5.1	9	5
231	EC718655	132	163	33.6	13.6	41	72.0	1.7	0.5	0.4	4.7	9	5
232	EC718654	132	163	31.2	18.0	59	110.0	1.8	0.8	0.7	5.0	5	9

S. No.	Accession	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of Branches/ plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Resistance to rust	Resistance to powdery mildew
233	EC718653	132	163	21.2	19.5	49	86.0	1.7	0.7	0.6	4.5	5	9
234	EC718652	132	166	44.0	16.0	218	420.0	1.9	0.8	3.3	10.0	5	9
235	EC741251	129	163	41.0	15.0	116	216.6	1.8	0.5	0.9	8.2	5	7
236	EC718672	132	163	20.7	15.0	79	145.0	1.8	0.6	1.4	4.9	5	7
237	EC718673	132	163	24.5	12.2	43	53.2	1.2	0.3	0.6	3.7	5	7
238	EC718651	96	145	56.5	4.2	26	37.0	1.5	0.5	0.2	3.2	5	7
239	EC718650	98	131	48.2	12.2	6	7.5	1.3	0.4	0.02	3.4	5	7
240	EC718649	96	157	59.7	14.0	43	56.2	1.3	0.2	0.4	5.0	5	7
241	EC718239	120	153	40.7	11.1	7	7.5	1.0	0.4	0.02	1.7	5	7
242	EC718237	97	132	67.0	3.2	73	110.2	1.5	0.6	0.7	3.1	5	9
243	EC718238	92	130	54.0	3.0	62	107.2	1.7	1.0	1.0	3.0	9	5
244	EC718644	111	146	43.2	2.0	9	10.0	1.3	1.2	0.1	2.1	7	9
245	EC718241	97	132	34.0	5.2	52	61.7	1.2	0.6	0.4	2.2	7	9
246	EC718242	95	132	48.0	5.7	122	188.7	1.5	0.5	1.3	3.9	7	5
247	EC718245	132	164	21.7	15.7	31	52.5	1.7	0.5	0.3	4.4	1	3
248	EC718246	131	164	26.0	22.7	8	13.5	1.7	0.4	0.05	3.0	3	7
249	EC718247	136	170	35.5	19.0	32	57.5	1.8	0.5	0.3	5.6	3	7
250	EC718248	132	164	50.7	16.0	33	61.2	1.8	0.7	0.4	5.0	3	7
251	EC718250	130	162	36.5	17.0	38	65.0	1.7	0.3	0.2	6.1	7	7
252	EC718251	134	176	31.5	17.0	133	250.1	1.8	0.3	0.9	8.6	7	7
253	EC718253	138	173	36.0	14.0	51	91.6	1.8	0.4	0.4	5.5	7	9
254	EC718254	138	173	35.8	13.0	56	108.0	1.9	0.5	0.5	3.9	3	7
255	EC718255	126	164	27.3	15.0	63	125.3	2.0	0.3	0.5	4.5	7	7
256	EC718256	128	173	32.0	17.0	39	65.0	1.6	0.4	0.3	5.5	7	7
257	EC718257	131	164	40.5	15.0	106	197.0	1.8	0.8	1.4	6.6	3	3
258	EC718258	132	164	40.3	15.0	66	90.1	1.3	0.5	0.7	6.7	3	3
259	EC718259	132	173	46.0	14.0	136	253.0	1.8	0.6	1.1	12.8	7	7
260	EC718682	132	164	36.5	13.5	141	234.5	1.6	1.1	2.0	6.2	3	3
261	EC718260	126	154	34.5	19.0	7	11.0	1.5	0.4	0.05	3.5	7	9

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262	EC718262	133	167	50.0	17.7	117	222.0	1.8	0.6	1.7	7.3	7	9
263	EC718263	132	164	27.2	17.0	22	37.5	1.7	0.8	0.2	6.8	7	9
264	EC718264	128	174	40.5	13.0	21	33.5	1.6	0.6	0.2	3.9	7	5
265	EC718265	126	164	36.0	19.0	74	123.0	1.6	0.5	0.5	5.2	7	9
266	EC718266	118	156	23.0	11.6	26	45.6	1.7	0.5	0.2	3.4	7	3
267	EC718267	138	170	24.3	14.0	32	58.3	1.8	0.5	0.3	4.1	7	7
268	EC718270	136	175	62.3	16.4	91	174.5	1.9	0.5	0.9	7.3	9	7
269	EC718271	132	164	30.8	14.4	9	15.0	1.6	0.4	0.06	3.5	9	7
270	EC718272	136	175	41.2	15.4	127	237.0	1.8	0.6	1.3	8.9	9	7
271	EC718273	138	173	52.0	15.4	153	275.0	1.7	0.9	2.3	15.3	9	9
272	EC718275	139	173	41.6	17.3	33	33.0	1.0	0.7	0.2	5.7	9	9
273	EC718250	116	153	35.5	7.0	7	9.0	1.3	1.0	0.7	4.1	5	7
274	EC718251	126	149	35.0	9.0	5	5.0	1.0	1.0	0.8	2.8	5	7
275	EC718252	97	149	43.5	9.0	57	87.5	1.2	0.4	0.7	1.6	5	7
276	EC718253	89	121	41.0	7.0	64	90.1	1.4	0.4	0.4	2.0	5	7
277	EC718645	125	154	51.0	11.0	50	79.5	1.5	0.6	0.5	2.3	5	5
278	EC718313	132	169	36.3	17.0	113	216.0	1.9	0.4	0.8	7.2	3	3
279	EC718314	132	168	40.5	17.0	147	285.5	1.9	0.5	1.2	7.6	3	3
280	EC718315	129	158	31.3	17.0	143	273.3	1.9	0.3	1.0	6.4	3	3
281	EC718316	141	170	31.0	13.0	34	60.1	1.7	0.4	0.2	5.6	7	5
282	EC718317	132	164	41.0	18.0	105	195.0	1.8	0.3	0.8	6.0	7	5
283	EC718318	131	160	31.0	16.0	45	81.6	1.8	0.3	0.2	4.9	7	5
284	EC718319	131	164	24.7	19.0	147	265.5	1.8	0.3	1.0	5.0	7	9
285	EC718320	131	164	30.3	21.0	72	133.3	1.8	0.4	0.4	4.4	5	9
286	EC718321	132	164	30.0	17.0	157	350.0	2.2	0.4	2.1	8.1	3	9
287	EC718322	132	164	35.5	16.0	284	561.5	1.9	0.5	2.7	9.2	7	9
288	EC718323	132	164	37.5	18.0	62	115.5	1.8	0.5	0.5	3.2	7	7
289	EC718324	132	164	35.8	17.0	40	40.1	1.0	0.5	0.2	3.5	5	7
290	EC718325	131	160	42.0	20.5	139	276.0	1.9	0.3	1.0	8.0	1	7



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291	EC718326	96	133	56.0	12.0	102	148.5	1.5	0.8	1.3	4.0	5	7
292	EC718646	96	133	57.0	11.0	96	140.5	1.5	0.8	1.0	3.3	5	7
293	EC718327	91	130	57.0	4.5	85	128.1	1.2	0.8	0.6	3.4	1	9
294	EC718328	127	168	33.0	14.0	37	62.5	1.6	0.5	0.3	2.0	5	9
295	EC718329	60	94	24.0	17.0	508	934.0	1.8	0.3	3.4	11.8	1	1
296	EC718330	97	134	59.0	4.5	108	152.5	1.2	0.8	1.0	3.6	5	5
297	EC718331	91	130	53.0	7.0	79	119.0	1.5	0.8	0.8	2.5	5	3
298	EC718333	83	134	23.0	16.0	45	78.7	1.7	1.1	0.4	4.3	5	5
299	EC718334	130	163	31.6	18.0	109	211.6	1.9	0.3	0.6	5.9	5	5
300	EC718335	91	130	45.0	7.0	60	88.5	1.3	0.4	0.5	2.4	5	5
301	EC718336	131	163	43.0	15.0	110	212.5	1.9	0.3	0.7	6.7	5	5
302	EC718647	118	156	53.0	4.2	24	41.1	1.1	0.3	0.9	1.3	9	3
303	EC718472	129	150	41.2	4.5	15	17.5	1.2	0.5	0.08	3.0	9	7
304	EC718337	131	163	39.6	17.0	44	79.3	1.8	0.2	0.2	6.5	9	7
305	EC718338	129	164	27.3	17.0	119	226.0	1.8	0.6	1.4	7.0	9	7
306	EC718339	131	163	43.6	12.4	116	223.3	1.9	0.5	1.1	7.3	9	7
307	EC718340	129	163	50.7	21.5	143	272.5	1.9	0.5	1.5	7.7	9	7
308	EC718341	129	163	48.0	21.0	124	240.0	1.9	0.4	1.0	6.8	7	7
309	EC718342	131	163	50.3	16.0	89	167.6	1.8	0.4	0.6	8.2	7	9
310	EC718343	128	165	40.2	21.0	132	243.7	1.8	0.4	1.0	6.0	1	9
311	EC718344	132	163	47.0	16.0	121	227.5	1.8	0.4	0.8	4.5	3	9
312	EC718345	128	165	34.3	18.0	210	406.6	1.9	0.4	1.7	8.4	3	9
313	EC718346	131	163	35.3	15.0	87	170.0	1.9	0.4	0.7	4.7	7	9
314	EC718347	130	163	51.0	16.8	97	193.2	1.9	0.5	0.8	5.8	7	9
315	EC718348	129	163	35.0	16.0	85	161.2	1.9	0.5	0.7	6.5	7	5
316	EC718349	131	163	43.6	15.7	117	230.4	1.9	0.3	0.9	6.2	7	5
317	EC718350	129	163	45.0	17.4	26	46.2	1.7	0.5	0.2	4.3	7	5
318	EC718351	129	161	46.8	21.8	172	341.0	1.9	0.5	1.5	5.1	9	5
319	EC718352	129	163	52.0	12.9	140	268.7	1.9	0.5	1.2	6.5	9	7

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320	EC718353	129	163	37.0	15.0	83	151.3	1.8	0.4	0.6	5.4	9	5
321	EC718354	131	163	44.6	15.0	108	213.4	1.9	0.5	0.8	5.5	1	3
322	EC718355	130	163	42.5	14.0	153	282.0	1.8	0.3	1.1	5.7	5	7
323	EC718356	129	164	32.0	15.9	96	177.5	1.8	0.4	0.9	6.6	5	7
324	EC718357	129	163	33.3	17.6	39	51.0	1.2	0.9	0.3	4.3	5	7
325	EC718360	126	161	37.3	11.6	10	16.6	1.6	0.4	0.1	3.6	9	3
326	EC718361	130	163	45.6	17.0	74	134.6	1.8	0.3	0.5	4.8	9	9
327	EC718362	126	161	46.0	18.0	139	247.2	1.7	0.5	1.1	5.5	5	9
328	EC718363	126	161	40.0	13.0	234	403.0	1.7	0.4	1.8	5.8	1	9
329	EC718365	129	163	40.0	15.0	194	350.0	1.8	0.4	1.2	4.9	7	9
330	EC718366	129	163	34.3	16.0	159	285.0	1.7	0.4	1.0	4.4	7	9
331	EC718367	126	161	34.0	18.0	85	161.2	1.9	0.3	0.8	3.8	9	9
332	EC718369	131	163	36.7	15.0	117	203.7	1.7	0.6	1.0	6.2	5	5
333	EC718370	65	104	20.8	10.0	355	525.0	1.4	0.8	4.8	25.5	1	1
334	EC718371	131	163	46.0	18.0	162	315.0	1.9	0.6	1.7	7.4	7	7
335	EC718372	131	163	34.0	18.0	46	78.3	1.6	0.4	0.3	4.3	7	3
336	EC718373	126	163	42.0	17.0	48	87.5	1.8	0.5	0.4	4.4	7	9
337	EC718374	127	163	28.0	8.0	3	3.0	1.0	1.0	0.5	3.1	7	9
338	EC718375	131	163	51.5	16.0	37	65.0	1.7	0.5	0.3	5.2	1	3
339	EC718376	131	163	45.3	13.0	53	83.3	1.5	0.4	0.3	4.6	7	7
340	EC718378	78	100	28.0	10.0	697	107.0	1.5	0.4	5.7	29.5	1	3
341	EC718379	65	100	28.0	13.0	184	290.1	1.5	0.8	1.2	6.8	1	3
342	EC718381	131	163	48.0	12.0	62	100.1	1.6	0.4	0.4	8.7	5	5
343	EC718383	65	101	26.0	16.0	403	682.0	1.6	0.4	3.0	14.2	1	1
344	EC718384	131	163	52.3	15.0	112	201.6	1.7	0.6	1.1	5.9	7	5
345	EC718386	129	163	54.0	16.0	199	378.5	1.9	0.5	1.9	6.2	7	7
346	EC718387	129	163	50.0	19.0	32	52.5	1.6	0.5	0.3	4.9	7	9
347	EC718388	73	101	22.0	7.0	4	7.0	1.7	2.0	0.1	2.2	1	3
348	EC718389	73	101	24.0	14.0	16	21.0	1.3	0.2	0.1	3.6	1	3

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349	EC718390	132	163	40.0	18.0	89	150.1	1.6	0.6	0.9	4.4	9	5
350	EC718391	124	163	36.5	17.0	137	246.0	1.7	0.4	1.2	4.3	9	5
351	EC718394	62	93	27.0	12.0	109	177.0	1.6	0.8	0.7	2.5	1	5
352	EC718398	130	163	40.0	17.0	126	237.6	1.8	0.3	1.06	6.4	9	5
353	EC718399	129	163	55.0	16.0	69	129.0	1.8	0.6	0.7	6.7	9	7
354	EC718400	129	163	33.5	13.0	184	353.5	1.9	0.5	1.7	6.8	9	7
355	EC718401	114	172	54.5	16.0	176	254.1	1.2	1.5	2.3	11.5	1	3
356	EC718402	131	163	33.6	17.0	65	127.2	1.9	0.3	0.6	4.0	9	9
357	EC718403	129	163	28.0	22.0	193	366.0	1.8	0.4	1.4	6.0	9	9
358	EC718404	60	103	25.0	16.0	478	761.1	1.5	0.8	3.2	9.4	3	9
359	EC718405	121	161	34.3	16.0	249	470.1	1.8	0.3	1.9	5.8	9	7
360	EC718406	129	163	50.7	15.0	184	365.0	1.9	0.7	2.1	7.4	9	7
361	EC718407	72	98	23.0	8.0	32	50.1	1.5	0.4	0.2	2.1	5	3
362	EC718408	131	163	41.4	17.0	97	199.1	2.0	0.3	0.8	5.5	7	5
363	EC718409	131	163	45.7	18.0	112	220.7	1.9	0.5	0.8	5.3	7	5
364	EC718410	67	100	26.0	15.0	23	38.0	1.6	0.3	0.1	2.3	1	3
365	EC718411	121	163	43.0	13.0	164	310.5	1.8	0.3	1.4	6.9	7	7
366	EC718412	129	163	42.0	21.0	74	137.5	1.8	0.3	0.6	5.6	7	7
367	EC718413	68	103	29.0	52.0	1002	1425.0	1.4	0.3	5.7	21.3	1	1
368	EC718414	78	100	22.0	9.0	22	30.1	1.3	0.3	0.1	1.2	7	1
369	EC718416	129	163	47.0	17.0	4	7.0	1.7	0.1	0.2	4.4	7	7
370	EC718417	129	163	36.0	20.0	22	37.5	1.7	0.3	0.2	6.5	7	7
371	EC718418	64	103	25.0	16.0	83	101.0	1.2	0.8	0.3	3.8	1	7
372	EC718419	129	163	28.0	17.0	31	43.0	1.3	0.1	0.2	3.5	9	1
373	EC718420	132	163	36.0	23.0	14	23.3	1.6	0.6	0.1	3.6	9	1
374	EC718421	131	163	38.2	17.7	58	117.5	2.0	0.4	0.4	5.2	9	9
375	EC718422	132	163	24.0	16.0	19	32.8	1.7	0.3	0.08	2.8	9	9
376	EC718423	129	163	20.8	15.0	14	23.0	1.6	0.4	0.1	3.3	5	1
377	EC718424	132	163	31.8	23.2	6	10.0	1.7	0.2	0.04	2.7	5	9

S. No.	Accession	Days to 50% flowering	Days to 80% maturity	Plant height (cm)	No. of Branches/ plant	No. of pods/ plant	No. of seeds/ plant	No. of seeds/ pod	100 seed weight (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Resistance to rust	Resistance to powdery mildew
378	EC718425	129	163	30.0	27.0	54	80.0	1.4	0.6	0.4	2.6	5	9
379	EC718426	129	163	25.6	18.6	62	118.0	1.9	0.2	0.1	5.0	7	9
380	EC718427	131	163	36.2	16.0	45	85.0	1.9	0.4	0.3	4.8	5	9
381	EC718428	73	100	23.0	21.0	245	419.5	1.7	0.8	2.1	7.5	1	1
382	EC718429	131	163	35.3	16.0	130	253.3	1.9	0.3	1.1	6.4	7	7
383	EC718430	131	163	37.0	14.0	177	342.5	1.9	0.4	1.1	6.0	7	7
384	EC718432	131	163	41.6	13.0	28	59.0	2.1	0.3	0.2	4.4	9	7
385	EC718433	131	163	36.6	18.0	73	141.0	1.9	0.6	0.9	4.0	9	5
386	EC718434	133	173	30.5	15.0	16	30.0	1.8	0.4	0.1	3.1	9	5
387	EC718435	133	173	27.0	7.5	4	6.0	1.5	0.1	0.05	4.5	9	7
388	EC718436	131	163	40.3	12.0	7	11.3	1.6	0.4	0.06	3.1	5	7
389	EC718437	133	163	41.5	12.0	13	20.0	1.5	0.4	0.1	7.8	5	7
390	EC718438	133	163	42.3	14.0	17	30.3	1.7	0.6	0.1	6.2	5	9
391	EC718439	67	106	21.3	16.3	163	258.6	1.5	0.8	4.1	16.8	1	1
392	EC718440	132	163	54.5	17.0	107	229.2	2.1	0.6	1.2	6.7	7	9
393	EC718441	133	163	41.5	10.5	18	30.0	1.7	0.6	0.1	6.7	7	9
394	EC718442	133	163	24.5	15.0	29	50.0	1.7	0.4	0.2	6.7	7	9
395	EC718448	133	163	41.3	15.0	58	116.6	2.0	0.5	0.7	6.6	9	7
396	EC718449	127	163	42.0	24.0	15	21.5	1.4	0.4	0.05	3.9	9	7
397	EC718648	92	130	54.0	6.0	89	159.5	1.7	1.5	1.5	3.9	9	5
398	EC718238	92	130	51.0	8.0	71	123.0	1.7	1.8	1.8	3.6	9	5
399	EC718252	129	165	37.7	15.0	105	205.0	1.9	0.6	1.05	8.1	9	5
400	EC718685	129	164	30.7	16.0	17	28.2	1.6	0.9	0.2	4.4	9	7
401	EC718686	129	158	43.3	16.0	43	90.6	2.1	0.9	0.8	6.3	7	7
402	EC718687	126	158	27.2	18.0	34	60.0	1.7	0.8	0.4	4.8	7	7
403	EC718688	126	158	36.0	17.0	8	13.7	1.7	0.6	0.1	4.2	7	9
404	EC718690	130	160	40.6	19.8	24	45.8	1.9	0.6	0.2	4.6	5	9
405	EC718692	126	164	47.5	12.0	186	364.0	1.9	0.6	2.7	9.9	5	9

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
1	L830	1	0	0	0	1	0	1	0	1	0	0	0	0	1
2	ILL10829	1	0	0	1	0	0	0	1	0	1	1	0	0	0
3	ILL8006	1	0	0	1	0	0	1	0	0	1	0	0	0	1
4	PRECOZ	1	0	0	1	0	0	0	1	0	1	0	0	0	1
5	EC718231	0	1	0	0	1	1	0	0	0	1	0	0	0	1
6	EC718232	0	1	0	0	1	1	0	0	0	1	0	0	0	1
7	EC718233	1	0	0	0	1	1	0	0	0	1	0	0	0	1
8	EC718234	0	1	0	1	0	1	0	0	1	0	0	0	0	1
9	EC718268	1	0	0	1	0	1	0	0	1	0	0	0	0	1
10	EC718326	0	1	0	0	1	1	0	0	1	0	0	0	0	1
11	EC718269	1	0	0	1	0	1	0	0	1	0	0	0	0	1
12	EC718250	1	0	0	0	1	1	0	0	0	1	0	0	0	1
13	EC718451	0	1	0	1	0	1	0	0	0	1	0	0	0	1
14	EC718452	1	0	0	1	0	1	0	0	0	1	0	0	0	1
15	EC718453	1	0	0	1	0	1	0	0	0	1	0	0	0	1
16	EC718454	1	0	0	1	0	1	0	0	0	1	0	0	0	1
17	EC718455	1	0	0	1	0	1	0	0	0	1	0	0	0	1
18	EC718456	1	0	0	1	0	1	0	0	0	1	0	0	0	1
19	EC718457	0	1	0	1	0	1	0	0	0	1	0	0	0	1
20	EC718458	0	1	0	1	0	1	0	0	0	1	0	0	0	1
21	EC718459	1	0	0	1	0	1	0	0	0	1	0	0	0	1
22	EC718460	0	1	0	1	0	1	0	0	0	1	0	0	0	1
23	EC718461	1	0	0	1	0	1	0	0	0	1	0	0	0	1
24	EC718462	0	1	0	1	0	1	0	0	0	1	0	0	0	1
25	EC718463	0	1	0	1	0	1	0	0	0	1	0	0	0	1
26	EC718465	0	1	0	1	0	1	0	0	0	1	0	0	0	1
27	EC718466	0	1	0	1	0	1	0	0	0	1	0	0	0	1
28	EC718467	0	1	0	1	0	1	0	0	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
29	EC718468	0	1	0	1	0	0	1	0	0	1	0	0	0	1
30	EC718469	0	1	0	1	0	1	0	0	0	1	0	0	0	1
31	EC718470	0	1	0	1	0	1	0	0	0	1	0	0	0	1
32	EC718472	0	1	0	1	0	1	0	0	0	1	0	0	0	1
33	EC718473	1	0	0	0	1	1	0	0	1	0	0	0	0	1
34	EC718474	0	1	0	1	0	0	1	0	1	0	0	0	0	1
35	EC718475	0	1	0	1	0	0	1	0	1	0	0	0	0	1
36	EC718476	0	1	1	0	0	0	0	1	0	1	0	0	0	1
37	EC718477	0	1	0	1	0	0	1	0	0	1	0	0	0	1
38	EC718478	0	1	0	0	1	1	0	0	0	1	0	0	0	1
39	EC718479	0	1	0	1	0	0	1	0	1	0	0	0	0	1
40	EC718480	0	1	0	1	0	1	0	0	0	1	0	0	0	1
41	EC718481	0	1	0	0	1	1	0	0	0	1	0	0	0	1
42	EC718482	0	1	0	1	0	1	0	0	0	1	0	0	0	1
43	EC718483	0	1	0	1	0	1	0	0	0	1	0	0	0	1
44	EC718484	0	1	0	1	0	1	0	0	0	1	0	0	0	1
45	EC718485	0	1	0	1	0	1	0	0	0	1	0	0	0	1
46	EC718486	0	1	0	1	0	1	0	0	0	1	0	0	0	1
47	EC718487	0	1	0	1	0	1	0	0	0	1	1	0	0	0
48	EC718488	0	1	0	1	0	0	1	0	1	0	0	0	0	1
49	EC718489	0	1	0	0	1	1	0	0	1	0	0	0	0	1
50	EC718490	0	1	0	0	1	0	1	0	0	1	1	0	0	0
51	EC718491	0	1	0	1	0	0	1	0	1	0	0	0	0	1
52	EC718492	1	0	0	1	0	1	0	0	0	1	0	0	0	1
53	EC718493	0	1	0	0	1	1	0	0	0	1	0	0	0	1
54	EC718494	0	1	0	1	0	1	0	0	0	1	0	0	0	1
55	EC718495	1	0	0	1	0	1	0	0	0	1	0	0	0	1
56	EC718496	0	1	0	1	0	1	0	0	0	1	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
57	EC718497	0	1	0	1	0	0	1	0	0	1	0	0	0	1
58	EC718498	0	1	0	1	0	0	1	0	0	1	0	0	0	1
59	EC718619	0	1	0	1	0	0	1	0	0	1	0	0	0	1
60	EC718620	0	1	0	1	0	0	1	0	0	1	0	0	0	1
61	EC718500	0	1	0	1	0	1	0	0	0	1	0	0	0	1
62	EC718501	0	1	0	0	1	1	0	0	1	0	0	0	0	1
63	EC718502	0	1	0	0	1	0	0	1	0	1	0	0	0	1
64	EC718503	0	1	0	1	0	1	0	0	1	0	0	0	0	1
65	EC718504	0	1	0	1	0	1	0	0	0	1	0	0	0	1
66	EC718505	0	1	0	0	1	0	1	0	0	1	0	0	0	1
67	EC718506	0	1	0	0	1	0	1	0	1	0	0	0	0	1
68	EC718507	0	1	0	0	1	1	0	0	0	1	0	0	0	1
69	EC718508	0	1	0	0	1	0	1	0	0	1	0	0	0	1
70	EC718509	0	1	0	1	0	0	1	0	0	1	0	0	0	1
71	EC718510	0	1	0	0	1	0	1	0	0	1	0	0	0	1
72	EC718511	0	1	0	1	0	0	1	0	0	1	0	0	0	1
73	EC718512	0	1	0	0	1	0	1	0	0	1	0	0	0	1
74	EC718513	0	1	0	0	1	0	1	0	0	1	1	0	0	0
75	EC718514	0	1	0	1	0	0	1	0	0	1	1	0	0	0
76	EC718515	0	1	0	1	0	0	1	0	1	0	1	0	0	0
77	EC718516	0	1	0	1	0	0	1	0	1	0	1	0	0	0
78	EC718517	0	1	0	0	1	0	1	0	1	0	1	0	0	0
79	EC718518	0	1	0	0	1	0	1	0	0	1	0	0	0	1
80	EC718519	0	1	0	0	1	0	1	0	0	1	1	0	0	0
81	EC718520	0	1	0	0	1	0	1	0	0	1	0	0	0	1
82	EC718521	0	1	0	0	1	0	1	0	0	1	1	0	0	0
83	EC718522	0	1	0	1	0	0	0	0	1	0	0	0	0	1
84	EC718523	0	1	0	1	0	0	1	0	1	0	0	0	0	1



S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
85	EC718524	0	1	0	0	1	0	1	0	1	0	0	0	0	1
86	EC718525	0	1	0	0	1	1	0	0	1	0	0	0	0	1
87	EC718526	0	1	0	0	1	1	0	0	0	1	0	0	0	1
88	EC718527	0	1	0	0	1	1	0	0	0	1	0	0	0	1
89	EC718528	0	1	0	1	0	1	0	0	1	0	0	0	0	1
90	EC718529	0	1	0	0	1	1	0	0	1	0	0	0	0	1
91	EC718530	0	1	0	0	1	1	0	0	1	0	0	0	0	1
92	EC718531	1	0	1	0	0	1	0	0	1	0	0	0	0	1
93	EC718533	0	1	0	0	1	0	1	0	0	1	0	0	0	1
94	EC718534	0	1	0	1	0	1	0	0	1	0	0	0	0	1
95	EC718535	0	1	0	1	0	1	0	0	1	0	0	0	0	1
96	EC718536	0	1	0	0	1	1	0	0	1	0	0	0	0	1
97	EC718537	0	1	0	0	1	0	1	0	0	1	0	0	0	1
98	EC718538	0	1	0	0	1	0	1	0	1	0	0	0	0	1
99	EC718539	0	1	0	1	0	1	0	0	1	0	0	0	0	1
100	EC718540	0	1	0	1	0	1	0	0	1	0	0	0	0	1
101	EC718541	0	1	0	1	0	1	0	0	0	1	0	0	0	1
102	EC718542	0	1	0	1	0	1	0	0	1	0	0	0	0	1
103	EC718543	0	1	0	1	0	1	0	0	1	0	0	0	0	1
104	EC718544	0	1	0	0	1	0	1	0	1	0	0	0	0	1
105	EC718545	0	1	0	0	1	0	1	0	1	0	0	0	0	1
106	EC718546	0	1	0	1	0	0	1	0	1	0	0	0	0	1
107	EC718547	0	1	0	1	0	0	1	0	1	0	0	0	0	1
108	EC718548	0	1	0	1	0	1	0	0	1	0	0	0	0	1
109	EC718549	0	1	0	1	0	1	0	0	1	0	0	0	0	1
110	EC718550	0	1	0	1	0	1	0	0	1	0	0	0	0	1
111	EC718551	0	1	0	1	0	1	0	0	1	0	0	0	0	1
112	EC718552	0	1	0	1	0	0	1	0	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
113	EC718553	0	1	0	1	0	1	0	0	1	0	0	0	0	1
114	EC718554	1	0	0	0	1	1	0	0	1	0	0	0	0	1
115	EC718555	0	1	0	0	1	1	0	0	1	0	0	0	0	1
116	EC718556	0	1	0	0	1	1	0	0	1	0	0	0	0	1
117	EC718557	1	0	0	1	0	0	1	0	0	1	0	0	0	1
118	EC718558	0	1	0	0	1	1	0	0	1	0	0	0	0	1
119	EC718559	0	1	0	0	1	1	0	0	1	0	0	0	0	1
120	EC718560	0	1	0	0	1	1	0	0	1	0	0	0	0	1
121	EC718561	0	1	0	1	0	0	1	0	0	1	0	0	0	1
122	EC718562	1	0	0	0	1	1	0	0	1	0	0	0	0	1
123	EC718563	1	0	0	1	0	1	0	0	1	0	0	0	0	1
124	EC718564	0	1	0	0	1	0	1	0	1	0	0	0	0	1
125	EC718565	0	1	0	0	1	0	1	0	1	0	0	0	0	1
126	EC718566	0	1	0	0	1	1	0	0	0	1	0	0	0	1
127	EC718567	0	1	1	0	0	0	1	0	0	1	0	0	0	1
128	EC718568	0	1	0	0	1	1	0	0	1	0	0	0	0	1
129	EC718569	0	1	0	1	0	0	1	0	1	0	0	0	0	1
130	EC718570	0	1	0	0	1	0	1	0	1	0	0	0	0	1
131	EC718571	0	1	1	0	0	0	1	0	0	1	0	0	0	1
132	EC718572	0	1	0	0	1	0	1	0	0	1	0	0	0	1
133	EC718573	0	1	0	0	1	0	1	0	1	0	0	0	0	1
134	EC718574	0	1	1	0	0	0	1	0	0	1	1	0	0	0
135	EC718575	0	1	0	1	0	1	0	0	1	0	0	0	0	1
136	EC718576	0	1	0	1	0	1	0	0	0	1	0	0	0	1
137	EC718577	0	1	0	1	0	1	0	0	0	1	0	0	0	1
138	EC718578	0	1	0	1	0	1	0	0	0	1	0	0	0	1
139	EC718579	0	1	0	1	0	1	0	0	0	1	0	0	0	1
140	EC718580	0	1	0	1	0	0	1	0	1	0	1	0	0	0

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
141	EC718582	0	1	0	1	0	0	1	0	1	0	0	0	0	1
142	EC718583	0	1	0	1	0	0	1	0	0	1	0	0	0	1
143	EC718584	0	1	1	0	0	1	0	0	0	1	0	0	0	1
144	EC718585	0	1	0	1	0	1	0	0	0	1	0	0	0	1
145	EC718586	0	1	0	0	1	1	0	0	0	1	0	0	0	1
146	EC718587	0	1	0	1	0	1	0	0	0	1	0	0	0	1
147	EC718588	0	1	0	1	0	1	0	0	0	1	0	0	0	1
148	EC718589	0	1	0	1	0	1	0	0	0	1	0	0	0	1
149	EC718590	0	1	0	1	0	1	0	0	0	1	0	0	0	1
150	EC718591	0	1	0	0	1	1	0	0	0	1	0	0	0	1
151	EC718592	0	1	0	1	0	1	0	0	0	1	0	0	0	1
152	EC718593	0	1	0	1	0	1	0	0	0	1	0	0	0	1
153	EC718594	0	1	0	1	0	1	0	0	0	1	0	0	0	1
154	EC718595	0	1	0	1	0	1	0	0	0	1	0	0	0	1
155	EC718596	0	1	0	0	0	1	0	0	0	1	0	0	0	1
156	EC718597	0	1	0	0	1	1	0	0	1	0	0	0	0	1
157	EC718598	0	1	0	1	0	1	0	0	0	1	1	0	0	0
158	EC718599	0	1	0	1	0	1	0	0	0	1	1	0	0	0
159	EC718600	0	1	0	1	0	1	0	0	1	0	0	0	0	1
160	EC718601	0	1	0	0	1	1	0	0	0	1	1	0	0	0
161	EC718602	0	1	0	0	1	1	0	0	1	0	0	0	0	1
162	EC718603	0	1	0	1	0	1	0	0	0	1	0	0	0	1
163	EC718604	0	1	0	1	0	0	1	0	0	1	0	0	0	1
164	EC718605	0	1	0	1	0	0	0	1	0	1	0	0	0	1
165	EC718606	0	1	0	0	1	1	0	0	0	1	1	0	0	0
166	EC718607	0	1	0	0	1	1	0	0	0	1	0	0	0	1
167	EC718609	0	1	0	1	0	1	0	0	0	1	0	0	0	1
168	EC718610	0	1	0	0	1	0	1	0	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
169	EC718611	0	1	0	0	1	0	1	0	0	1	0	0	0	1
170	EC718612	1	0	0	1	0	1	0	0	0	1	0	0	0	1
171	EC718613	0	1	0	1	0	1	0	0	0	1	0	0	0	1
172	EC718614	1	0	0	1	0	1	0	0	0	1	0	0	0	1
173	EC718615	0	1	0	0	1	0	1	0	0	1	0	0	0	1
174	EC718616	0	1	0	1	0	1	0	0	0	1	0	0	0	1
175	EC718617	0	1	0	1	0	0	1	0	0	1	0	0	0	1
176	EC718236	0	1	0	0	1	0	1	0	0	1	0	0	0	1
177	EC718243	1	0	1	0	0	1	0	0	0	1	0	0	0	1
178	EC718274	0	1	0	1	0	1	0	0	0	1	0	0	0	1
179	EC718246	0	1	0	1	0	0	1	0	0	1	0	0	0	1
180	EC718276	0	1	0	1	0	1	0	0	1	0	0	0	0	1
181	EC718277	1	0	0	1	0	1	0	0	1	0	0	0	0	1
182	EC718462	0	1	0	0	1	0	1	0	0	1	0	0	0	1
183	EC718464	0	1	0	1	0	0	1	0	0	1	0	0	0	1
184	EC718675	0	1	0	0	1	0	1	0	0	1	0	0	0	1
185	EC718676	0	1	0	1	0	1	0	0	0	1	0	0	0	1
186	EC718677	0	1	0	1	0	1	0	0	0	1	0	0	0	1
187	EC718279	0	1	0	0	1	0	1	0	0	1	0	0	0	1
188	EC718281	0	1	0	0	1	0	1	0	0	1	0	0	0	1
189	EC718282	0	1	0	0	1	0	1	0	0	1	0	0	0	1
190	EC718283	0	1	0	0	1	0	1	0	1	0	0	0	0	1
191	EC718287	0	1	0	0	1	0	0	1	0	1	0	0	0	1
192	EC718288	0	1	0	0	1	0	1	0	0	1	0	0	0	1
193	EC718289	0	1	0	0	1	1	0	0	0	1	0	0	0	1
194	EC718291	0	1	0	0	1	1	0	0	0	1	0	0	0	1
195	EC718292	0	1	0	0	1	0	1	0	1	0	0	0	0	1
196	EC718293	0	1	0	0	1	0	1	0	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
197	EC718294	0	1	0	0	1	0	1	0	0	1	0	0	0	1
198	EC718664	0	1	0	1	0	1	0	0	0	1	0	0	0	1
199	EC718295	0	1	0	1	0	0	1	0	0	1	0	0	0	1
200	EC718297	0	1	0	0	1	0	1	0	1	0	0	0	0	1
201	EC718298	0	1	0	0	1	1	0	0	0	1	0	0	0	1
202	EC718299	0	1	0	0	1	1	0	0	0	1	0	0	0	1
203	EC718301	0	1	0	1	0	0	1	0	0	1	0	0	0	1
204	EC718302	1	0	0	0	1	1	0	0	0	1	0	0	0	1
205	EC718303	0	1	0	0	1	0	1	0	0	1	0	0	0	1
206	EC718304	0	1	0	0	1	1	0	0	0	1	0	0	0	1
207	EC718305	0	1	0	0	1	0	1	0	0	1	0	0	0	1
208	EC718691	0	1	0	0	1	0	1	0	0	1	0	0	0	1
209	EC718306	0	1	0	0	1	0	1	0	0	1	0	0	0	1
210	EC718307	0	1	0	1	0	1	0	0	0	1	0	0	0	1
211	EC718308	0	1	0	1	0	0	1	0	0	1	0	0	0	1
212	EC718309	0	1	0	1	0	0	1	0	0	1	0	0	0	1
213	EC718310	0	1	0	1	0	0	1	0	0	1	0	0	0	1
214	EC718311	0	1	0	1	0	0	1	0	0	1	0	0	0	1
215	EC718312	0	1	0	0	1	0	1	0	0	1	0	0	0	1
216	EC718693	0	1	0	0	1	0	1	0	0	1	0	0	0	1
217	EC718694	0	1	0	1	0	0	1	0	0	1	0	0	0	1
218	EC718446	1	0	0	1	0	1	0	0	0	1	0	0	0	1
219	EC718471	0	1	0	0	1	0	1	0	0	1	0	0	0	1
220	EC718473	0	1	0	0	1	0	1	0	0	1	0	0	0	1
221	EC718477	1	0	0	0	1	1	0	0	0	1	1	0	0	0
222	EC718658	1	0	0	1	0	0	1	0	1	0	0	0	0	1
223	EC718659	0	1	0	1	0	1	0	0	1	0	0	0	0	1
224	EC718443	0	1	0	0	1	0	1	0	0	1	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
225	EC718444	0	1	0	0	1	0	1	0	0	1	0	0	0	1
226	EC718445	0	1	0	0	1	1	0	0	0	1	0	0	0	1
227	EC718447	0	1	0	0	1	0	1	0	0	1	0	0	0	1
228	EC718695	0	1	0	0	1	0	1	0	0	1	0	0	0	1
229	EC718656	0	1	0	0	1	0	1	0	0	1	0	0	0	1
230	EC718657	0	1	0	0	1	0	1	0	0	1	0	0	0	1
231	EC718655	0	1	0	0	1	0	1	0	0	1	0	0	0	1
232	EC718654	0	1	0	0	1	0	0	1	0	1	0	0	0	1
233	EC718653	0	1	0	0	1	0	1	0	0	1	0	0	0	1
234	EC718652	0	1	0	0	1	0	1	0	0	1	0	0	0	1
235	EC741251	0	1	0	1	0	0	1	0	0	1	0	0	0	1
236	EC718672	0	1	0	0	1	0	1	0	0	1	0	0	0	1
237	EC718673	0	1	0	0	1	0	1	0	0	1	0	0	0	1
238	EC718651	0	1	0	1	0	1	0	0	0	1	0	0	0	1
239	EC718650	0	1	1	0	0	1	0	0	0	1	0	0	0	1
240	EC718649	0	1	0	1	0	1	0	0	0	1	0	0	0	1
241	EC718239	1	0	0	1	0	1	0	0	0	1	0	0	0	1
242	EC718237	1	0	1	0	0	1	0	0	0	1	0	0	0	1
243	EC718238	1	0	1	0	0	1	0	0	0	1	0	0	0	1
244	EC718644	1	0	0	0	1	1	0	0	0	1	0	0	0	1
245	EC718241	0	1	1	0	0	1	0	0	0	1	0	0	0	1
246	EC718242	0	1	0	0	1	1	0	0	0	1	0	0	0	1
247	EC718245	1	0	0	1	0	1	0	0	0	1	0	0	0	1
248	EC718246	1	0	0	1	0	1	0	0	0	1	0	0	0	1
249	EC718247	0	1	0	1	0	1	0	0	1	0	0	0	0	1
250	EC718248	0	1	0	1	0	0	5	0	0	1	0	0	0	1
251	EC718250	0	1	1	0	0	1	0	0	0	1	0	0	0	1
252	EC718251	0	1	0	1	0	1	0	0	0	1	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
253	EC718253	1	0	1	0	0	1	0	0	0	1	0	0	0	1
254	EC718254	1	0	0	1	0	0	1	0	0	1	0	0	0	1
255	EC718255	1	0	0	1	0	1	0	0	0	1	0	0	0	1
256	EC718256	1	0	1	0	0	1	0	0	1	0	0	0	0	1
257	EC718257	1	0	0	1	0	0	1	0	1	0	0	0	0	1
258	EC718258	1	0	0	0	1	1	0	0	0	1	0	0	0	1
259	EC718259	1	0	0	0	1	1	0	0	0	1	0	0	0	1
260	EC718682	0	1	0	1	0	0	0	1	1	0	0	0	0	1
261	EC718260	0	1	0	1	0	1	0	0	1	0	0	0	0	1
262	EC718262	0	1	0	0	1	1	0	0	0	1	0	0	0	1
263	EC718263	0	1	0	1	0	1	0	0	1	0	0	0	0	1
264	EC718264	1	0	0	1	0	1	0	0	0	1	1	0	0	0
265	EC718265	0	1	0	1	0	1	0	0	1	0	0	0	0	1
266	EC718266	0	1	0	1	0	1	0	0	0	1	0	0	0	1
267	EC718267	0	1	0	0	1	1	0	0	0	1	0	0	0	1
268	EC718270	0	1	0	1	0	0	1	0	0	1	1	0	0	0
269	EC718271	0	1	0	1	0	1	0	0	0	1	0	0	0	1
270	EC718272	1	0	0	0	1	1	0	0	0	1	0	0	0	1
271	EC718273	0	1	0	1	0	1	0	0	0	1	1	0	0	0
272	EC718275	1	0	0	0	1	1	0	0	0	1	1	0	0	0
273	EC718250	0	1	0	1	0	0	1	0	0	1	0	0	0	1
274	EC718251	0	1	0	1	0	0	1	0	0	1	0	0	0	1
275	EC718252	0	1	0	1	0	0	1	0	0	1	0	0	0	1
276	EC718253	0	1	0	1	0	0	1	0	0	1	0	0	0	1
277	EC718645	0	1	0	1	0	0	1	0	0	1	0	0	0	1
278	EC718313	0	1	1	0	0	0	1	0	0	1	0	0	0	1
279	EC718314	0	1	1	0	0	0	1	0	1	0	0	0	0	1
280	EC718315	0	1	1	0	0	1	0	0	1	0	0	0	0	1



S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
281	EC718316	0	1	1	0	0	1	0	0	0	1	0	0	0	1
282	EC718317	0	1	1	0	0	1	0	0	1	0	0	0	0	1
283	EC718318	0	1	1	0	0	1	0	0	1	0	0	0	0	1
284	EC718319	1	0	1	0	0	1	0	0	1	0	0	0	0	1
285	EC718320	0	1	1	0	0	1	0	0	0	1	0	0	0	1
286	EC718321	0	1	0	1	0	0	1	0	0	1	0	0	0	1
287	EC718322	0	1	0	1	0	1	0	0	0	1	0	0	0	1
288	EC718323	0	1	0	1	0	1	0	0	0	1	0	0	0	1
289	EC718324	0	1	1	0	0	1	0	0	0	1	0	0	0	1
290	EC718325	1	0	1	0	0	0	1	0	1	0	0	0	0	1
291	EC718326	1	0	1	0	0	1	0	0	0	1	0	0	0	1
292	EC718646	1	0	1	0	0	1	0	0	0	1	0	0	0	1
293	EC718327	1	0	1	0	0	1	0	0	0	1	0	0	0	1
294	EC718328	1	0	0	1	0	1	0	0	0	1	0	0	0	1
295	EC718329	0	1	0	1	0	1	0	0	0	1	0	0	0	1
296	EC718330	1	0	1	0	0	0	0	1	0	1	0	0	0	1
297	EC718331	1	0	1	0	0	0	0	1	0	1	0	0	0	1
298	EC718333	0	1	0	1	0	1	0	0	0	1	0	0	0	1
299	EC718334	0	1	1	0	0	1	0	0	0	1	0	0	0	1
300	EC718335	1	0	1	0	0	0	0	1	0	1	0	0	0	1
301	EC718336	0	1	0	1	0	1	0	0	1	0	0	0	0	1
302	EC718647	0	1	0	0	1	0	1	0	0	1	0	1	0	0
303	EC718472	1	0	0	1	0	1	0	0	0	1	0	0	0	1
304	EC718337	0	1	0	1	0	0	1	0	1	0	0	0	0	1
305	EC718338	0	1	0	0	1	0	1	0	1	0	0	0	0	1
306	EC718339	0	1	1	0	0	0	1	0	0	1	0	0	0	1
307	EC718340	0	1	1	0	0	0	0	1	0	1	0	0	0	1
308	EC718341	1	0	1	0	0	0	0	1	0	1	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
309	EC718342	0	1	0	1	0	0	0	1	0	1	0	0	0	1
310	EC718343	0	1	0	1	0	0	0	1	0	1	0	0	0	1
311	EC718344	0	1	0	1	0	0	0	1	0	1	0	0	0	1
312	EC718345	0	1	0	1	0	0	0	1	0	1	0	0	0	1
313	EC718346	0	1	1	0	0	0	1	0	0	1	0	0	0	1
314	EC718347	0	1	1	0	0	0	0	1	0	1	0	0	0	1
315	EC718348	0	1	0	1	0	0	1	0	0	1	0	0	0	1
316	EC718349	0	1	0	1	0	0	0	1	0	1	0	0	0	1
317	EC718350	0	1	0	1	0	0	1	0	0	1	0	0	0	1
318	EC718351	0	1	0	1	0	0	0	1	0	1	0	0	0	1
319	EC718352	0	1	0	1	0	0	0	1	0	1	0	0	0	1
320	EC718353	0	1	0	1	0	0	1	0	0	1	0	0	0	1
321	EC718354	0	1	0	1	0	0	1	0	0	1	0	0	0	1
322	EC718355	0	1	0	1	0	0	1	0	0	1	0	0	0	1
323	EC718356	0	1	0	1	0	0	1	0	0	1	0	0	0	1
324	EC718357	0	1	0	1	0	1	0	0	0	1	0	0	0	1
325	EC718360	0	1	0	0	1	0	1	0	1	0	0	0	0	1
326	EC718361	0	1	0	1	0	0	1	0	0	1	0	0	0	1
327	EC718362	0	1	0	1	0	0	0	1	0	1	0	0	0	1
328	EC718363	0	1	0	1	0	0	1	0	0	1	0	0	0	1
329	EC718365	1	0	0	1	0	0	1	0	0	1	0	0	0	1
330	EC718366	0	1	0	1	0	0	1	0	0	1	0	0	0	1
331	EC718367	0	1	0	1	0	0	1	0	0	1	0	0	0	1
332	EC718369	0	1	0	1	0	1	0	0	1	0	0	0	0	1
333	EC718370	0	1	0	1	0	1	0	0	1	0	0	0	0	1
334	EC718371	0	1	0	1	0	1	0	0	0	1	0	0	0	1
335	EC718372	0	1	0	1	0	1	0	0	0	1	0	0	0	1
336	EC718373	0	1	0	0	1	0	1	0	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
337	EC718374	1	0	0	1	0	1	0	0	1	0	0	0	0	1
338	EC718375	0	1	0	1	0	0	1	0	1	0	0	0	0	1
339	EC718376	0	1	0	1	0	0	1	0	0	1	0	0	0	1
340	EC718378	0	1	0	1	0	0	1	0	0	1	0	0	0	1
341	EC718379	0	1	0	1	0	1	0	0	0	1	0	0	0	1
342	EC718381	0	1	0	1	0	0	1	0	0	1	0	0	0	1
343	EC718383	0	1	0	1	0	1	0	0	0	1	0	0	0	1
344	EC718384	0	1	0	1	0	1	0	0	0	1	0	0	0	1
345	EC718386	0	1	1	0	0	0	1	0	0	1	0	0	0	1
346	EC718387	1	0	0	1	0	0	1	0	0	1	0	0	0	1
347	EC718388	1	0	0	0	1	1	0	0	1	0	0	0	0	1
348	EC718389	1	0	0	1	0	1	0	0	1	0	0	0	0	1
349	EC718390	1	0	0	1	0	0	1	0	0	1	0	0	0	1
350	EC718391	0	1	0	1	0	0	1	0	0	1	0	0	0	1
351	EC718394	0	1	1	0	0	0	1	0	0	1	0	0	0	1
352	EC718398	0	1	0	1	0	0	1	0	0	1	0	0	0	1
353	EC718399	0	1	0	1	0	0	1	0	0	1	0	0	0	1
354	EC718400	0	1	0	1	0	0	1	0	0	1	0	0	0	1
355	EC718401	0	1	0	1	0	1	0	0	1	0	0	0	0	1
356	EC718402	0	1	0	1	0	1	0	0	0	1	0	0	0	1
357	EC718403	1	0	1	0	0	0	1	0	0	1	0	0	0	1
358	EC718404	0	1	1	0	0	1	0	0	0	1	0	0	0	1
359	EC718405	0	1	1	0	0	0	1	0	0	1	0	0	0	1
360	EC718406	0	1	0	1	0	0	1	0	0	1	0	0	0	1
361	EC718407	0	1	1	0	0	1	0	0	1	0	0	0	0	1
362	EC718408	0	1	0	1	0	0	1	0	0	1	0	0	0	1
363	EC718409	0	1	0	1	0	0	1	0	0	1	0	0	0	1
364	EC718410	0	1	1	0	0	1	0	0	0	1	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
365	EC718411	0	1	0	1	0	0	0	1	0	1	0	0	0	1
366	EC718412	0	1	1	0	0	1	0	0	1	0	0	0	0	1
367	EC718413	1	0	1	0	0	1	0	0	0	1	0	0	0	1
368	EC718414	0	1	0	1	0	0	1	0	0	1	0	0	0	1
369	EC718416	0	1	1	0	0	0	1	0	1	0	0	0	0	1
370	EC718417	1	0	1	0	0	0	1	0	1	0	0	0	0	1
371	EC718418	0	1	0	1	0	0	1	0	0	1	0	0	0	1
372	EC718419	0	1	1	0	0	1	0	0	1	0	0	0	0	1
373	EC718420	0	1	0	1	0	0	1	0	1	0	0	0	0	1
374	EC718421	0	1	1	0	0	0	1	0	0	1	0	0	0	1
375	EC718422	0	1	0	1	0	1	0	0	1	0	0	0	0	1
376	EC718423	0	1	1	0	0	0	1	0	0	1	0	0	0	1
377	EC718424	0	1	1	0	0	1	0	0	1	0	0	0	0	1
378	EC718425	1	0	0	1	0	1	0	0	1	0	0	0	0	1
379	EC718426	1	0	0	1	0	1	0	0	1	0	0	0	0	1
380	EC718427	0	1	0	1	0	1	0	0	1	0	0	0	0	1
381	EC718428	0	1	1	0	0	1	0	0	0	1	0	0	0	1
382	EC718429	0	1	0	1	0	1	0	0	1	0	0	0	0	1
383	EC718430	0	1	0	1	0	1	0	0	0	1	0	0	0	1
384	EC718432	0	1	0	1	0	1	0	0	1	0	0	0	0	1
385	EC718433	0	1	1	0	0	1	0	0	1	0	0	0	0	1
386	EC718434	1	0	1	0	0	1	0	0	1	0	0	0	0	1
387	EC718435	1	0	0	1	0	1	0	0	1	0	0	0	0	1
388	EC718436	0	1	0	0	1	0	1	0	1	0	0	0	0	1
389	EC718437	0	1	0	1	0	0	1	0	0	1	0	0	0	1
390	EC718438	0	1	0	1	0	0	1	0	0	1	0	0	0	1
391	EC718439	1	0	1	0	0	1	0	0	1	0	0	0	0	1
392	EC718440	0	1	0	1	0	0	0	1	1	0	0	0	0	1

S. No.	Accessions	Seedling stem pigmentation		Leaf pubescence			Leaflet size			Tendrill length		Flower colour			
		Absent	Present	Absent	Slight	Dense	Small	Medium	Large	Rudimentary	Prominent	White	Yellow	Red	Purple
393	EC718441	0	1	0	1	0	1	0	0	0	1	0	0	0	1
394	EC718442	0	1	0	1	0	1	0	0	0	1	0	0	0	1
395	EC718448	0	1	0	1	0	0	1	0	0	1	0	0	0	1
396	EC718449	0	1	0	1	0	0	1	0	0	1	0	0	0	1
397	EC718648	1	0	1	0	0	0	1	0	0	1	0	0	0	1
398	EC718238	1	0	1	0	0	0	1	0	0	1	0	0	0	1
399	EC718252	0	1	1	0	0	0	1	0	1	0	0	0	0	1
400	EC718685	0	1	0	1	0	0	1	0	1	0	0	0	0	1
401	EC718686	0	1	1	0	0	0	1	0	1	0	0	0	0	1
402	EC718687	0	1	0	1	0	1	0	0	1	0	1	0	0	0
403	EC718688	0	1	0	1	0	0	1	0	1	0	0	0	0	1
404	EC718690	0	1	0	1	0	1	0	0	0	1	0	0	0	1
405	EC718692	0	1	0	1	0	0	1	0	0	1	1	0	0	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
1	L830	0	0	1	0	0	0	1	0	0	0	0	1	0
2	ILL10829	0	0	1	0	0	1	0	0	0	0	0	1	0
3	ILL8006	0	0	1	0	0	0	1	0	0	0	0	1	0
4	PRECOZ	0	0	1	0	0	1	0	0	0	0	1	0	0
5	EC718231	0	0	1	0	0	0	0	0	1	0	0	1	0
6	EC718232	0	1	0	0	0	0	0	0	1	0	0	1	0
7	EC718233	0	0	1	0	0	0	0	1	0	0	0	1	0
8	EC718234	0	1	0	0	0	0	0	0	1	0	0	1	0
9	EC718268	0	1	0	0	0	0	0	0	1	0	1	0	0
10	EC718326	1	0	0	0	0	0	0	0	1	0	0	1	0
11	EC718269	0	1	0	0	0	0	0	0	1	0	1	0	0
12	EC718250	0	0	1	0	0	0	0	0	0	1	0	1	0
13	EC718451	0	1	0	0	0	0	0	1	0	0	0	1	0
14	EC718452	0	0	1	0	0	0	0	0	1	0	1	0	0
15	EC718453	0	0	1	0	0	0	0	0	1	0	1	0	0
16	EC718454	0	0	1	0	0	0	0	0	1	0	0	1	0
17	EC718455	0	0	1	0	0	0	0	0	1	0	0	1	0
18	EC718456	0	0	1	0	0	0	0	0	1	0	0	1	0
19	EC718457	0	0	1	0	0	0	0	0	1	0	0	1	0
20	EC718458	0	0	1	0	0	0	0	0	1	0	0	1	0
21	EC718459	0	0	1	0	0	0	1	0	0	0	0	1	0
22	EC718460	0	0	1	0	0	0	1	0	0	0	0	1	0
23	EC718461	0	1	0	0	0	1	0	0	0	0	0	1	0
24	EC718462	0	0	1	0	0	0	0	0	1	0	1	0	0
25	EC718463	0	0	1	0	0	0	0	0	1	0	0	1	0
26	EC718465	0	0	1	0	0	0	0	0	1	0	0	1	0
27	EC718466	0	0	1	0	0	0	0	0	1	0	0	1	0
28	EC718467	0	0	1	0	0	0	0	0	1	0	0	1	0
29	EC718468	0	0	1	0	0	0	1	0	0	0	0	1	0
30	EC718469	0	0	1	0	0	0	0	0	0	1	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
31	EC718470	0	0	1	0	0	0	1	0	0	0	0	1	0
32	EC718472	0	0	1	0	0	0	0	0	1	0	0	1	0
33	EC718473	0	1	0	0	0	0	0	0	1	0	0	1	0
34	EC718474	0	0	1	0	0	0	0	0	0	1	0	1	0
35	EC718475	0	0	1	0	0	0	0	0	1	0	0	1	0
36	EC718476	0	1	0	0	0	0	0	0	1	0	0	1	0
37	EC718477	0	0	1	0	0	0	0	0	1	0	0	1	0
38	EC718478	0	0	1	0	0	0	0	0	1	0	0	1	0
39	EC718479	0	0	1	0	0	1	0	0	0	0	0	1	0
40	EC718480	0	0	1	0	0	0	0	0	1	0	0	1	0
41	EC718481	0	0	1	0	0	0	0	0	1	0	0	1	0
42	EC718482	0	0	1	0	0	0	0	0	1	0	1	0	0
43	EC718483	0	0	1	0	0	0	0	0	1	0	0	1	0
44	EC718484	0	0	1	0	0	0	0	0	1	0	0	1	0
45	EC718485	0	0	1	0	0	0	0	0	1	0	0	1	0
46	EC718486	0	0	1	0	0	0	0	0	1	0	0	1	0
47	EC718487	0	0	1	0	0	0	0	0	1	0	0	1	0
48	EC718488	0	0	1	0	0	0	0	0	1	0	0	1	0
49	EC718489	0	0	1	0	0	0	1	0	0	0	0	1	0
50	EC718490	0	0	1	0	0	0	0	0	1	0	0	1	0
51	EC718491	0	1	0	0	0	0	1	0	0	0	1	0	0
52	EC718492	0	1	0	0	0	0	0	0	1	0	0	1	0
53	EC718493	0	0	1	0	0	0	0	0	1	0	0	1	0
54	EC718494	0	0	1	0	0	0	0	0	1	0	0	1	0
55	EC718495	0	0	1	0	0	0	0	0	1	0	1	0	0
56	EC718496	0	0	1	0	0	0	0	0	1	0	1	0	0
57	EC718497	0	0	1	0	0	0	0	0	1	0	0	1	0
58	EC718498	0	0	1	0	0	0	0	0	1	0	0	1	0
59	EC718619	0	0	1	0	0	0	0	0	1	0	0	1	0
60	EC718620	0	0	1	0	0	0	0	0	1	0	0	1	0



S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
61	EC718500	0	0	1	0	0	0	0	0	1	0	0	1	0
62	EC718501	0	0	1	0	0	0	0	0	1	0	0	1	0
63	EC718502	0	0	1	0	0	0	0	0	1	0	0	1	0
64	EC718503	0	0	1	0	0	0	0	0	1	0	0	1	0
65	EC718504	0	0	1	0	0	0	0	0	1	0	0	1	0
66	EC718505	0	0	1	0	0	0	0	0	1	0	0	1	0
67	EC718506	0	0	1	0	0	0	0	0	1	0	0	1	0
68	EC718507	0	0	1	0	0	0	0	0	1	0	0	1	0
69	EC718508	0	0	1	0	0	0	0	0	1	0	0	1	0
70	EC718509	0	0	1	0	0	0	0	0	0	1	0	1	0
71	EC718510	0	0	1	0	0	0	0	0	1	0	0	1	0
72	EC718511	0	0	1	0	0	0	0	0	0	1	0	1	0
73	EC718512	0	1	0	0	0	0	0	0	1	0	0	1	0
74	EC718513	0	0	1	0	0	0	0	1	0	0	0	1	0
75	EC718514	0	0	1	0	0	0	1	0	0	0	0	1	0
76	EC718515	0	0	1	0	0	0	0	0	1	0	0	1	0
77	EC718516	0	0	1	0	0	0	0	0	1	0	0	1	0
78	EC718517	0	0	1	0	0	0	0	0	1	0	0	1	0
79	EC718518	0	1	0	0	0	0	0	0	1	0	0	1	0
80	EC718519	0	0	1	0	0	0	0	0	1	0	0	1	0
81	EC718520	0	1	0	0	0	0	1	0	0	0	0	1	0
82	EC718521	0	0	1	0	0	0	0	0	1	0	0	1	0
83	EC718522	0	0	1	0	0	0	0	0	1	0	0	1	0
84	EC718523	0	0	1	0	0	0	1	0	0	0	0	1	0
85	EC718524	0	0	1	0	0	0	0	0	1	0	0	1	0
86	EC718525	0	0	1	0	0	0	0	0	1	0	0	1	0
87	EC718526	0	0	1	0	0	0	0	1	0	0	0	1	0
88	EC718527	0	0	1	0	0	0	0	0	1	0	0	1	0
89	EC718528	0	0	1	0	0	0	0	0	1	0	0	1	0
90	EC718529	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
91	EC718530	0	0	1	0	0	0	0	0	1	0	0	1	0
92	EC718531	0	0	1	0	0	0	0	0	1	0	0	1	0
93	EC718533	0	0	1	0	0	0	1	0	0	0	0	1	0
94	EC718534	0	1	0	0	0	0	0	0	1	0	0	1	0
95	EC718535	0	1	0	0	0	0	0	0	1	0	0	1	0
96	EC718536	0	1	0	0	0	0	0	0	1	0	0	1	0
97	EC718537	0	0	1	0	0	0	1	0	0	0	0	1	0
98	EC718538	0	0	1	0	0	0	0	0	0	1	0	1	0
99	EC718539	0	1	0	0	0	0	0	0	1	0	0	1	0
100	EC718540	0	1	0	0	0	0	0	0	1	0	0	1	0
101	EC718541	0	0	1	0	0	0	0	0	1	0	0	1	0
102	EC718542	0	0	1	0	0	0	0	0	1	0	0	1	0
103	EC718543	0	0	1	0	0	0	0	0	1	0	0	1	0
104	EC718544	0	0	1	0	0	0	1	0	0	0	0	1	0
105	EC718545	0	0	1	0	0	0	0	0	1	0	0	1	0
106	EC718546	0	0	1	0	0	0	0	0	1	0	0	1	0
107	EC718547	0	0	1	0	0	0	0	0	1	0	0	1	0
108	EC718548	0	0	1	0	0	0	0	0	1	0	0	1	0
109	EC718549	0	0	1	0	0	0	0	0	1	0	0	1	0
110	EC718550	0	0	1	0	0	0	0	0	1	0	0	1	0
111	EC718551	0	0	1	0	0	0	1	0	0	0	0	1	0
112	EC718552	0	0	1	0	0	0	1	0	0	0	0	1	0
113	EC718553	0	0	1	0	0	0	1	0	0	0	0	1	0
114	EC718554	0	0	1	0	0	0	1	0	0	0	0	1	0
115	EC718555	0	0	1	0	0	0	1	0	0	0	0	1	0
116	EC718556	0	0	1	0	0	0	1	0	0	0	0	1	0
117	EC718557	0	0	1	0	0	0	1	0	0	0	0	1	0
118	EC718558	0	0	1	0	0	0	0	1	0	0	0	1	0
119	EC718559	0	0	1	0	0	0	0	1	0	0	0	1	0
120	EC718560	0	0	1	0	0	0	1	0	0	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
121	EC718561	0	0	1	0	0	0	0	0	1	0	0	1	0
122	EC718562	0	0	1	0	0	0	1	0	0	0	0	1	0
123	EC718563	0	0	1	0	0	0	1	0	0	0	0	1	0
124	EC718564	0	0	1	0	0	0	0	1	0	0	0	1	0
125	EC718565	0	0	1	0	0	0	1	0	0	0	0	1	0
126	EC718566	0	0	1	0	0	0	0	0	0	1	0	1	0
127	EC718567	0	0	1	0	0	0	0	1	0	0	0	1	0
128	EC718568	0	0	1	0	0	0	0	0	1	0	0	1	0
129	EC718569	0	0	1	0	0	0	0	0	0	1	0	1	0
130	EC718570	0	0	1	0	0	0	0	0	1	0	0	1	0
131	EC718571	0	0	1	0	0	0	0	0	0	1	0	1	0
132	EC718572	0	0	1	0	0	0	0	1	0	0	0	1	0
133	EC718573	0	0	1	0	0	0	0	0	1	0	0	1	0
134	EC718574	0	0	1	0	0	0	0	0	0	1	0	1	0
135	EC718575	0	0	1	0	0	0	1	0	0	0	0	1	0
136	EC718576	0	0	1	0	0	0	1	0	0	0	0	1	0
137	EC718577	0	0	1	0	0	0	1	0	0	0	0	1	0
138	EC718578	0	0	1	0	0	0	0	0	1	0	0	1	0
139	EC718579	0	0	1	0	0	0	0	0	1	0	0	1	0
140	EC718580	0	0	1	0	0	0	0	0	0	1	0	1	0
141	EC718582	0	1	0	0	0	0	0	0	0	1	0	1	0
142	EC718583	0	0	1	0	0	0	0	0	1	0	0	1	0
143	EC718584	0	0	1	0	0	0	0	0	1	0	0	1	0
144	EC718585	0	0	1	0	0	0	0	1	0	0	0	1	0
145	EC718586	0	0	1	0	0	0	0	1	0	0	0	1	0
146	EC718587	0	0	1	0	0	0	0	1	0	0	0	1	0
147	EC718588	0	0	1	0	0	0	0	1	0	0	0	1	0
148	EC718589	0	0	1	0	0	0	0	1	0	0	0	1	0
149	EC718590	0	0	1	0	0	0	0	0	0	1	0	1	0
150	EC718591	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
151	EC718592	0	0	1	0	0	0	0	0	0	1	0	1	0
152	EC718593	0	0	1	0	0	0	0	0	0	1	0	1	0
153	EC718594	0	0	1	0	0	0	0	0	0	1	0	1	0
154	EC718595	0	0	1	0	0	0	0	0	0	1	0	1	0
155	EC718596	0	0	1	0	0	0	0	1	0	0	0	1	0
156	EC718597	0	0	1	0	0	0	0	1	0	0	0	1	0
157	EC718598	0	0	1	0	0	0	1	0	0	0	0	1	0
158	EC718599	0	0	1	0	0	0	0	0	1	0	0	1	0
159	EC718600	0	0	1	0	0	0	0	1	0	0	0	1	0
160	EC718601	0	0	1	0	0	0	0	0	1	0	0	1	0
161	EC718602	0	0	1	0	0	0	0	1	0	0	0	1	0
162	EC718603	0	0	1	0	0	0	0	1	0	0	0	1	0
163	EC718604	0	0	1	0	0	0	0	1	0	0	0	1	0
164	EC718605	0	0	1	0	0	0	0	1	0	0	0	1	0
165	EC718606	0	0	1	0	0	0	1	0	0	0	0	1	0
166	EC718607	0	0	1	0	0	0	0	1	0	0	0	1	0
167	EC718609	0	0	1	0	0	0	0	1	0	0	0	1	0
168	EC718610	0	0	1	0	0	0	0	0	0	1	0	1	0
169	EC718611	0	0	1	0	0	0	0	1	0	0	0	1	0
170	EC718612	0	0	1	0	0	0	0	1	0	0	0	1	0
171	EC718613	0	0	1	0	0	0	0	1	0	0	0	1	0
172	EC718614	0	0	1	0	0	0	0	1	0	0	0	1	0
173	EC718615	0	0	1	0	0	0	0	1	0	0	0	1	0
174	EC718616	0	0	1	0	0	0	0	1	0	0	0	1	0
175	EC718617	0	0	1	0	0	0	0	1	0	0	0	1	0
176	EC718236	0	0	1	0	0	0	0	0	1	0	0	1	0
177	EC718243	0	0	1	0	0	0	1	0	0	0	1	0	0
178	EC718274	0	0	1	0	0	0	0	0	0	1	1	0	0
179	EC718246	0	0	1	0	0	0	0	0	1	0	0	1	0
180	EC718276	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
181	EC718277	0	0	1	0	0	0	0	0	0	1	1	0	0
182	EC718462	0	0	1	0	0	0	0	0	0	1	1	0	0
183	EC718464	0	1	0	0	0	0	0	0	0	1	1	0	0
184	EC718675	0	0	1	0	0	0	0	0	1	0	0	1	0
185	EC718676	0	0	1	0	0	0	0	0	0	1	1	0	0
186	EC718677	0	0	1	0	0	0	0	0	1	0	1	0	0
187	EC718279	0	0	1	0	0	0	0	0	0	1	0	1	0
188	EC718281	0	0	1	0	0	0	0	0	0	1	1	0	0
189	EC718282	0	0	1	0	0	0	0	1	0	0	1	0	0
190	EC718283	0	1	0	0	0	0	0	0	0	1	1	0	0
191	EC718287	0	1	0	0	0	0	0	0	0	1	0	1	0
192	EC718288	0	0	1	0	0	0	1	0	0	0	0	1	0
193	EC718289	0	0	1	0	0	0	0	0	0	1	1	0	0
194	EC718291	0	0	1	0	0	0	0	1	0	0	1	0	0
195	EC718292	0	0	1	0	0	0	1	0	0	0	1	0	0
196	EC718293	0	1	0	0	0	0	0	0	0	1	1	0	0
197	EC718294	0	0	1	0	0	0	0	0	0	1	1	0	0
198	EC718664	0	0	1	0	0	0	0	0	0	1	1	0	0
199	EC718295	0	0	1	0	0	0	0	0	0	1	1	0	0
200	EC718297	0	1	0	0	0	0	0	0	0	1	1	0	0
201	EC718298	0	0	1	0	0	0	0	0	0	1	1	0	0
202	EC718299	0	0	1	0	0	0	0	0	0	1	1	0	0
203	EC718301	0	1	0	0	0	0	0	0	1	0	1	0	0
204	EC718302	0	0	1	0	0	0	0	0	0	1	0	1	0
205	EC718303	0	1	0	0	0	0	0	0	0	1	1	0	0
206	EC718304	0	1	0	0	0	0	0	0	0	1	1	0	0
207	EC718305	0	0	1	0	0	0	0	0	0	1	1	0	0
208	EC718691	0	1	0	0	0	0	0	1	0	0	1	0	0
209	EC718306	0	1	0	0	0	0	0	0	0	1	1	0	0
210	EC718307	0	1	0	0	0	0	0	0	0	1	1	0	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
211	EC718308	0	0	1	0	0	0	0	0	0	1	1	0	0
212	EC718309	0	0	1	0	0	0	0	0	0	1	1	0	0
213	EC718310	0	0	1	0	0	0	0	0	0	1	1	0	0
214	EC718311	0	0	1	0	0	0	0	1	0	0	1	0	0
215	EC718312	0	1	0	0	0	0	0	0	0	1	1	0	0
216	EC718693	0	1	0	0	0	0	0	0	0	1	0	1	0
217	EC718694	0	0	1	0	0	0	0	0	0	1	1	0	0
218	EC718446	0	1	0	0	0	0	0	0	0	1	0	1	0
219	EC718471	0	0	1	0	0	0	0	0	0	1	0	1	0
220	EC718473	0	0	1	0	0	0	0	0	0	1	0	1	0
221	EC718477	0	0	1	0	0	0	0	0	1	0	0	1	0
222	EC718658	0	0	1	0	0	0	0	0	1	0	0	1	0
223	EC718659	0	0	1	0	0	0	0	0	1	0	0	1	0
224	EC718443	0	0	1	0	0	0	0	0	1	0	0	1	0
225	EC718444	0	0	1	0	0	0	0	0	1	0	0	1	0
226	EC718445	0	0	1	0	0	0	0	0	1	0	0	1	0
227	EC718447	0	0	1	0	0	0	0	0	1	0	0	1	0
228	EC718695	0	0	1	0	0	0	0	0	1	0	0	1	0
229	EC718656	0	0	1	0	0	0	0	0	1	0	0	1	0
230	EC718657	0	0	1	0	0	0	0	0	1	0	0	1	0
231	EC718655	0	0	1	0	0	1	0	0	0	0	0	1	0
232	EC718654	0	0	1	0	0	0	0	0	1	0	0	1	0
233	EC718653	0	0	1	0	0	0	0	1	0	0	0	1	0
234	EC718652	0	0	1	0	0	0	0	0	0	1	0	1	0
235	EC741251	0	0	1	0	0	0	0	0	1	0	0	1	0
236	EC718672	0	0	1	0	0	0	0	0	1	0	0	1	0
237	EC718673	0	0	1	0	0	0	0	0	1	0	0	1	0
238	EC718651	0	0	1	0	0	0	0	0	1	0	0	1	0
239	EC718650	0	0	1	0	0	0	0	0	1	0	0	1	0
240	EC718649	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
241	EC718239	0	0	1	0	0	0	0	1	0	0	1	0	0
242	EC718237	0	0	1	0	0	0	0	1	0	0	1	0	0
243	EC718238	0	0	1	0	0	0	1	0	0	0	1	0	0
244	EC718644	0	0	1	0	0	0	0	0	0	1	0	1	0
245	EC718241	0	0	1	0	0	1	0	0	0	0	1	0	0
246	EC718242	0	0	1	0	0	0	1	0	0	0	1	0	0
247	EC718245	0	1	0	0	0	0	0	0	0	1	1	0	0
248	EC718246	0	1	0	0	0	0	0	0	0	1	1	0	0
249	EC718247	0	0	1	0	0	0	0	1	0	0	0	1	0
250	EC718248	0	1	0	0	0	0	0	1	0	0	1	0	0
251	EC718250	0	0	1	0	0	0	0	0	1	0	0	1	0
252	EC718251	0	0	1	0	0	0	0	0	1	0	1	0	0
253	EC718253	0	1	0	0	0	0	0	0	1	0	0	1	0
254	EC718254	0	0	1	0	0	0	0	0	1	0	0	1	0
255	EC718255	0	0	1	0	0	0	0	0	1	0	0	1	0
256	EC718256	0	1	0	0	0	0	0	0	1	0	0	1	0
257	EC718257	0	1	0	0	0	0	0	0	1	0	0	1	0
258	EC718258	0	0	1	0	0	0	0	1	0	0	0	1	0
259	EC718259	0	0	1	0	0	0	0	0	1	0	0	1	0
260	EC718682	0	0	1	0	0	0	0	0	1	0	1	0	0
261	EC718260	0	1	0	0	0	0	0	0	0	1	0	1	0
262	EC718262	0	0	1	0	0	0	0	0	1	0	0	1	0
263	EC718263	0	0	1	0	0	0	0	0	1	0	0	1	0
264	EC718264	0	0	1	0	0	0	0	0	1	0	0	1	0
265	EC718265	0	0	1	0	0	0	0	0	1	0	0	1	0
266	EC718266	0	1	0	0	0	0	0	0	0	1	1	0	0
267	EC718267	0	0	1	0	0	0	1	0	0	0	0	1	0
268	EC718270	0	0	1	0	0	0	1	0	0	0	0	1	0
269	EC718271	0	0	1	0	0	0	0	1	0	0	0	1	0
270	EC718272	0	1	0	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
271	EC718273	0	1	0	0	0	0	1	0	0	0	0	1	0
272	EC718275	0	0	1	0	0	0	0	0	1	0	0	1	0
273	EC718250	0	0	1	0	0	0	0	0	1	0	0	1	0
274	EC718251	0	0	1	0	0	0	0	0	1	0	0	1	0
275	EC718252	0	0	1	0	0	0	0	0	1	0	0	1	0
276	EC718253	0	0	1	0	0	0	0	0	1	0	0	1	0
277	EC718645	0	0	1	0	0	0	0	0	1	0	0	1	0
278	EC718313	0	1	0	0	0	0	0	0	1	0	0	1	0
279	EC718314	0	1	0	0	0	0	0	0	1	0	0	1	0
280	EC718315	0	0	1	0	0	0	0	0	1	0	0	1	0
281	EC718316	0	0	1	0	0	0	0	0	0	1	0	1	0
282	EC718317	0	0	1	0	0	0	0	0	1	0	0	1	0
283	EC718318	0	0	1	0	0	0	1	0	0	0	1	0	0
284	EC718319	0	0	1	0	0	0	0	0	1	0	0	1	0
285	EC718320	0	0	1	0	0	0	0	0	1	0	0	1	0
286	EC718321	0	0	1	0	0	1	0	0	0	0	0	1	0
287	EC718322	0	1	0	0	0	0	0	0	1	0	1	0	0
288	EC718323	0	0	1	0	0	0	0	0	1	0	0	1	0
289	EC718324	0	0	1	0	0	1	0	0	0	0	0	1	0
290	EC718325	0	1	0	0	0	0	0	0	1	0	1	0	0
291	EC718326	1	0	0	0	0	0	1	0	0	0	1	0	0
292	EC718646	1	0	0	0	0	0	1	0	0	0	1	0	0
293	EC718327	0	0	1	0	0	0	1	0	0	0	1	0	0
294	EC718328	0	0	1	0	0	0	0	0	1	0	0	1	0
295	EC718329	0	0	1	0	0	0	0	0	1	0	0	1	0
296	EC718330	0	0	1	0	0	0	0	1	0	0	1	0	0
297	EC718331	0	0	1	0	0	0	0	1	0	0	1	0	0
298	EC718333	0	1	0	0	0	0	0	0	1	0	0	1	0
299	EC718334	0	0	1	0	0	0	0	0	1	0	0	1	0
300	EC718335	1	0	0	0	0	0	1	0	0	0	1	0	0



S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
301	EC718336	0	0	1	0	0	0	0	0	1	0	0	1	0
302	EC718647	0	0	1	0	0	0	0	0	1	0	0	1	0
303	EC718472	0	1	0	0	0	0	0	0	1	0	0	1	0
304	EC718337	0	0	1	0	0	0	0	1	0	0	0	1	0
305	EC718338	0	1	0	0	0	0	0	1	0	0	1	0	0
306	EC718339	0	0	1	0	0	0	1	0	0	0	0	1	0
307	EC718340	0	0	1	0	0	0	0	0	1	0	0	1	0
308	EC718341	0	0	1	0	0	0	1	0	0	0	0	1	0
309	EC718342	0	0	1	0	0	0	0	0	1	0	0	1	0
310	EC718343	0	1	0	0	0	0	0	0	1	0	0	1	0
311	EC718344	0	0	1	0	0	0	0	0	1	0	0	1	0
312	EC718345	0	0	1	0	0	0	0	0	1	0	1	0	0
313	EC718346	0	0	1	0	0	0	0	0	1	0	0	1	0
314	EC718347	0	1	0	0	0	0	0	0	1	0	0	1	0
315	EC718348	0	0	1	0	0	0	0	0	1	0	0	1	0
316	EC718349	0	0	1	0	0	0	0	0	1	0	0	1	0
317	EC718350	0	0	1	0	0	0	0	0	1	0	0	1	0
318	EC718351	0	0	1	0	0	0	0	0	1	0	0	1	0
319	EC718352	0	0	1	0	0	0	0	0	1	0	0	1	0
320	EC718353	0	1	0	0	0	0	0	1	0	0	1	0	0
321	EC718354	0	0	1	0	0	0	0	0	1	0	0	1	0
322	EC718355	0	0	1	0	0	0	0	0	1	0	0	1	0
323	EC718356	0	0	1	0	0	0	0	0	0	1	0	1	0
324	EC718357	0	0	1	0	0	0	0	0	1	0	0	1	0
325	EC718360	0	0	1	0	0	0	0	0	1	0	0	1	0
326	EC718361	0	0	1	0	0	0	0	0	1	0	0	1	0
327	EC718362	0	0	1	0	0	0	0	0	1	0	0	1	0
328	EC718363	0	1	0	0	0	0	0	0	1	0	0	1	0
329	EC718365	0	1	0	0	0	0	0	0	1	0	0	1	0
330	EC718366	0	1	0	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
331	EC718367	0	1	0	0	0	0	0	0	1	0	0	1	0
332	EC718369	0	1	0	0	0	0	0	0	1	0	0	1	0
333	EC718370	0	1	0	0	0	0	0	1	0	0	0	1	0
334	EC718371	0	0	1	0	0	0	0	0	1	0	0	1	0
335	EC718372	0	1	0	0	0	0	0	0	1	0	0	1	0
336	EC718373	0	0	1	0	0	0	0	1	0	0	0	1	0
337	EC718374	0	0	1	0	0	1	0	0	0	0	0	1	0
338	EC718375	0	0	1	0	0	0	1	0	0	0	0	1	0
339	EC718376	0	0	1	0	0	0	0	1	0	0	0	1	0
340	EC718378	0	1	0	0	0	0	1	0	0	0	0	1	0
341	EC718379	0	1	0	0	0	0	1	0	0	0	0	1	0
342	EC718381	0	0	1	0	0	1	0	0	0	0	0	1	0
343	EC718383	0	0	1	0	0	0	0	0	1	0	0	1	0
344	EC718384	0	0	1	0	0	0	0	0	1	0	1	0	0
345	EC718386	0	0	1	0	0	0	0	0	1	0	0	1	0
346	EC718387	0	1	0	0	0	0	1	0	0	0	0	1	0
347	EC718388	0	0	1	0	0	0	0	1	0	0	0	1	0
348	EC718389	0	0	1	0	0	0	0	1	0	0	0	1	0
349	EC718390	0	1	0	0	0	0	1	0	0	0	0	1	0
350	EC718391	0	1	0	0	0	0	0	0	1	0	0	1	0
351	EC718394	0	1	0	0	0	0	1	0	0	0	0	1	0
352	EC718398	0	0	1	0	0	0	0	0	1	0	1	0	0
353	EC718399	0	1	0	0	0	0	0	0	1	0	0	1	0
354	EC718400	0	1	0	0	0	0	0	0	1	0	0	1	0
355	EC718401	0	0	1	0	0	0	0	0	1	0	0	1	0
356	EC718402	0	0	1	0	0	0	0	0	1	0	0	1	0
357	EC718403	0	0	1	0	0	0	0	0	1	0	1	0	0
358	EC718404	0	0	1	0	0	0	0	0	1	0	0	1	0
359	EC718405	0	1	0	0	0	0	0	0	1	0	1	0	0
360	EC718406	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
361	EC718407	0	0	1	0	0	0	0	1	0	0	0	1	0
362	EC718408	0	1	0	0	0	0	1	0	0	0	1	0	0
363	EC718409	0	0	1	0	0	0	0	0	1	0	0	1	0
364	EC718410	0	0	1	0	0	0	0	0	1	0	0	1	0
365	EC718411	0	0	1	0	0	0	0	0	1	0	0	1	0
366	EC718412	0	0	1	0	0	0	0	0	1	0	1	0	0
367	EC718413	0	0	1	0	0	0	0	0	1	0	0	1	0
368	EC718414	0	1	0	0	0	1	0	0	0	0	0	1	0
369	EC718416	0	0	1	0	0	0	0	0	0	1	0	1	0
370	EC718417	0	0	1	0	0	0	0	0	1	0	0	1	0
371	EC718418	0	1	0	0	0	1	0	0	0	0	0	1	0
372	EC718419	0	0	1	0	0	0	0	1	0	0	0	1	0
373	EC718420	0	0	1	0	0	0	0	0	1	0	0	1	0
374	EC718421	0	0	1	0	0	0	0	0	1	0	1	0	0
375	EC718422	0	0	1	0	0	0	0	0	1	0	0	1	0
376	EC718423	0	0	1	0	0	0	0	0	1	0	0	1	0
377	EC718424	0	0	1	0	0	0	0	0	1	0	0	1	0
378	EC718425	0	0	1	0	0	0	0	0	1	0	0	1	0
379	EC718426	0	0	1	0	0	0	0	0	1	0	0	1	0
380	EC718427	0	0	1	0	0	0	0	0	1	0	0	1	0
381	EC718428	0	1	0	0	0	0	1	0	0	0	0	1	0
382	EC718429	0	0	1	0	0	0	0	0	1	0	0	1	0
383	EC718430	0	0	1	0	0	0	0	0	1	0	1	0	0
384	EC718432	0	0	1	0	0	0	0	0	1	0	0	1	0
385	EC718433	0	0	1	0	0	0	0	0	0	1	0	1	0
386	EC718434	0	0	1	0	0	0	0	0	1	0	0	1	0
387	EC718435	0	0	1	0	0	0	0	1	0	0	0	1	0
388	EC718436	0	0	1	0	0	0	0	0	1	0	0	1	0
389	EC718437	0	0	1	0	0	0	0	0	1	0	0	1	0
390	EC718438	0	0	1	0	0	0	0	0	1	0	0	1	0

S. No.	Accessions	Ground colour of testa					Pattern of testa					Cotyledon colour		
		Green	Grey	Brown	Black	Pink	Absent	Dotted	Spotted	Marbled	Complex	Yellow	Orange/ red	Olive- green
391	EC718439	0	1	0	0	0	0	0	1	0	0	0	1	0
392	EC718440	0	0	1	0	0	0	0	0	0	1	0	1	0
393	EC718441	0	0	1	0	0	0	0	0	1	0	0	1	0
394	EC718442	0	0	1	0	0	0	0	0	1	0	0	1	0
395	EC718448	0	0	1	0	0	0	0	0	1	0	0	1	0
396	EC718449	0	0	1	0	0	0	0	0	1	0	0	1	0
397	EC718648	0	0	1	0	0	0	1	0	0	0	1	0	0
398	EC718238	0	0	1	0	0	0	1	0	0	0	1	0	0
399	EC718252	0	1	0	0	0	0	0	1	0	0	0	1	0
400	EC718685	0	1	0	0	0	0	0	0	1	0	1	0	0
401	EC718686	0	1	0	0	0	0	0	0	1	0	1	0	0
402	EC718687	0	1	0	0	0	0	0	0	1	0	1	0	0
403	EC718688	0	0	1	0	0	0	0	0	1	0	1	0	0
404	EC718690	0	0	1	0	0	0	0	0	0	1	1	0	0
405	EC718692	0	0	1	0	0	0	0	0	0	1	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
1	L830	1	0	0	0	1	0	0	0
2	ILL10829	1	0	0	0	1	0	0	0
3	ILL8006	1	0	0	0	1	0	0	0
4	PRECOZ	1	0	0	0	1	0	0	0
5	EC718231	0	0	0	1	0	0	1	0
6	EC718232	0	0	0	1	0	0	1	0
7	EC718233	0	0	0	1	0	0	1	0
8	EC718234	0	0	0	1	0	0	1	0
9	EC718268	0	0	0	1	0	0	1	0
10	EC718326	0	0	0	1	0	0	1	0
11	EC718269	0	0	0	1	0	0	1	0
12	EC718250	0	0	0	1	0	0	1	0
13	EC718451	0	0	0	1	0	0	1	0
14	EC718452	0	0	0	1	0	0	1	0
15	EC718453	0	0	0	1	0	0	1	0
16	EC718454	0	0	0	1	0	0	1	0
17	EC718455	0	0	0	1	0	0	1	0
18	EC718456	0	0	0	1	0	0	1	0
19	EC718457	0	0	0	1	0	0	1	0
20	EC718458	0	0	0	1	0	0	1	0
21	EC718459	0	0	0	1	0	0	1	0
22	EC718460	0	0	0	1	0	0	1	0
23	EC718461	0	0	0	1	0	0	1	0
24	EC718462	0	0	0	1	0	0	1	0
25	EC718463	0	0	0	1	0	0	1	0
26	EC718465	0	0	0	1	0	0	1	0
27	EC718466	0	0	0	1	0	0	1	0
28	EC718467	0	0	0	1	0	0	1	0
29	EC718468	0	0	0	1	0	0	1	0
30	EC718469	0	0	0	1	0	0	1	0
31	EC718470	0	0	0	1	0	0	1	0
32	EC718472	0	0	0	1	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
33	EC718473	0	0	0	1	0	0	1	0
34	EC718474	0	0	0	1	0	0	1	0
35	EC718475	0	0	0	1	0	0	1	0
36	EC718476	0	0	0	1	0	0	1	0
37	EC718477	0	0	0	1	0	0	1	0
38	EC718478	0	0	0	1	0	0	1	0
39	EC718479	0	0	0	1	0	0	1	0
40	EC718480	0	0	0	1	0	0	1	0
41	EC718481	0	0	0	1	0	0	1	0
42	EC718482	0	0	0	1	0	0	1	0
43	EC718483	0	0	0	1	0	0	1	0
44	EC718484	0	0	0	1	0	0	1	0
45	EC718485	0	0	0	1	0	0	0	1
46	EC718486	0	0	0	1	0	0	1	0
47	EC718487	0	0	0	1	0	0	1	0
48	EC718488	0	0	0	1	0	0	1	0
49	EC718489	0	0	0	1	0	0	1	0
50	EC718490	0	0	0	1	0	0	1	0
51	EC718491	0	0	0	1	0	0	1	0
52	EC718492	0	0	0	1	0	0	1	0
53	EC718493	0	0	0	1	0	0	1	0
54	EC718494	0	0	0	1	0	0	1	0
55	EC718495	0	0	0	1	0	0	1	0
56	EC718496	0	0	0	1	0	0	1	0
57	EC718497	0	0	0	1	0	0	1	0
58	EC718498	0	0	1	0	0	0	1	0
59	EC718619	0	0	1	0	0	0	1	0
60	EC718620	0	0	1	0	0	0	1	0
61	EC718500	0	0	0	1	0	0	1	0
62	EC718501	0	0	1	0	0	0	1	0
63	EC718502	0	0	0	1	0	0	1	0
64	EC718503	0	0	1	0	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
65	EC718504	0	0	0	1	0	0	1	0
66	EC718505	0	0	0	1	0	0	1	0
67	EC718506	0	0	0	1	0	0	1	0
68	EC718507	0	0	0	1	0	0	1	0
69	EC718508	0	0	0	1	0	0	1	0
70	EC718509	0	0	0	1	0	0	1	0
71	EC718510	0	0	0	1	0	0	1	0
72	EC718511	0	0	0	1	0	0	1	0
73	EC718512	0	0	0	1	0	0	1	0
74	EC718513	0	0	1	0	0	0	0	1
75	EC718514	0	0	0	1	0	0	1	0
76	EC718515	0	0	0	1	0	0	1	0
77	EC718516	0	0	0	1	0	0	1	0
78	EC718517	0	0	0	1	0	0	1	0
79	EC718518	0	0	0	1	0	0	1	0
80	EC718519	0	0	0	1	0	0	1	0
81	EC718520	0	0	0	1	0	0	1	0
82	EC718521	0	0	1	0	0	0	1	0
83	EC718522	0	0	0	1	0	0	1	0
84	EC718523	0	0	1	0	0	0	1	0
85	EC718524	0	0	0	1	0	0	0	1
86	EC718525	0	0	0	1	0	0	1	0
87	EC718526	0	0	0	1	0	0	1	0
88	EC718527	0	0	0	1	0	0	1	0
89	EC718528	0	0	1	0	0	0	1	0
90	EC718529	0	0	1	0	0	0	1	0
91	EC718530	0	0	1	0	0	0	1	0
92	EC718531	0	0	1	0	0	0	1	0
93	EC718533	0	0	0	1	0	0	1	0
94	EC718534	0	0	1	0	0	0	1	0
95	EC718535	0	0	1	0	0	0	1	0
96	EC718536	0	0	1	0	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
97	EC718537	0	0	0	1	0	0	0	1
98	EC718538	0	0	0	1	0	0	1	0
99	EC718539	0	0	1	0	0	0	1	0
100	EC718540	0	0	1	0	0	0	1	0
101	EC718541	0	0	1	0	0	0	1	0
102	EC718542	0	0	1	0	0	0	0	1
103	EC718543	0	0	1	0	0	0	0	1
104	EC718544	0	0	0	1	0	0	0	1
105	EC718545	0	0	0	1	0	0	1	0
106	EC718546	0	0	1	0	0	0	0	1
107	EC718547	0	0	1	0	0	0	0	1
108	EC718548	0	0	1	0	0	0	0	1
109	EC718549	0	0	1	0	0	0	1	0
110	EC718550	0	0	1	0	0	0	0	1
111	EC718551	0	0	1	0	0	0	0	1
112	EC718552	0	0	1	0	0	0	0	1
113	EC718553	0	0	1	0	0	0	0	1
114	EC718554	0	1	0	0	0	1	0	0
115	EC718555	0	0	1	0	0	0	0	1
116	EC718556	0	0	1	0	0	0	0	1
117	EC718557	0	0	0	1	0	0	0	1
118	EC718558	0	0	1	0	0	0	0	1
119	EC718559	0	0	1	0	0	0	0	1
120	EC718560	0	0	1	0	0	0	0	1
121	EC718561	0	0	0	1	0	0	1	0
122	EC718562	0	0	1	0	0	0	0	1
123	EC718563	0	0	1	0	0	0	0	1
124	EC718564	0	0	1	0	0	0	0	1
125	EC718565	0	0	0	1	0	0	1	0
126	EC718566	0	0	0	1	0	0	1	0
127	EC718567	0	0	1	0	0	0	0	1
128	EC718568	0	0	0	1	0	0	1	0



S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
129	EC718569	0	0	0	1	0	0	1	0
130	EC718570	0	0	0	1	0	0	1	0
131	EC718571	0	0	1	0	0	0	0	1
132	EC718572	0	0	0	1	0	0	1	0
133	EC718573	0	0	0	1	0	0	1	0
134	EC718574	0	0	1	0	0	0	0	1
135	EC718575	0	0	1	0	0	0	0	1
136	EC718576	0	1	0	0	0	0	1	0
137	EC718577	0	0	1	0	0	0	0	1
138	EC718578	0	0	1	0	0	0	1	0
139	EC718579	0	0	0	1	0	0	1	0
140	EC718580	0	1	0	0	0	1	0	0
141	EC718582	0	0	0	1	0	0	1	0
142	EC718583	0	0	0	1	0	0	1	0
143	EC718584	0	0	0	1	0	0	1	0
144	EC718585	0	0	1	0	0	0	0	1
145	EC718586	0	0	1	0	0	0	0	1
146	EC718587	0	0	0	1	0	0	1	0
147	EC718588	0	0	1	0	0	0	0	1
148	EC718589	0	0	1	0	0	0	0	1
149	EC718590	0	0	1	0	0	0	0	1
150	EC718591	0	0	0	1	0	0	1	0
151	EC718592	0	0	1	0	0	0	0	1
152	EC718593	0	0	1	0	0	0	0	1
153	EC718594	0	0	1	0	0	0	0	1
154	EC718595	0	0	1	0	0	0	0	1
155	EC718596	0	0	1	0	0	0	0	1
156	EC718597	0	0	1	0	0	0	0	1
157	EC718598	0	0	0	1	0	0	1	0
158	EC718599	0	0	0	1	0	0	1	0
159	EC718600	0	0	1	0	0	0	0	1
160	EC718601	0	0	0	1	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
161	EC718602	0	0	1	0	0	0	0	1
162	EC718603	0	0	1	0	0	0	0	1
163	EC718604	0	0	1	0	0	0	0	1
164	EC718605	0	0	1	0	0	0	0	1
165	EC718606	0	0	0	1	0	0	1	0
166	EC718607	0	0	0	1	0	0	1	0
167	EC718609	0	1	0	0	0	0	0	1
168	EC718610	0	0	0	1	0	0	1	0
169	EC718611	0	0	0	1	0	0	1	0
170	EC718612	0	1	0	0	0	0	0	1
171	EC718613	0	1	0	0	0	0	0	1
172	EC718614	0	1	0	0	0	0	0	1
173	EC718615	0	0	0	1	0	0	1	0
174	EC718616	0	1	0	0	0	0	0	1
175	EC718617	0	0	0	1	0	0	1	0
176	EC718236	0	0	1	0	0	0	1	0
177	EC718243	0	0	0	1	0	1	0	0
178	EC718274	0	0	0	1	0	1	0	0
179	EC718246	0	0	0	1	0	1	0	0
180	EC718276	0	0	1	0	0	0	1	0
181	EC718277	0	0	0	1	0	1	0	0
182	EC718462	0	0	0	1	0	1	0	0
183	EC718464	0	0	1	0	0	0	1	0
184	EC718675	0	1	0	0	0	0	1	0
185	EC718676	0	1	0	0	0	0	1	0
186	EC718677	0	1	0	0	0	1	0	0
187	EC718279	0	0	1	0	0	0	1	0
188	EC718281	0	0	1	0	0	0	1	0
189	EC718282	0	0	1	0	0	0	1	0
190	EC718283	0	0	1	0	0	0	1	0
191	EC718287	0	0	1	0	0	0	1	0
192	EC718288	0	0	1	0	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
193	EC718289	0	0	1	0	0	0	1	0
194	EC718291	0	0	1	0	0	0	1	0
195	EC718292	0	0	1	0	0	0	1	0
196	EC718293	0	1	0	0	0	1	0	0
197	EC718294	0	0	1	0	0	0	1	0
198	EC718664	0	1	0	0	0	1	0	0
199	EC718295	0	0	1	0	0	0	1	0
200	EC718297	0	0	1	0	0	0	1	0
201	EC718298	0	0	1	0	0	0	1	0
202	EC718299	0	0	1	0	0	0	1	0
203	EC718301	0	0	1	0	0	0	1	0
204	EC718302	0	0	1	0	0	0	1	0
205	EC718303	0	0	1	0	0	0	1	0
206	EC718304	0	0	1	0	0	0	1	0
207	EC718305	0	0	1	0	0	0	1	0
208	EC718691	0	0	0	1	0	0	1	0
209	EC718306	0	0	0	1	0	0	1	0
210	EC718307	0	0	1	0	0	0	1	0
211	EC718308	0	0	1	0	0	0	1	0
212	EC718309	0	0	1	0	0	0	1	0
213	EC718310	0	0	1	0	0	0	1	0
214	EC718311	0	1	0	0	0	0	1	0
215	EC718312	0	1	0	0	0	0	1	0
216	EC718693	0	1	0	0	0	0	1	0
217	EC718694	0	0	0	1	0	0	1	0
218	EC718446	0	0	0	1	0	0	0	1
219	EC718471	0	0	0	1	0	0	1	0
220	EC718473	0	0	0	1	0	0	1	0
221	EC718477	0	0	1	0	0	0	0	1
222	EC718658	0	0	0	1	0	0	1	0
223	EC718659	0	0	0	1	0	0	1	0
224	EC718443	0	0	0	1	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
225	EC718444	0	0	0	1	0	0	1	0
226	EC718445	0	0	0	1	0	0	1	0
227	EC718447	0	0	1	0	0	0	1	0
228	EC718695	0	0	0	1	0	0	0	1
229	EC718656	0	0	1	0	0	0	1	0
230	EC718657	0	0	0	1	0	0	1	0
231	EC718655	0	0	1	0	0	0	1	0
232	EC718654	0	0	1	0	0	0	1	0
233	EC718653	0	0	0	1	0	0	1	0
234	EC718652	0	0	1	0	0	0	0	1
235	EC741251	0	0	0	1	0	0	0	1
236	EC718672	0	0	0	1	0	0	0	1
237	EC718673	0	0	1	0	0	0	1	0
238	EC718651	0	1	0	0	0	0	1	0
239	EC718650	0	1	0	0	0	0	1	0
240	EC718649	0	1	0	0	0	1	0	0
241	EC718239	0	0	0	1	0	1	0	0
242	EC718237	0	0	0	1	0	1	0	0
243	EC718238	0	0	0	1	0	1	0	0
244	EC718644	0	0	0	1	0	0	0	1
245	EC718241	0	0	0	1	0	0	0	1
246	EC718242	0	0	0	1	0	0	0	1
247	EC718245	0	0	0	1	0	0	1	0
248	EC718246	0	0	1	0	0	1	0	0
249	EC718247	0	0	1	0	0	0	1	0
250	EC718248	0	0	1	0	0	1	0	0
251	EC718250	0	0	1	0	0	0	1	0
252	EC718251	0	0	1	0	0	0	1	0
253	EC718253	0	0	1	0	0	0	1	0
254	EC718254	0	0	1	0	0	0	1	0
255	EC718255	0	0	1	0	0	0	1	0
256	EC718256	0	0	1	0	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
257	EC718257	0	0	0	1	0	0	0	1
258	EC718258	0	0	0	1	0	0	1	0
259	EC718259	0	0	1	0	0	0	1	0
260	EC718682	0	1	0	0	0	0	1	0
261	EC718260	0	0	0	0	0	0	1	0
262	EC718262	0	0	1	0	0	0	0	1
263	EC718263	0	0	1	0	0	0	1	0
264	EC718264	0	0	1	0	0	0	1	0
265	EC718265	0	1	0	0	0	0	1	0
266	EC718266	0	0	1	0	0	0	1	0
267	EC718267	0	0	1	0	0	0	1	0
268	EC718270	0	0	1	0	0	0	1	0
269	EC718271	0	0	1	0	0	0	1	0
270	EC718272	0	0	1	0	0	0	1	0
271	EC718273	0	1	0	0	0	0	1	0
272	EC718275	0	1	0	0	0	0	1	0
273	EC718250	0	0	0	1	0	0	0	1
274	EC718251	0	0	0	1	0	0	0	1
275	EC718252	0	0	0	1	0	0	0	1
276	EC718253	0	0	0	1	0	0	0	1
277	EC718645	0	0	0	1	0	0	0	1
278	EC718313	0	0	0	1	0	0	1	0
279	EC718314	0	0	0	1	0	0	1	0
280	EC718315	0	0	0	1	0	0	1	0
281	EC718316	0	1	0	0	0	1	0	0
282	EC718317	0	0	0	1	0	0	1	0
283	EC718318	0	0	1	0	0	0	1	0
284	EC718319	0	0	0	1	0	0	0	1
285	EC718320	0	0	1	0	0	0	1	0
286	EC718321	0	0	0	1	0	0	1	0
287	EC718322	0	0	0	1	0	0	0	1
288	EC718323	0	0	0	1	0	0	0	1

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
289	EC718324	0	0	0	1	0	0	0	1
290	EC718325	0	0	0	1	0	0	0	1
291	EC718326	0	0	0	1	0	0	0	1
292	EC718646	0	0	1	0	0	0	0	1
293	EC718327	0	0	1	0	0	0	0	1
294	EC718328	0	0	0	1	0	0	1	0
295	EC718329	0	0	1	0	0	0	0	1
296	EC718330	0	0	1	0	0	0	0	1
297	EC718331	0	0	1	0	0	0	0	1
298	EC718333	0	0	0	1	0	0	1	0
299	EC718334	0	0	0	1	0	0	1	0
300	EC718335	0	0	1	0	0	0	0	1
301	EC718336	0	0	0	1	0	0	1	0
302	EC718647	0	0	0	1	0	0	0	1
303	EC718472	0	0	0	1	0	0	0	1
304	EC718337	0	0	0	1	0	0	1	0
305	EC718338	0	0	1	0	0	0	1	0
306	EC718339	0	0	1	0	0	0	1	0
307	EC718340	0	0	0	1	0	0	1	0
308	EC718341	0	0	0	1	0	0	1	0
309	EC718342	0	0	0	1	0	0	1	0
310	EC718343	0	0	0	1	0	0	1	0
311	EC718344	0	0	0	1	0	0	0	1
312	EC718345	0	0	0	1	0	0	1	0
313	EC718346	0	0	0	1	0	0	1	0
314	EC718347	0	0	0	1	0	0	1	0
315	EC718348	0	0	0	1	0	0	1	0
316	EC718349	0	0	0	1	0	0	1	0
317	EC718350	0	0	0	1	0	0	1	0
318	EC718351	0	0	0	1	0	0	1	0
319	EC718352	0	0	0	1	0	0	1	0
320	EC718353	0	0	0	1	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
321	EC718354	0	0	0	1	0	0	1	0
322	EC718355	0	0	0	1	0	0	1	0
323	EC718356	0	0	0	1	0	0	1	0
324	EC718357	0	0	0	1	0	0	1	0
325	EC718360	0	0	0	1	0	0	1	0
326	EC718361	0	0	0	1	0	0	1	0
327	EC718362	0	0	0	1	0	0	1	0
328	EC718363	0	0	0	1	0	0	1	0
329	EC718365	0	0	0	1	0	0	1	0
330	EC718366	0	0	0	1	0	0	1	0
331	EC718367	0	0	0	1	0	0	1	0
332	EC718369	0	0	0	1	0	0	1	0
333	EC718370	0	1	0	0	0	1	0	0
334	EC718371	0	0	0	1	0	0	1	0
335	EC718372	0	0	0	1	0	0	1	0
336	EC718373	0	0	0	1	0	0	1	0
337	EC718374	0	0	0	1	0	0	1	0
338	EC718375	0	0	1	0	0	0	1	0
339	EC718376	0	0	0	1	0	0	0	1
340	EC718378	0	0	1	0	0	0	0	1
341	EC718379	0	0	1	0	0	0	0	1
342	EC718381	0	0	1	0	0	0	1	0
343	EC718383	0	0	1	0	0	0	0	1
344	EC718384	0	0	0	1	0	0	1	0
345	EC718386	0	0	0	1	0	0	1	0
346	EC718387	0	0	0	1	0	0	1	0
347	EC718388	0	1	0	0	0	1	0	0
348	EC718389	0	1	0	0	0	1	0	0
349	EC718390	0	0	0	1	0	0	1	0
350	EC718391	0	0	1	0	0	0	1	0
351	EC718394	0	1	0	0	0	1	0	0
352	EC718398	0	0	0	1	0	0	1	0

S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
353	EC718399	0	0	0	1	0	0	1	0
354	EC718400	0	0	0	1	0	0	1	0
355	EC718401	0	0	0	1	0	0	0	1
356	EC718402	0	0	0	1	0	0	1	0
357	EC718403	0	0	0	1	0	0	1	0
358	EC718404	0	0	1	0	0	0	0	1
359	EC718405	0	0	0	1	0	0	1	0
360	EC718406	0	0	0	1	0	0	1	0
361	EC718407	0	1	0	0	0	1	0	0
362	EC718408	0	0	0	1	0	0	1	0
363	EC718409	0	0	0	1	0	0	1	0
364	EC718410	0	0	1	0	0	0	0	1
365	EC718411	0	0	0	1	0	0	1	0
366	EC718412	0	0	0	1	0	0	1	0
367	EC718413	0	0	1	0	0	0	0	1
368	EC718414	0	0	1	0	0	0	0	1
369	EC718416	0	0	0	1	0	0	1	0
370	EC718417	0	0	0	1	0	0	1	0
371	EC718418	0	0	1	0	0	0	0	1
372	EC718419	0	0	0	1	0	0	1	0
373	EC718420	0	1	0	0	0	1	0	0
374	EC718421	0	0	0	1	0	0	1	0
375	EC718422	0	0	0	1	0	0	1	0
376	EC718423	0	0	0	1	0	0	1	0
377	EC718424	0	0	0	1	0	0	1	0
378	EC718425	0	0	0	1	0	0	0	1
379	EC718426	0	0	0	1	0	0	1	0
380	EC718427	0	0	0	1	0	0	1	0
381	EC718428	0	0	1	0	0	0	0	1
382	EC718429	0	0	0	1	0	0	1	0
383	EC718430	0	0	0	1	0	0	1	0
384	EC718432	0	0	0	1	0	0	1	0



S. No.	Accessions	Pod shedding				Pod dehiscence			
		None	Low	Medium	High	None	Low	Medium	High
385	EC718433	0	0	0	1	0	0	1	0
386	EC718434	0	0	0	1	0	0	1	0
387	EC718435	0	1	0	0	0	1	0	0
388	EC718436	0	0	0	1	0	0	1	0
389	EC718437	0	0	0	1	0	0	1	0
390	EC718438	0	0	0	1	0	0	1	0
391	EC718439	0	1	0	0	0	1	0	0
392	EC718440	0	0	0	1	0	0	0	1
393	EC718441	0	0	0	1	0	0	1	0
394	EC718442	0	0	0	1	0	0	1	0
395	EC718448	0	0	0	1	0	0	0	1
396	EC718449	0	0	0	1	0	0	0	1
397	EC718648	0	1	0	0	0	1	0	0
398	EC718238	0	1	0	0	0	1	0	0
399	EC718252	0	0	0	1	0	0	0	1
400	EC718685	0	1	0	0	0	1	0	0
401	EC718686	0	1	0	0	0	1	0	0
402	EC718687	0	1	0	0	0	0	1	0
403	EC718688	0	1	0	0	0	0	1	0
404	EC718690	0	0	1	0	0	0	1	0
405	EC718692	0	0	1	0	0	0	1	0

## About the Authors

**Dr. Mohar Singh** has made an outstanding contribution in the management of plant genetic resources for food and agriculture in India. His research interest reflects a continuum of high quality basic and strategic research in pulses. He has developed 03 core sets, 02 reference sets, registered 08 genetic stocks, 25 gene sequences, 06 farmer varieties and collaborated in the development of 2 lentil varieties for lower rainfed areas of north-western Indian Himalaya. He had conducted 10 explorations on crop wild relatives (CWRs) and explored more than 900 wild germplasm of cereals, oilseeds and pulses. He has been instrumental to initiate pre-breeding in chickpea and lentil in India for securing national nutritional demand. His pioneer research work on understanding the population structure and diversity assessment of global wild species of lentil and chickpea is very well known. This has led to the identification of most target gene sources in the secondary and tertiary gene pool of chickpea and lentil for biofortification of cultivated varieties as several yield and major biotic and abiotic stress related traits were successfully incorporated in cultivated backgrounds of these two important pulse crops. Successful deployment of marker assisted breeding for introgression of two most promising superior haplotypes with high seed weight and pod number from cultivated and wild species into high yielding varieties of chickpea for improving their overall yield and productivity. Dr Singh has a distinguished record of high quality peer research publications viz.; *DNA Research, Plant Science, Frontiers in Plant Science, Frontiers in Genetics, Scientific Reports, PLOS ONE, Plant Breeding, Crop Science, Euphytica, Genetic Resources and Crop Evolution, Journal of Genetics, Biodiversity and Conservation, Journal of Experimental Biology, Plant Genetic Resources: Cambridge, Indian J. Genet and Indian J. Agri. Sci. etc.* He also holds three authored and eight edited books to his credit. Dr Singh is recipient of Harbhajan Singh Memorial and Dr B.R. Barwale Awards for his significant contributions in PGR management.



**Dr. Ashutosh Sarker**, a native of Bangladesh, acquired 41 years of research and academic experience in the field of food legume research. He obtained B.Sc. Ag. (Hons) and M.Sc. Ag. (Genetics & Plant Breeding) from Bangladesh Agricultural University, Mymensingh, Bangladesh; and Ph.D. in Genetics from the Indian Agricultural Research Institute, New Delhi, India. He started his research career as a pulse breeder at the Bangladesh Agricultural Research Institute in 1979, and joined ICARDA in 1996 as the Lentil Breeder. Since 2008, Dr Sarker is serving as ICARDA's Regional Coordinator of South Asia and China Program. Recently he is appointed as the Head of Food Legume Research Platform in India and associated with R & D of food legumes in the region. Dr Sarker is author of more than 200 scientific articles in reputed international journals, symposia proceedings, popular articles and book chapters. Dr Sarker has been directly involved in the development of more than 45 pulse varieties, majority of them in lentil which have made significant impact at farmers level across the globe. He is recipient of several national and international awards in recognition of his contribution to legume R & D. He is an active member of several professional bodies, and participated and contributed to more than 40 international symposia/conferences. Dr Sarker acts as research supervisor of MS/PhD students to develop new generation of scientists.



**Dr. Sandeep Kumar** earned his master and doctoral degrees in Biochemistry from Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana. He joined Indian Council of Agricultural Research (ICAR) as Scientist (Biochemistry) in 2007. Presently, he is working as Principal Scientist (Biochemistry) in Division of Germplasm Evaluation at ICAR-National Bureau of Plant Genetic Resources (ICAR-NBPGR), New Delhi. He has contributed in the development of two core sets and one reference set, and identification of trait-specific genetic stocks. He is involved in targeted/untargeted metabolite profiling of field crops, contributing towards quality improvement and identification of biomarkers for resistance to biotic and abiotic stresses. He has edited three books and contributed in more than 50 scientific publications including journals/publishers of national and international repute including *Environmental and Experimental Botany*, *Frontiers in Plant Science*, *Scientific Reports*, *PLoS ONE*, *Animal Feed science and Technology*, *Journal of American Oil Chemists Society*, *Crop Science*, *Genetic Resources and Crop Evolution*, *Arthropod-Plant Interactions* etc.



**Dr. Nikhil Malhotra** is a Molecular Biologist having more than eight years of experience on designing and performing experiments with the focus on genomics, transcriptomics and metabolomics of high-value plant species. With profound interest in agricultural sciences, he also has been working on OMICS-assisted promotion of pseudocereals to convalesce nutritional security. He has utilized comparative genomics, metabolic & nutritional profiling along with NGS analysis to provide first time insights into molecular aspects of secondary metabolites biosynthesis and nutritional assessment of plethora of NW Himalayan plant species. In a short research tenure, he has published more than 10 research articles in reputed international journals, namely, *Phytochemistry*, *Planta*, *Scientific Reports*, *Acta Physiologiae Plantarum*, *3Biotech*, *PLoS ONE*, *Molecular Biology Reports*, *Applied Biochemistry & Biotechnology* and *Plant Breeding*.



**Dr. Ashok Kumar** is presently working as Director (Acting) of ICAR-National Bureau of Plant Genetic Resources, New Delhi. He has long working experience of >35 years with various aspects of plant genetic resources management. Received M Phil/ Ph. D in Agricultural Botany (Genetics & Plant Breeding) and joined ARS as Scientist (Plant Breeding) at ICAR-NRRI (the then CRRI), Cuttack in 1986 and moved to ICAR-NBPGR in 1988. Visited USA for three months for Professional Enhancement Programme on Plant Genetic Resources under USAID Project. He was associated with the planning, monitoring and execution of NATP Sub-project “Sustainable Management of Bio-diversity” in Mission mode which was included under Prime Minister’s coveted “Jai Vigyan National Science and Technology Mission on Conservation of Agro-Biodiversity (PGR)”. Associated with the development of value rich genetic stocks, technologies and databases for utilization of genetic resources.



As Head, Division of Germplasm Evaluation, ICAR-NBPGR, he has planned, executed and coordinated the activities of germplasm evaluation at national level and established linkages with crop based institutes and state /central agricultural universities for characterization, evaluation and utilization of PGR. He has organized several Germplasm Field Days/ visits for enhanced utilization of germplasm in applied and basic research. He has also coordinated the activity of characterization and evaluation at national level through Consortium Research Platform (CRP) on Agro biodiversity of ICAR.

He has been associated with the identification of several trait specific germplasm and registered 35 trait specific accessions as unique genetic stocks with Plant Germplasm Registration Committee (PGRC) of ICAR. He has more than 150 publications comprising research papers published in national and international journals, book, book chapters, training manuals, invited lectures, extended summaries, abstracts etc. In addition, he has participated and presented papers in national and international seminars, symposia, conferences etc. He is member of several professional societies and has been recognized as Fellow of various professional societies.

**Dr. Shiv Kumar** holds a Ph.D. in Plant Breeding from the GB Pant University of Agriculture and Technology, Pantnagar, India. His area of expertise includes crop improvement through resistance breeding, widening the genetic base through pre-breeding, and development of genetic and genomic resources in food legumes. His contribution in identifying donors for new plant type in rice, extra early genotypes in chickpea, lentil, and mung bean, basic information on genetics of important traits, and pre-breeding populations in *Vigna*, *Lens* and *Lathyrus* species, are noteworthy.



During the 30 years of professional career, he in collaboration with national partners has contributed in development of 41 lentil, 5 mung bean, 2 urdbean, 1 rice, and 3 grass pea varieties and published 196 peer-reviewed journal articles, 72 book chapters, 9 books, 7 technical bulletins, and 2 training manuals. He is a Fellow of professional societies including International Legumes Society, Indian Society of Genetics and Plant Breeding, and Indian Society of Pulses Research and Development. Dr Kumar has received many academic distinctions, fellowships including Rockefeller, and awards from national and international organizations/societies in recognition of his contribution in food legumes. Presently, Dr. Kumar is leading ICARDA's Food legumes program which aims to deliver improved germplasm of lentil, kabuli chickpea, faba bean and grass pea to national partners in South Asia, Sub-Saharan Africa, West Asia, and North Africa. He works on developing short duration climate smart varieties of lentil and grass pea with high iron and zinc content for sustainable intensification of cereal based cropping systems.

**Dr. Kuldeep Singh** received his Master and Ph.D. degrees in Plant Breeding from Punjab Agricultural University Ludhiana and is recipient of Sardar Iqbal Singh Gold Medal. He did post-doc studies at IRRI, Philippines and worked at Punjab Agriculture University for nearly 25 years as Plant Breeder, Sr. Molecular Geneticist, Director School of Agricultural Biotechnology. He is elected Fellow of the National Academy of Agricultural Sciences. Has worked in the area of Genomics, Molecular Breeding and Wide Hybridization with the objective of creating diversity in crop gene base, developing biotic/



abiotic stress tolerant varieties, enhancing iron and zinc in grains. He has identified about a dozen new genes in rice and wheat which confer resistance to diseases, insects, nutritional and productivity traits. He was involved in developing three varieties of wheat and 11 of rice with Punjab Basmati 1 being the first MAS based semi-dwarf and bacterial blight resistant variety. He has more than 143 research publications, published in peer reviewed international journals such as *Science*, *Scientific Reports*, *PNAS*, *Genetics*, *Theor Appl Gene*, *PLoS ONE*, *Crop Science*, *Molecular Breeding*, *Euphytica*, *GRACE*, *Indian J Genet* etc. He guided 14 M.Sc. and 14 Ph.D. students and five of them were recipients of Monsanto Beachel - Borlaug International Scholarships. At ICAR-NBPGR, his major emphasis was on Focussed identification of germplasm and collection based on gap analysis especially of the crop wild relatives, trait identification and gene mapping and large-scale characterization and utilization of germplasm. Dr. Singh is recipient of SciGenom Research Foundation Excellence in Science award - 2018 and The Borlaug Global Rust Initiative Gene Stewardship Award - 2018.









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