Strengthening the impact of plant genetic resources through collaborative collection, conservation, characterization and evaluation: a tribute to the legacy of Dr Clive Francis

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Strengthening the impact of plant genetic resources through collaborative collection, conservation, characterization and evaluation: a tribute to the legacy of Dr. Clive Francis

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Abstract

This paper is a tribute to the legacy of Dr. Clive Francis who directly and indirectly collected > 14,000 accessions across 60 genera of pasture, forage and crop species and their wild relatives around the Mediterranean basin, Eastern Africa, Central and South Asia from 1973 to 2005. This was achieved by a collaborative approach that built strong interactions between disparate organizations (ICARDA, VIR, CLIMA and Australian genebanks) based on germplasm exchange, conservation and documentation, capacity building and joint collection. These activities greatly strengthened Australian pasture, forage and crop genebanks, and led to widespread germplasm utilization that has waned in the last 5 years, reflecting changing priorities among industry funding bodies and research providers. This situation must be reversed, given the pivotal role genetic resource collections must play to broaden the genetic and adaptive base of plant breeding, to meet the challenge of feeding an increasing population in a depleting resource base.

Because the use of germplasm subsets that facilitate phenotyping will stimulate wider utilization of genetic resources, we discuss the application of core collection and germplasm selection through habitat characterization/filtering in Australian collections. Both are valid entry points into large collections, but the latter has the advantage of enabling both trait discovery *and* investigation of plant adaptation, and because it is based on *a priori* hypothesis testing, increases understanding even when the trait of interest is not identified.

Keywords

Plant genetic resources, core collection, habitat characterization, FIGS

Introduction

From 1973 to 2005 Dr. Clive Francis collected > 8,600 accessions across 60 genera, and assisted in the collection of >5,450 additional accessions by helping to organize collection missions manned by colleagues throughout Australia and internationally (Table 1). While Clive's early collection activities were strongly focused on the Mediterranean rim (Fig. 1a), in time his missions expanded to the east and south, from Iraq in 1980, to Iran (1988, 95), Nepal (1996, 98), Ethiopia (1997), Kazakhstan (2002), Azerbaijan (2004) and finally Armenia (2004, 2005). With the exception of the genus *Lupinus* (Berger *et al.* 2013), Clive's early and abiding focus was on Mediterranean pasture legumes, particularly *Medicago* and *Trifolium* (Table 1, Fig. 2a). However, from the early 1990s onwards, Clive and colleagues also began to collect forage and grain legume crops, such as *Cicer, Lathyrus, Lens, Pisum* and *Vicia*, expanding to cereals, such as *Aegilops, Hordeum*, *Triticum* and *Zea*, and even under-utilized oilseeds such as *Guizotia abyssinica* in Nepal (Table 1, Fig. 1). This widespread interest in genetic resource collection was remarkable, both in terms of taxa that were collected, and the range of habitats and regions that were sampled. To honour this legacy this paper summarizes Dr. Francis' contribution to germplasm collection and utilization, emphasising how his collaborative approach built strong interaction between disparate organizations separated by borders and political systems. Unfortunately we also demonstrate a decline in these collaborations as a consequence of reduced funding for genetic resources. Finally, without ongoing utilization, plant genetic resource collections are fated to become static museum exhibits (Maxted *et al.* 1997), and therefore the bulk of this paper is focused on methodologies for data mining to increase the utilization of collections, be it for furthering our understanding of plant adaptation, or identifying useful traits.

Collaborative genetic resource collection and conservation

Dr. Francis' career in plant genetic resources was characterized by long-standing collaboration with a wide range of institutes with an interest in plant collection, as well as with the local agricultural research community in those countries in which the genetic resources were found (Table 2). Perhaps Dr. Francis' most significant contribution to fostering collaboration among the genetic resources community was his interaction with the N. I. Vavilov Institute (VIR) in St. Petersburg, Russia from the early 1990s onwards (Table 2). On a visit to VIR shortly after the dismantling of the former USSR, Dr. Francis and Dr. Rade Matic (vetch breeder, SARDI) became aware of how a funding crisis was placing the collection at risk, as stored germplasm was losing viability, while seed regeneration facilities in the Central Asia - Caucasus region (CAC) were lost. Discussions were opened between the Centre of Legumes in Mediterranean Agriculture (CLIMA) and

VIR as to how this parlous situation could be resolved. These were soon expanded to include the International Centre for Agricultural Research in the Dry Areas (ICARDA) in Aleppo, Syria, where seed regeneration was feasible for cereal and legume germplasm. Recognizing the value of this germplasm, the Grains Research and Development Corporation (GRDC, Australia) funded a short term project (1997-99) to regenerate seed at ICARDA, start evaluation of the material and replenish the reserves at VIR. These activities were subsequently expanded to include genebanks in Australia (Australian Winter Wheat Collection (AWWC) Tamworth and Australian Temperate Field Crops Collection (ATFCC) Horsham) and Germany (IPK Gatersleben (Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung)), as well as a wide range of regional institutes in Central Asia, the western and eastern Mediterranean (Table 2). This facilitated international germplasm exchange for safety duplication and evaluation, prompting greater interaction among the genetic resources community through reciprocal visits, capacity building (training, sabbaticals, PhD scholarships) and joint collection missions. Leveraging this activity, the Crawford Fund provided scholarships for staff from VIR (Alexandrova *et al.* 2000) and the Institut National de la Recherche Agronomique (INRA), Morocco (Bennett *et al.* 1998) amongst others. Moreover, emphasis was given to passport data retrieval to increase the value of the germplasm, as outlined in the subsequent section on data mining. For example, records at VIR comprise hand written field books of collecting missions dating back to the 1920s, and include agricultural surveys, local crop management practices, end-uses, and evaluation data, reflecting the holistic approach to collecting and recording landrace data initiated by N.I. Vavilov. Through the joint projects, these data were (and continue to be) digitised and GPS coordinates assigned from reconstructed maps of collecting missions – often problematic given changes over time in place names, administrative boundaries and access roads. As a result of the VIR-ICARDA-Australian collaboration the breadth of germplasm in the ATFCC and AWWC has been substantially increased (e.g. field pea, n=1556; chickpea, n=1194; lentil, n=420; faba bean, n=365), and now whole landrace collections in different crops are being screened for herbicide and disease resistances.

These international linkages, established in the late 1990s, led to further collaboration in the Mediterranean basin (funded by GRDC), Caucasus and Central Asia (funded by the Australian Centre for International Agricultural Research (ACIAR)) until 2006 and 2011, respectively (Table 2). The Mediterranean collections included annual pasture legumes from short season and low latitude regions in the Canary Islands, Morocco, south-east Spain, Israel (Snowball *et al.* 2008), Eritrea (Snowball *et al.* 2012), Turkey, Greece and the Cyclades islands (Folegandros, Sikinos, Ios, Naxos and Milos); *Melilotus siculus* and other salt tolerant species from Andalusia and Valencia (Nichols *et al.* 2010). Subsequently perennial pasture legumes were also targeted, including *Lotus* from Cape

Verde, Canary Islands and Azores (Sandral *et al.* 2006); and drought tolerant *Bituminaria bituminosa* var. *albomarginata* (Albo Tedera) from the Canary Islands. This most recent interest in Tedera was largely initiated as a result of the long standing relationship between Dr Francis and the Spanish pasture legume specialist, Enrique Correal Castellanos, who forged a close friendship from the early 1970s onwards. These activities stimulated wider pasture collection outside of the Mediterranean basin, such as drought tolerant perennial *Lessertia, Lebeckia and Lotononis* from South Africa and *Syrmatium glabrum* from southern California. The Central Asian linkages were pivotal in the search for germplasm which could reduce recharge and manage discharge for the control of dryland salinity in southern Australia (Dear and Ewing 2008; Hughes *et al.* 2008). The Central Asian-Caucasian collections included Armenia, Azerbaijan, Kazakhstan and Turkmenistan. Target species included lucerne (*Medicago sativa* subsp. *sativa*) and its wild relatives (Auricht *et al.* 2010) and *Trifolium tumens* (Hall *et al.* 2013). The Asian interests extended as far as the subcontinent. As a result of associations developed in joint projects with the Nepal Agricultural Research Council (Table 2), collections of the underutilised crop *G. abyssinica* were undertaken (Clements *et al.* 2002), leading to the selection and release of a cultivar in Nepal. Indeed, Table 3 lists a wide range of pasture, forage and crop cultivars aimed at different soil types, pH and rainfall ranges in southern Australia, that were developed as a result of the genetic resource activities of Dr. Francis and colleagues.

Nevertheless, from the mid 2000s plant genetic resource activities began to decline due to changing priorities among industry funding bodies and research providers. Target regions moved away from Mediterranean climate areas to the Pacific-Rim, while the advent of the requirement of a Memorandum of Understanding (MoU) and Mutual Transfer Agreement (MTA) prior to plant collecting overseas increased the recognition of the value of plant genetic resources in less developed countries. This was one of the aims of the agreements, and rightly so, but in some cases increased costs levied by host countries to prohibitive levels, and therefore plant collection ceased. Within Australia the Australian Quarantine Inspection Service (AQIS) changed the importation procedure. Prior to 1999 species not included on a prohibited list could be imported to Australia with relatively little quarantine requirements. Subsequently, only those species on a permitted list could easily be imported. This was an important change for AQIS as it substantially reduced the potential for the introduction of noxious weeds into Australia, but further increased the cost of funding collection (Bennett and Virtue 2004), particularly where new species were collected, as all material must now be screened in PC2 glasshouses prior to release for evaluation. In many cases, species of agricultural potential not on the new permitted species list were prohibited, or their introduction seriously delayed while submissions were made to have the list amended. Others failed the weed risk assessment and remain prohibited today.

Thus, the relative decline in Table 2 is reflected across the plant genetic resource community as a whole, and typified by the situation in the Australian temperate and tropical pasture genebanks (Australian *Medicago* Genetic Resource Centre, Adelaide; the Australian *Trifolium* Genetic Resource Centre, Perth; and the Australian Tropical Crops and Pasture Collection, Biloela) and lupin collections (Australian Lupin Collection, Perth) in particular. Since 2008 there has been no external funding for these genetic resource centres, which have struggled to meet their obligations to maintain, let alone exchange material. In some species the costs associated with the importation of germplasm into Australia are now being borne by individual researcher's projects (e.g. *Lupinus* other than *L. angustifolius*). This is a disincentive to widen the Australian Lupin Collection, and particularly untimely (Berger *et al.* 2013), given that the industry is based on very limited genetic diversity which is constraining adaptation and yield potential (Berger *et al.* 2012a; Berger *et al.* 2012b). (However, it should be noted that GRDC are underwriting the quarantine import program at ATFCC Horsham for pulse germplasm, and at the winter cereals collection in Tamworth for wheat and barley germplasm). Reluctantly the Australian *Medicago* GRC has been forced to charge end-users to access germplasm, which they recognize is unlikely to stimulate germplasm utilization. Indeed, in the last decade there has been a dramatic decline in germplasm evaluation compared to the peak dispatch numbers in the mid 1990s and 2000s (Fig. 2b). Sadly it appears that due to a lack of resources to perform fundamental conservation and utilisation work; including documentation, seed viability testing, regeneration and seed distribution, the Australian collections *are* at risk of becoming static museum exhibits (Maxted *et al.* 1997). This is a poor use of a valuable asset, as the subsequent section on stimulating germplasm use through appropriate data mining methodologies will attest. It is to be hoped that the ongoing negotiations for a viable cost sharing model to fund an Australian Pasture and Forage Genebank between funding bodies, state and federal research providers are completed before valuable germplasm and the capacity to properly evaluate it is lost. The recent decision to establish the Australian Grains Genebank at Horsham for all field crops, both temperate and tropical, gives some hope for future operational funding for germplasm phenotyping and genotyping projects in partnership with breeders and research institutions. Such steps, including conservation of wild relatives, are a necessity for the targeted and informed exploitation of genetic resources in crop improvement.

Mining germplasm collections

It is in their utilization that genetic resource collections become valuable; a static collection that is used neither for plant improvement, nor to enhance our understanding of adaptation and evolution, consumes resources and has little intrinsic value. As collections grow ever larger there is an increasing risk that much of the material remains filed away inside genebanks, playing no role in plant improvement or scientific research. Typically the problem is one of scale. Improvements in experimental design and analysis notwithstanding, it is often infeasible and potentially meaningless to screen 1000s of accessions because of the difficulties of comparing traits over time (e.g. when different accessions are evaluated over years) or space (e.g. when trials become very large, with correspondingly increasing extraneous variation). In this context, the evaluation of smaller germplasm subsets likely to contain the trait of interest is an attractive alternative. A common approach to this problem is the evaluation of core collections that capture a high proportion of total collection diversity, ideally >70% according to Brown (1989) in a subset of samples (often 10 to 20% of the full collection) filtered by different criteria which increasingly include molecular data. The underlying assumption here is that variation in the trait of interest is related to diversity *per se*, even though there may not be a direct marker-trait link, especially for complex traits. This approach has gained traction with the increasing genomic characterization of plant genetic resources, and has been applied to a wide range of grain legumes (see references in Upadhyaya et al. (2011)). Indeed, in collections which are particularly large these authors advocate the use of mini-cores that subsample the primary core (Upadhyaya *et al.* 2011; Upadhyaya and Ortiz 2001).

Core collections based on ecogeographic, plant morphological and molecular data have been developed for *Lupinus* spp (*L. angustifolius, L. albus, L. luteus*), Chinese pea landraces (Zong *et al.* 2009), *Trifolium subterraneum* (Ghamkhar *et al.* 2010), *T. spumosum* (Ghamkhar *et al.* 2008), annual *Medicago* (Ellwood *et al.* 2006a; Skinner *et al.* 1999) and *Biserrula pelecinus* (Ghamkhar *et al.* 2012). In each case a maximisation strategy (Gouesnard *et al.* 2001) was employed to determine the ideal size of each core and select multiple cores or iterations that were used to arrive at a final core of lines or phenotypes. In the case of *T. subterraneum* the first subset of accessions was selected using collecting site data, the second subset of phenotypes was selected using plant agro-morphological characters, and the final core collection of phenotypes was selected using plant molecular data from SSR markers. From the whole collection of 7,800 phenotypes (originating from 2,870 collecting sites) a core collection of 97 phenotypes was developed. Currently it is being screened for methane production in sheep, soil phosphorus response, and acid soil tolerance at the University of Western Australia. The development of annual *Medicago* cores has been instrumental in the identification of discreet genotypes with disease and insect resistant traits (Ballard *et al.* 2012; Ellwood *et al.* 2006b; Kamphuis *et al.* 2012) and the continued use of *M. truncatula* as the pre-eminent model species for legume genetics research (Nair *et al.* 2006). The continued use of molecular studies in phenotyping is providing a successful model for future work in the development of core collections. Finally, the lupin core collection has been used to identify genetic variation and phenotypic plasticity for a range of root traits in *L. angustifolius* (Chen *et al.* 2011).

Core collections based on genetic diversity offer an easy entry point for germplasm screening. Once individual phenotypes have been identified with the trait of interest, closely related accessions can then be identified in the phylogenetic tree or dendrogram, and then evaluated. If by chance there is an association between the diversity data and the trait of interest, then there is an enhanced likelihood of recovering the trait of interest in this new germplasm subset. However, given that in general the relationship between any trait of interest and the diversity data is unknown, there is an implicit assumption that 'diversity cores' can usefully be screened for an infinite number of traits of interest; which seems to be supported by the *Medicago* experience outlined above, but may or may not be correct. The disadvantage of the core approach is that it does not encourage hypothesis testing while screening germplasm, and therefore does little to further our understanding of plant biology.

An alternative to the core collection approach is to filter germplasm by variables in the passport data, a methodology commonly referred to as FIGS (focused identification of germplasm subsets) in the bread wheat literature (Mackay *et al.* 2007; Street *et al.* 2008). The underlying assumption here is that plant populations evolve into locally-adapted ecotypes in response to environmental selection pressures across their habitat range (Allard 1988). By characterizing collection site habitats, local selection pressures can be described, and used to select germplasm subsets that evolved under contrasting selection, assuming that the habitat at the point of collection is responsible for the evolution of the population. (Note that habitat can be defined widely, including both the biophysical environment as well as human selection pressure imposed by the demands of the farming system, market or end users). The advantage of this approach over the core selection method is that it facilitates hypothesis testing of population responses to local selection pressures, and therefore increases understanding of adaptation even when the trait of interest is not found.

The FIGS approach has been used in bread wheat (Mackay *et al.* 2007; Street *et al.* 2008), chickpea (Berger 2007; Berger and Turner 2007), field pea (Ling *et al.* 2013), *C. judaicum* (Ben-David *et al.* 2010), and lupin collections (Berger *et al.* 2008a; Berger *et al.* 2008b). It is most effective in high quality collections-in which accessions were indeed collected where the passport data suggests, and where habitats have been well characterized. Our capacity to do this has been greatly improved by the advent of user-friendly, freely-available GIS software and high resolution descriptive data surfaces (Hijmans *et al.* 2005; Hijmans *et al.* 2001; New *et al.* 2002) that can be linked to collection site coordinates. Upadhyaya et al. (2011) outline a methodology for habitat characterization and germplasm selection using a procedure to:

1. Geo-reference collection sites.
2. Extract site-specific climate data by site coordinates.
3. Define seasonal rules to calculate crop and site-specific bioclimatic variables.
4. Characterize habitats holistically using multivariate techniques to facilitate the selection of germplasm subsets from contrasting habitats that highlight the stress of interest.

The above methodology largely captures climate-based selection pressures, and is therefore particularly apt for the annual lifecycle in which phenology balances stress avoidance against yield potential. This is critical to plant improvement, where yield is often the highest priority criterion. Characterization of Mediterranean habitats (*Lupinus* spp, chickpea and wild relatives) typically reveal terminal drought gradients between cool, sometimes frost-prone, higher elevation/rainfall sites and higher temperature, low rainfall sites with little precipitation and rapidly rising temperatures in the reproductive phase (Ben-David *et al.* 2010; Berger *et al.* 2008a; Berger *et al.* 2008b; Berger and Turner 2007). To a large extent these trends are also expressed in Chinese pea collection sites (Ling *et al.* 2013). While winter- and spring-sowing regions in central-southern and northern China respectively, were clearly separated by vegetative phase rainfall and frost incidence, both contained the aforementioned terminal drought contrast: reproductive frost-prone high altitude versus high minimum and maximum temperature, low elevation sites (Ling *et al.* 2013).

Thus in Mediterranean climates and beyond, winter cold and spring/summer terminal drought are the twin climatic stresses that are negotiated by plants using appropriate phenology. Terminal drought prone habitats select for early flowering and short lifecycles as a drought escape mechanism, limiting biomass production and yield potential. Conversely, cool, high rainfall habitats select for delayed phenology to minimize exposure of the sensitive reproductive phase to low temperature stress, also facilitating increased biomass production, supporting a higher reproductive effort. These trends have been reported widely in both wild and domesticated Mediterranean annuals (Ehrman and Cocks 1996), including grasses (Volis 2007), crucifers (Petrů *et al.* 2006), yellow lupin (*Lupinus luteus* L.) (Berger *et al.* 2008a), narrow-leafed lupin (Clements and Cowling 1994), annual *Trifolium* from Sardinia (Bennett and Galwey 2002) and Turkey (Bennett 2000),*T. glomeratum* L. (Bennett 1997), *T. subterraneum* L. (Piano *et al.* 1996), *T. tomentosum* (Bennett 1999), *Cicer judaicum* Boiss (Ben-David *et al.* 2010) and chickpea (*C. arietinum* L.) (Berger *et al.* 2006; Berger *et al.* 2004).

The latter species is a particularly good example of the application of FIGS to highlight the role of different habitats in selecting for appropriate phenology through different mechanisms. Chickpea is extremely sensitive to chilling stress at the reproductive phase, delaying pod set significantly in temperatures as high as 18°C (Berger *et al.* 2012c). A comparison of chilling tolerance of germplasm sourced from contrasting reproductive temperature habitats revealed very limited, albeit statistically significant differences (Berger *et al.* 2012c), suggesting that the principal strategy in chickpea is stress escape. Indeed, photothermal modelling of diverse FIGS–characterized germplasm demonstrates that temperature responsiveness of flowering is strongly correlated to collection site vegetative phase temperature (r = 0.8) (Berger *et al.* 2011). Accordingly, temperature responses increase from winter- to spring-sown Mediterranean and Australian material, and then to north, central and southern India. This prevents Mediterranean chickpea from flowering too early, and being exposed to deleteriously low temperatures, and facilitates increasing drought escape as temperatures increase with decreasing latitude in South Asia. Moreover, by combining temperature and photoperiod response in a strong negative relationship (r = -0.8), Eastern Mediterranean chickpea eliminates the inherent risk of flowering too late as a result of low temperature responsiveness (Berger *et al.* 2011).

In lupin the FIGS approach has been used to further evaluate adaptive strategies to contrasting Mediterranean climates (Berger and Ludwig 2013a; Berger and Ludwig 2013b). As implied above, long-season, high rainfall habitats selected strongly for competitive traits. Thus, delayed phenology facilitated high biomass production, manifested both above- and below-ground, and in high leaf area. These traits led to greater productivity and fecundity, but also higher water-use, and the earlier onset of stress compared to lupins from terminal drought-prone environments, characterized by ruderal traits that facilitate drought escape/avoidance but limit reproductive potential. Interestingly, in yellow lupin, high rainfall habitats appear to have selected for drought tolerance, as these ecotypes reaches a lower critical leaf water potential, maintaining higher relative leaf water content (RWC) than their lower rainfall counterparts (Berger and Ludwig 2013a). While this at first seems contradictory, this tolerance capacity may have evolved in response to intermittent self-imposed droughts driven by the large biomass/water-use of high rainfall ecotypes. Given that lupins are predominantly found in sandy soils with little water holding capacity, this drought tolerance strategy of high rainfall ecotypes may be an important 'insurance policy' to facilitate a competitive, resource acquisitive growth habit. By contrast, in Tunisian *Medicago truncatula* and *M. laciniata* populations, osmotic adjustment and maintenance of elevated RWC under terminal drought was higher in low, rather than high rainfall ecotypes (Yousfi *et al.* 2010). Because of the lack of physiological studies of ecotypic responses to drought stress using germplasm collected along rainfall gradients, at the present time it is difficult to interpret this apparent contradiction.

In field pea the FIGS approach has provided a short list of accessions from contrasting environments which are currently being screened by the Waite Agricultural Research Institute (University of Adelaide) for field responses to frost stress in the Adelaide hills, to be followed by growth chamber tests for heat tolerance and by the Qingdao Academy of Agricultural Sciences, Shandong Province, China for cold and frost tolerance. Given the contrasting nature of these stresses in both the Chinese winter and spring-sown regions, this approach will deliver good insight into adaptive strategies in pea, and hopefully identify useful germplasm.

The previous examples are illustrations of plant populations responding directly to climatic selection pressure. However, climate can also indirectly impose selection pressure on plant populations by influencing the incidence of pests and diseases. This approach has been used in bread wheat to identify resistance to Sunn pest (*Eurygaster integriceps* Puton) (El Bouhssini *et al.* 2011; El Bouhssini *et al.* 2009), Russian wheat aphid (*Diuraphis noxia* Kurd) (Street *et al.* 2008), powdery mildew (*Blumeria graminis* f. sp. Tritici D. C. Speer) (Bhullar *et al.* 2009), and stem rust (*Puccinia graminis* f. sp. *tritici*) (Bari *et al.* 2012; Endresen *et al.* 2012). Germplasm collections were filtered by country, latitude, agro-climatic zone, altitude, annual rain and winter temperatures (Street *et al.* 2008). As a result, the size of the screening subsets were reduced to manageable proportions (n~500), returning 10-12 resistant genotypes of Sunn pest and Russian wheat aphid, respectively, a vast improvement on previous efforts where random screening of >2000 genotypes did not uncover a single source of resistance (Street *et al.* 2008). In powdery mildew, a reverse engineering approach was used to define the habitat characteristics of 400 known resistant genotypes in the USDA-ARS National Small-Grains Collection, and this information used as a multivariate filter to select 1,320 landraces from a total of 17,000 (Kaur *et al.* 2008), identifying new sources of resistance leading to the isolation of 7 new resistance alleles (Bhullar *et al.* 2009).

Conclusions and future priorities

We preface these conclusions with the observation that to feed the projected population of ~9 billion by the year 2050, global food supply will need to double (Parry and Hawkesford 2010), in a diminishing resource base that is under threat due to land degradation, peak P and N supply, reduced agricultural investment and climate change. Furthermore, productivity gains in crop yields – positively correlated to research and development investment, have been declining over the last 30 years (Beintema and Elliott 2009; Fischer *et al.* 2009). There is therefore an urgent need to increase food production per unit land area and per unit input, which will require the development of better adapted, higher yielding, more resource efficient crop and pasture cultivars. To this end, the effective utilization of plant genetic resources is essential to break current bottlenecks in plant improvement.

The career of Dr. Clive Francis is testament to the value of international collaboration in strengthening the impact of plant genetic resources. Collection, conservation and utilization all proceed more effectively in an engaging, collaborative environment, where ideas and technology are actively exchanged. It is in this context that securing long term funding for ongoing Australian plant genetic resource collection, conservation and evaluation activities is a top priority. These activities should include characterization of both habitats and germplasm in new and existing collections to facilitate the formation of germplasm subsets that are amenable to evaluation. Moreover, this is essential information for the identification of gaps *and* redundancy in existing collections, to maximize the efficient use of scarce financial resources.

Large collections become more accessible when smaller germplasm subsets are generated to facilitate evaluation. Core formation and FIGS characterization are both valid approaches to this end. The use of cores has facilitated screening for biotic and abiotic stress resistance, and other traits of interest in a range of species, and is an excellent entry into collections when there is no *a priori* reason for comparing specific genotypes or groups of genotypes. The downside with this approach is that in the absence of an *a priori* hypothesis, there is nothing to be learnt, and nothing to be gained if the trait of interest is not identified in the core. FIGS characterization has been invaluable in the investigation of plant adaptation *and* trait discovery, and because it is based on *a priori* hypothesis testing, has the advantage of increasing understanding even when the trait of interest is not identified. In this context, ecophysiological studies of plant populations from contrasting environments that highlight selection pressures that are likely to become increasingly important in future climates (e.g. terminal drought, high temperature, winter frost (Giannakopoulos *et al.* 2009; Turner *et al.* 2011)) are an important priority. This approach will inform our capacity to meet future climate challenges by adapting crops and pastures appropriately, and is heavily reliant on the use of germplasm from well described environments. Our review demonstrates that the approach has been applied more to Australian crop, rather than pasture collections, when in fact it could be argued that the latter represent a better resource for ecophysiology on the basis of their much more comprehensive collection (Fig. 1). Habitat characterization will improve as higher resolution datasets become increasingly available, but it may be more important to validate existing collections to ensure that material really was collected where the passport data indicates.

Finally, the genetic and adaptive diversity that resides in genetic resource collections must be used to broaden the genetic and adaptive base of plant breeding programs. This will require a good understanding of marker- (and ultimately gene-) trait relationships in order to retain traits of interest in the breeding program, as outlined in the companion chapter on genetic resources in lupin improvement (Berger *et al.* 2013). This methodology can then be reapplied to genetic resource collections to further our understanding of plant responses to selection pressure by quantifying marker or gene frequencies in populations from contrasting environments.

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Table headings

Table 1: Germplasm collected directly by Dr. Clive Francis and indirectly by colleagues in missions arranged with Clive's assistance, categorized by genus (bold) and species.

Comment [ber181 1]: To the editor. We realize that this is a massive table that may be difficult to include in the hard copy of the published paper. It's a reflection of Clive's widespread collection activities over the years. If necessary the table could be truncated in the print version to only list the genera Clive collected.

Table 2: Dr. Clive Francis' interests in plant genetic resource collection, conservation and evaluation; summarized by project title, international and regional collaborators.

Table 3: Pasture, forage and crop cultivar releases flowing from the genetic resource activities of Dr. Francis and colleagues.

Fig headings

Fig. 1: Genetic resource collection focus of Dr. Clive Francis and colleagues from 1973-2005: collection sites of major genera (accession n>60).

Fig. 2: The rise and fall of plant genetic resources activity. (A) Dr. Clive Francis' annual collection effort categorized by plant use; (B) germplasm dispatch of Dr. Francis' material by the Australian *Medicago* Genetic Resource Collection.

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Table 1: Germplasm collected directly by Dr. Clive Francis and indirectly by colleagues in missions arranged with Clive's assistance, categorized by genus (bold) and species.

Comment [ber181 1]: To the editor. We realize that this is a massive table that may be difficult to include in the hard copy of the published paper. It's a reflection of Clive's widespread collection activities over the years. If necessary the table could be truncated in the print version to only list the genera Clive collected.

Genus & species	Direct	Indirect	Total
Aegilops	**61**		**61**
biuncialis	1		1
cylindrica	19		19
geniculata	1		1
neglecta	4		4
sp.	7		7
tauschii	16		16
triuncialis	13		13
Agropyron		**2**	**2**
sp.		2	2
Agrostis		**19**	**19**
capillaris		1	1
rubra		1	1
sp.		16	16
tenius		1	1
Allium	**4**		**4**
sp.	4		4
Anethum	**7**		**7**
graveolens	6		6
sp.	1		1
Anthyllis	**4**	**6**	**10**
sp.		2	2
tetraphylla	1		1
vulneraria	3	4	7
Apium	**6**		**6**
graveolens	6		6
Astragalus	**24**	**62**	**86**
asterias	1		1
boeticus	4		4
corrugatus	1		1
falcatus	1		1
glycyphyllos	1		1
goktschaicus	2		2
hamosus	11	38	49
lydius		1	1
pelecinus		1	1
sevangensis	3		3
sp.		21	21
vulnerariae		1	1
Avena	**6**		**6**
fatua	6		6
Beta	**11**		**11**
vulgaris	11		11
Biserrula	**17**	**79**	**96**
pelecinus	17	79	96
Bituminaria		**3**	**3**

bituminosa		3	3
Brassica	**4**		**4**
oleracea	4		4
Bromus		**3**	**3**
hordeaceus		1	1
sp.		2	2
Cajanus	**24**		**24**
cajan	24		24
Calamagrostis		**2**	**2**
sp.		2	2
Capsicum	**5**		**5**
sp.	5		5
Carthamus	**1**		**1**
tinctorius	1		1
Chelidonium	**1**		**1**
majus	1		1
Cicer	**165**	**19**	**184**
anatolicum	1		1
arietinum	164	18	182
sp.		1	1
Citrullus	**2**		**2**
vulgaris	2		2
Colutea		**2**	**2**
sp.		2	2
Coriandrum	**6**		**6**
sativum	6		6
Coronilla	**7**	**34**	**41**
orientalis		1	1
scorpioides	4	6	10
sp.	1	16	17
varia	2	11	13
Cucumis	**12**		**12**
melo	2		2
sativus	10		10
Cucurbita	**12**		**12**
pepo	12		12
Dactylis	**1**	**18**	**19**
glomerata		18	18
sp.	1		1
Daucus	**2**		**2**
carota	2		2
Dolichos	**7**		**7**
biflorus	7		7
Dorycnium		**4**	**4**
graecum		1	1
hirsutum		2	2
pentaphyllum		1	1
Galega		**3**	**3**
officinalis		3	3
Glycine	**1**		**1**
max	1		1

Glycyrrhiza		**1**	**1**
sp.		1	1
Guizotia		**84**	**84**
abyssinica		84	84
Hedysarum		**4**	**4**
sp.		4	4
Hibiscus	**1**		**1**
esculentus	1		1
Hippocrepis	**9**	**20**	**29**
bisiliqua	2		2
ciliata		1	1
emerus		1	1
multisiliquosa	3	1	4
sp.		7	7
unisiliquosa	4	10	14
Holcus		**2**	**2**
lanatus		2	2
Hordeum	**29**		**29**
bulbosum	4		4
vulgare	25		25
Hymenocarpus	**7**	**70**	**77**
circinnatus	7	70	77
Lathyrus	**332**	**194**	**526**
angulatus	1		1
annus	15	17	32
aphaca	21	39	60
articulatus	69		69
belinensis		1	1
blepharicarpus		2	2
cassius	2		2
chloranthus	3		3
cicera	38	25	63
clymenum	3		3
digitatus		6	6
gorgoni	1	1	2
hierosolymitanus		21	21
hirsutus	7	2	9
inconspicuus	5	3	8
incurvus	1		1
laxiflorus	3	14	17
marmoratus		3	3
nissolia	6	9	15
ochrus	11	1	12
pratensis	2		2
rotundifolius	5		5
sativus	117		117
saxatilis	1		1
setifolius	5	3	8
sp.	5	34	39
sphaericus	7	8	15
stenophyllus		1	1

tingitanus	4		4
undulatus		4	4
Lens	**126**	**42**	**168**
culinaris	117	32	149
ervoides	8	4	12
orientalis		5	5
sp.	1	1	2
Lepidium	**4**		**4**
sp.	4		4
Leucaena	**2**		**2**
leucocephala	2		2
Linum	**2**		**2**
usitatissimum	2		2
Lolium		**37**	**37**
loliaceum		5	5
multiflorum		2	2
perenne		21	21
rigidum		4	4
sp.		5	5
Lotus	**24**	**98**	**122**
angustissimus		1	1
arenarius	3		3
corniculatus	14	33	47
creticus	5		5
edulis	1	10	11
glaber		4	4
halophilus		2	2
ornithopodioides		28	28
parviflorus		10	10
schoelleri	1		1
sp.		10	10
Lupinus	**267**	**75**	**342**
albus	154		154
angustifolius	57	48	105
atlanticus	7		7
cosentinii	11		11
luteus	8		8
micranthus	5	7	12
pilosus	24	9	33
sp.	1	11	12
Lycopersicon	**2**		**2**
sp.	2		2
Medicago	**3469**	**681**	**4150**
aculeata	3		3
arabica	71	35	106
arborea		2	2
astroites	2		2
blancheana	11		11
ciliaris	17		17
constricta	38	2	40
coronata	1	16	17

disciformis	17	24	41
doliata	153		153
granadensis	8		8
intertexta	17		17
italica	85		85
laciniata	69		69
littoralis	222	6	228
lupulina	5	52	57
marina		1	1
minima	92	72	164
monantha	1		1
monspeliaca		4	4
murex	206	24	230
noeana	13		13
orbicularis	162	117	279
polymorpha	1071	128	1199
praecox	24	4	28
radiata	15		15
rigidula	309	62	371
rotata	26		26
rugosa	15	1	16
sativa	14	37	51
scutellata	13	7	20
sp.	10	35	45
syriaca	16		16
tenoreana	2		2
tornata	4		4
truncatula	722	37	759
turbinata	35	15	50
Melilotus	**11**	**6**	**17**
albus		1	1
elegans	1	2	3
indicus	7	1	8
officinalis	3		3
sp.		1	1
spicatus		1	1
Ocimum	**2**		**2**
basilicum	2		2
Onobrychis	**12**	**36**	**48**
aequidentata	1		1
amoena		9	9
armena		5	5
bungei	4		4
caput-galli		9	9
crista-galli		1	1
michauxii	1		1
radiata	3		3
sp.	3	8	11
viciifolia		4	4
Ononis		**1**	**1**
sp.		1	1

Ornithopus	**123**	**105**	**228**
compressus	112	89	201
isthmocarpus	7		7
pinnatus	4	16	20
Petroselinum	**3**		**3**
sativum	3		3
Phalaris	**3**		**3**
aquatica	2		2
sp.	1		1
Phaseolus	**75**	**47**	**122**
coccineus	4		4
sp.	1		1
vulgaris	70	47	117
Phleum		**4**	**4**
pratense		4	4
Phsorolea		**1**	**1**
sp.		1	1
Pisum	**233**	**67**	**300**
arvense	4		4
sativum	228	62	290
sp.	1	5	6
Plantago		**20**	**20**
lanceolata		19	19
rubra		1	1
Poa		**7**	**7**
pratensis		5	5
sp.		2	2
Polypogon		**1**	**1**
monspeliensis		1	1
Psoralea	**1**		**1**
sp.	1		1
Puccinellia		**1**	**1**
ciliata		1	1
Raphanus	**5**		**5**
sativus	5		5
Rumex	**1**		**1**
crispus	1		1
Sanguisorba		**13**	**13**
minor		13	13
Satureja	**1**		**1**
hortensis	1		1
Scorpiurus	**16**	**28**	**44**
muricatus	13	27	40
sp.		1	1
vermiculatus	3		3
Secale	**1**	**1**	**2**
cereale	1		1
sp.		1	1
Securigera	**1**	**11**	**12**
cretica		2	2
securidaca	1	9	10

Solanum	**1**		**1**
tuberosum	1		1
Tetragonolobus	**1**		**1**
palaestinus	1		1
Torilis		**1**	**1**
nodosa		1	1
Trifolium	**2293**	**2721**	**5014**
affine		1	1
aintabense	85		85
alexandrinum	7		7
alpestre	4	36	40
ambiguum	14		14
angustifolium	100	121	221
apertum		8	8
argutum	7	45	52
arvense	2	75	77
batmanicum	28	6	34
billardierei		1	1
boissieri	6	16	22
brutium	2	2	4
campestre	8	58	66
canescens	1		1
caudatum		1	1
cernuum	5	2	7
cherleri	213	135	348
clusii	3	1	4
clypeatum	4	41	45
constantinopolitanum	4	3	7
dasyurum	5	6	11
diffusum	2	26	28
dubium		14	14
echinatum	50	115	165
eriosphaerum		1	1
fragiferum	45	70	115
glanduliferum	1	25	26
globosum	4	45	49
glomeratum	35	50	85
grandiflorum	10	35	45
haussknechtii	1		1
hirtum	54	135	189
hybridum	6	30	36
isthmocarpum	27		27
lappaceum	60	115	175
leucanthum	4	11	15
ligusticum	2		2
medium	1		1
michelianum	17	36	53
nigrescens	64	162	226
obscurum	2		2
pallescens		2	2
pallidum	30	49	79

pannonicum		8	8
patens		5	5
pauciflorum	18	2	20
phleoides		3	3
physodes	21	13	34
pilulare	42	26	68
plebeium		1	1
pratense	12	59	71
purpureum	112	107	219
repens	12	98	110
resupinatum	146	108	254
retusum	1	20	21
scabrum	7	103	110
scutatum	25	7	32
setiferum		1	1
sp.	11	163	174
spadiceum	2		2
speciosum		1	1
spumosum	51	198	249
squamosum	2	1	3
squarrosum		2	2
stellatum	23	43	66
striatum	2	9	11
subterraneum	845	93	938
suffocatum	2		2
sylvaticum	1	19	20
tomentosum	34	146	180
trichocephalum	1		1
tumens	9		9
uniflorum		4	4
velivolum		1	1
vesiculosum	1	1	2
Trigonella	**28**	**102**	**130**
balansae		45	45
corniculata		1	1
fischeriana		5	5
foenum-graecum	16		16
gladiata		2	2
monspeliaca	1	10	11
sp.	3	28	31
spicata	8	11	19
Tripodion		**4**	**4**
tetraphyllum		4	4
Triticum	**104**		**104**
aestivum	88		88
monococcum	2		2
turgidum	14		14
Vicia	**1036**	**738**	**1774**
abbreviata	2		2
anatolica	1		1
articulata	1	4	5

balansae	1		1
benghalensis	27		27
bithynica	5	16	21
botanica		1	1
cappadocica	6		6
cassia	3		3
ciliatula	12		12
cracca	2	12	14
cuspidata	1	15	16
eristaloides		2	2
ervilia	47	12	59
faba	261	84	345
grandiflora	4	7	11
hetrasperma		1	1
hirsuta	6	5	11
hybrida	25	81	106
hyrcanica	6		6
johannis	11	12	23
lathyroides	2	6	8
laxiflora		2	2
lutea	50	42	92
melanops	1	1	2
meyeri		3	3
monantha	11		11
narbonensis	24	27	51
onobrychioides	3		3
palaestina	1		1
pannonica	33	21	54
peregrina	28	28	56
pisiformis	1		1
sativa	399	211	610
sericocarpa	2		2
sp.	7	54	61
tenuifolia	7		7
tetrasperma	7	12	19
villosa	39	79	118
Vigna	**22**	**3**	**25**
mungo	12		12
radiata	9		9
sp.		1	1
unguiculata	1	2	3
Zea	**14**		**14**
mays	14		14
Grand Total	**8651**	**5482**	**14133**

Table 2: Dr. Clive Francis' interests in plant genetic resource collection, conservation and evaluation; summarized by project title, international and regional collaborators.

Year	Funder	Title	International collaborators	Regional collaborators
1973-1994	N/A	Various: N/A	Australia: DAFWA Syria: ICARDA	Greece: Nicosia Agricultural Research Institute (NARI) Israel: Volcani Institute of Agricultural Research (VIAR) Iran: Forest & Range Organization of Iran (IFAO) Iraq: Ministry of Agriculture, National Herbarium (IMA) Italy: Istituto Sperimentale Colture Foraggere (ISCF), Centro di Studio sui Pascoil Mediterranei, National Research Centre (CNR) Morocco: Institut National de la Recherche Agronomique (INRA), Arididoculture Centre (AC) Portugal: INIA, Consejeria de Agricultura y Comercio (CAC)
1994-1998	ACIAR	Development and conservation of plant genetic resources for the Mediterranean basin and West Africa	Australia: ATFCC, CLIMA, DAFWA, DPI Tasmania, Pastoral Research and Veterinary Institute, VIDA Syria: ICARDA, IBPGR UK: University of Birmingham	Bangladesh : Bangladesh Agricultural Research Institute Ethiopia: Ethiopian Agricultural Research Organization (EARO), Biodiversity Institute (BDI), Addis Ababa University Italy: ISCF, CNR Morocco: INRA Nepal : Nepal Agricultural Research Centre Pakistan: Pakistan Agricultural Research Council, National Agricultural Research Council
1994-1998	GRDC	Conservation and evaluation utilisation of grain legume genetic resources from the Eastern Mediterranean region	Australia: ATFCC, CLIMA, DAFWA, DPI Tasmania, SARDI Russia: VIR Syria: ICARDA UK: University of Birmingham	Greece: National Gene Bank, Thessaloniki Iran: Forest and Range Organization of Iran (FROI), Challus, Iran Turkey: Plant Genetic Resources Institute, Aegean Agricultural Research Institute (AARI)
1994-1998	GRDC	Faba bean multiplication-ICARDA collection	Australia: CLIMA, DAFWA, NSW Ag, SARDI Syria: ICARDA	

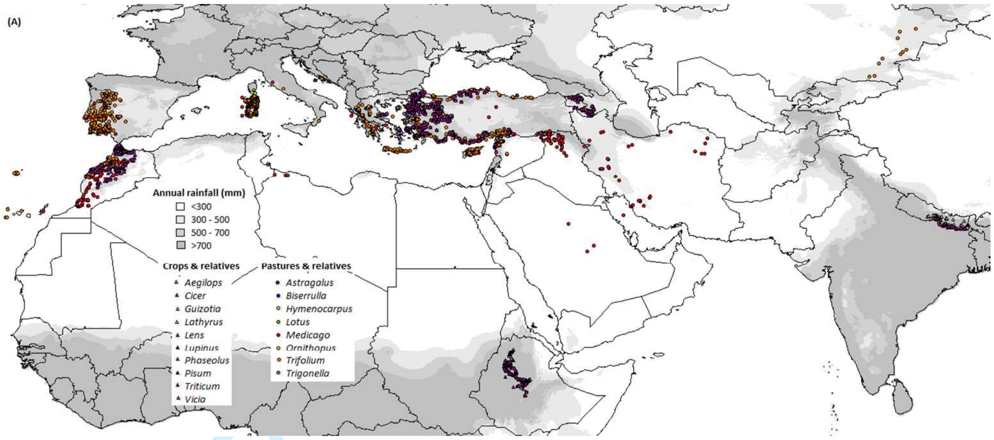
1996-1999	ACIAR	Improvement in drought and disease resistance in lentils in Nepal, Pakistan and Australia	Australia: CLIMA, DAFWA, VIDA	Nepal: NARC Pakistan: PARC
1997-1999	GRDC	Preservation & utilization of the unique pulse & cereal genetic resources of the Vavilov Institute	Australia: CLIMA Russia: VIR Syria: ICARDA	
1997-2001	GRDC	International selection, introduction and fast tracking of Kabuli chickpea with large seed size, high biomass, yield and Ascochyta resistance	Australia: CLIMA, DAFWA, NSW Ag Syria: ICARDA	Turkey: AARI
1998-2003	GRDC	International linkages for crop plant genetic resources	Australia: ATFCC, AWCC, CLIMA, NSW Ag, SARDI,VIDA, TIAR Germany: IPK Gatersleben Russia: VIR Syria: ICARDA	Armenia: Armenian Agricultural Institute (AAI) Georgia: Institute of Farming Kazakhstan/Kyrgyzstan: Botanical Institute, Department of Forage Crops, Aral Sea Experiment Station for Plant Genetic Resources Portugal: Estacao Nacional de Melhoramento de Plantes, Portuguese Vegetal Germplasm Bank Romania: Suceava Gene Bank Tajikistan: UZB Plant Research Institute Turkmenistan: TIDFF, Scientific Production Experimental Centre of PGR Uzbekistan: Uzbek Research Institute of Plant Production (UZRIPI), UZARIC
1998-2001	GRDC	Offshore evaluation of international field pea germplasm for resistance to blackspot & agronomic merit	Australia: CLIMA, SARDI, VIDA Russia: VIR Syria: ICARDA USA: USDA	Ethiopia: EARO New Zealand: Institute for Food and Crop Research
2001-	GRDC	An international program for selection of lupins with improved resistance to anthracnose and Fusarium wilt	Australia: CLIMA, DAFWA Portugal: INIA Russia: VIR	France: University of Auburn Poland: Institute of Plant Genetics Russia: Russian Lupin Research Institute
2001-	GRDC	Germplasm collection of *Trifolium*	Australia: CLIMA, DAFWA,	Eritrea: Genetic Resource Centre of Eritrea, Hal Hale Research Centre

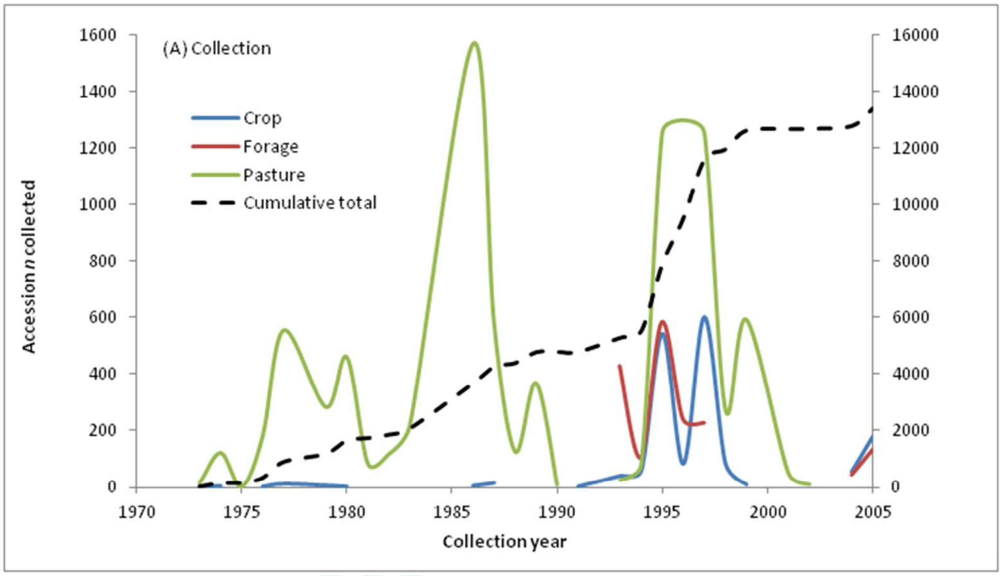
2006		and other pasture legume species from short season, low latitude regions in the Mediterranean	NSW Ag, SARDI Syria: ICARDA	Israel: Volcani Centre/Genebank, Hebrew University of Jerusalem, Israeli Genebank, Mt. Scopus Botanic Garden Lebanon: Lebanese Agricultural Research Institute (LARI) Morocco: INRA Spain: University of Murcia, University of Alicante, Botanic Gardens Tenerife
2000-2003	ACIAR	Development and conservation of plant genetic resources from the Central Asian Republics and associated regions	Australia: AWCC, CLIMA Russia: VIR Syria: ICARDA	Armenia: AAI Ethiopia: BDI Kazakhstan: National Academic Center of Agricultural Sciences (NACAS) Kyrgyzstan: Agrarian Academy (AA) Tajikistan: Tajik Academy of Agricultural Sciences (TAAS) Turkmenistan: Turkmen Academy of Agricultural Sciences (TAAS) Uzbekistan: UZRIPI
2001-2004	ACIAR	Conservation, evaluation and utilisation of plant genetic resources from Central Asia and the Caucasus	Australia: ATFCC, AWCC, CLIMA, DAFWA, SARDI, TIAR Syria: ICARDA Russia: VIR USA: USDA	Armenia: AAI Azerbaijan: Scientific Production Association, Azerbaijan Agrarian Academy Georgia: Research Institute of Crop Husbandry (RICH), Georgian Academy of Agricultural Sciences Kazakhstan: Chelkar Research Station, NACAS Kyrgyzstan: AA Tajikistan: TAAS Turkmenistan: Garragalinsky Scientific Production Centre, Scientific Institute of Plant Genetic Resources, TAAS Uzbekistan: UZRIPI, Uzbek Scientific Production Centre of Agriculture, Academy of Sciences, CGIAR Program Facilitation Unit
2004-2011	ACIAR	Plant genetic conservation, documentation and utilization in central Asia and the Caucasus	Australia: ATFCC, AWCC, CLIMA, DAFWA Syria: ICARDA Russia: VIR	Armenia: Armenian Botanic Institute (ABI) Azerbaijan: Research Institute of Genetic Resources Georgia: RICH Kazakhstan: Cereals Department Kyrgyzstan: Research Institute of Crop Husbandry and Plant Industry Tajikistan: TAAS Turkmenistan: Turkmen Research Institute of Cereals and Legumes

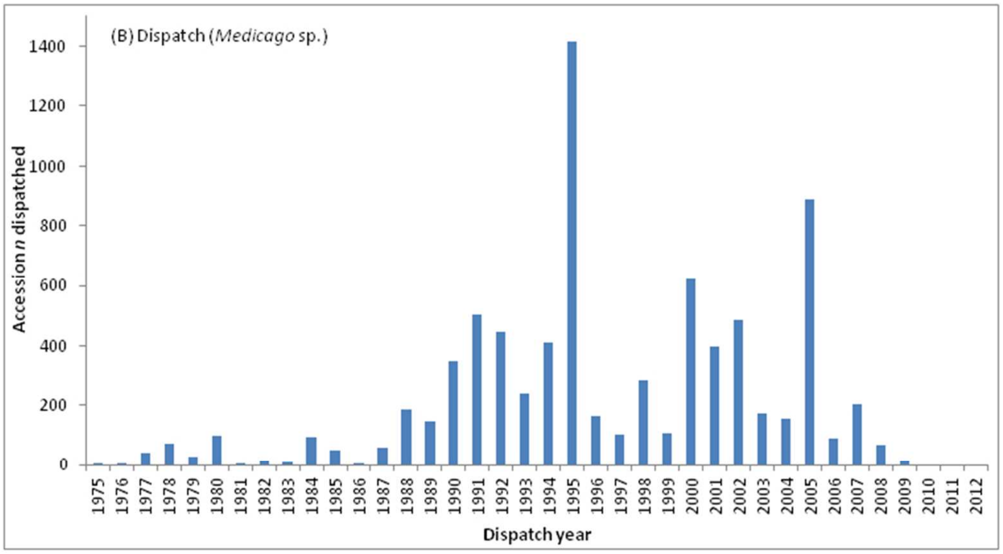
				Uzbekistan: Uzbek Research Institute of Plant Industry

Table 3: Pasture, forage and crop cultivar releases flowing from the genetic resource activities of Dr. Francis and colleagues.

Species	Cultivar name	Release date	Country
Pasture			
Subterranean clover (*Trifolium subterraneum*)	Rosedale	1988	Australia
Yellow serradella (*Ornithopus compressus*)	Madeira	1988	Australia
Murex medic *(Medicago murex)*	Zodiac	1988	Australia
Subterranean clover (*Trifolium subterraneum*)	Denmark	1992	Australia
Subterranean clover (*Trifolium subterraneum*)	Goulburn	1992	Australia
Subterranean clover (*Trifolium subterraneum*)	Leura	1992	Australia
Subterranean clover (*Trifolium subterraneum*)	York	1995	Australia
Purple clover (*Trifolium purpureum*)	Electra	2005	Australia
Subterranean clover (*Trifolium subterraneum*)	Izmir	2006	Australia
Bladder clover *(Trifolium spumosum)*	Bartolo	2009	Australia
Forage			
Bitter vetch (*Vicia ervilia*)	Cazar	1998	Australia
Chickling (*Lathyrus cicera*)	Chalus	1999	Australia
Crop			
Desi chickpea (*Cicer arietinum*)	Sona	1997	Australia
Desi chickpea (*Cicer arietinum*)	Heera	1997	Australia
Lentil (*Lens culinaris*)	Cassab	1998	Australia
Lentil (*Lens culinaris*)	Cumra	1998	Australia
Yellow lupin (*Lupinus luteus*)	Wodjil	1998	Australia
Niger, noog (*Guizotia abyssinica*)	Nawalpur Jhusetil 1	2000	Nepal
Kabuli chickpea (*Cicer arietinum*)	Almaz	2005	Australia
Kabuli chickpea (*Cicer arietinum*)	Nafice	2005	Australia
Kabuli chickpea (*Cicer arietinum*)	Kimberly Large	2005	Australia
Indian mustard (*Brassica juncea*)	Caza	2009	Australia


(A)
Annual rainfall (mm)
☐ <300
☐ 300 - 500
☐ 500 - 700
☐ >700
Crops & relatives
▲ Aegilops
▲ Cicer
▲ Guizotia
▲ Lathyrus
▲ Lens
▲ Lupinus
▲ Phaseolus
▲ Pisum
▲ Triticum
▲ Vicia
Pastures & relatives
● Astragalus
● Biserrulla
● Hymenocarpus
● Lotus
● Medicago
● Ornithopus
● Trifolium
● Trigonella


(A) Collection
Crop
Forage
Pasture
Cumulative total
Accession n collected
0
200
400
600
800
1000
1200
1400
1600
0
2000
4000
6000
8000
10000
12000
14000
16000
1970
1975
1980
1985
1990
1995
2000
2005
Collection year


(B) Dispatch (*Medicago* sp.)
Accession *n* dispatched
0
200
400
600
800
1000
1200
1400
Dispatch year
1975
1976
1977
1978
1979
1980
1981
1982
1983
1984
1985
1986
1987
1988
1989
1990
1991
1992
1993
1994
1995
1996
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1998
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2001
2002
2003
2004
2005
2006
2007
2008
2009
2010
2011
2012