

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

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16

17 **Abstract**

18 This paper is a tribute to the legacy of Dr. Clive Francis who directly and indirectly collected >
19 14,000 accessions across 60 genera of pasture, forage and crop species and their wild relatives
20 around the Mediterranean basin, Eastern Africa, Central and South Asia from 1973 to 2005. This was
21 achieved by a collaborative approach that built strong interactions between disparate organizations
22 (ICARDA, VIR, CLIMA and Australian genebanks) based on germplasm exchange, conservation and
23 documentation, capacity building and joint collection. These activities greatly strengthened
24 Australian pasture, forage and crop genebanks, and led to widespread germplasm utilization that
25 has waned in the last 5 years, reflecting changing priorities among industry funding bodies and
26 research providers. This situation must be reversed, given the pivotal role genetic resource
27 collections must play to broaden the genetic and adaptive base of plant breeding, to meet the
28 challenge of feeding an increasing population in a depleting resource base.

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

35 **Keywords**

36 Plant genetic resources, core collection, habitat characterization, FIGS

38 From 1973 to 2005 Dr. Clive Francis collected > 8,600 accessions across 60 genera, and
39 assisted in the collection of >5,450 additional accessions by helping to organize collection missions
40 manned by colleagues throughout Australia and internationally (Table 1). While Clive's early
41 collection activities were strongly focused on the Mediterranean rim (Fig. 1), in time his missions
42 expanded to the east and south, from Iraq in 1980, to Iran (1988, 95), Nepal (1996, 98), Ethiopia
43 (1997), Kazakhstan (2002), Azerbaijan (2004) and finally Armenia (2004, 2005). With the exception
44 of the genus *Lupinus* (Berger *et al.* 2013), Clive's early and abiding focus was on Mediterranean
45 pasture legumes, particularly *Medicago* and *Trifolium* (Table 1, Fig. 2a). However, from the early
46 1990s onwards, Clive and colleagues also began to collect forage and grain legume crops, such as
47 *Cicer*, *Lathyrus*, *Lens*, *Pisum* and *Vicia*, expanding to cereals, such as *Aegilops*, *Hordeum*, *Triticum* and
48 *Zea*, and even under-utilized oilseeds such as *Guizotia abyssinica* in Nepal (Table 1, Fig. 1). This
49 widespread interest in genetic resource collection was remarkable, both in terms of taxa that were
50 collected, and the range of habitats and regions that were sampled. To honour this legacy this
51 paper summarizes Dr. Francis' contribution to germplasm collection and utilization, emphasising
52 how his collaborative approach built strong interaction between disparate organizations separated
53 by borders and political systems. Unfortunately we also demonstrate a decline in these
54 collaborations as a consequence of reduced funding for genetic resources. Finally, without ongoing
55 utilization, plant genetic resource collections are fated to become static museum exhibits (Maxted *et*
56 *al.* 1997), and therefore the bulk of this paper is focused on methodologies for data mining to
57 increase the utilization of collections, be it for furthering our understanding of plant adaptation, or
58 identifying useful traits.

Collaborative genetic resource collection and conservation

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

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

96 These international linkages, established in the late 1990s, led to further collaboration in the
97 Mediterranean basin (funded by GRDC), Caucasus and Central Asia (funded by the Australian Centre
98 for International Agricultural Research (ACIAR)) until 2006 and 2011, respectively (Table 2). The
99 Mediterranean collections included annual pasture legumes from short season and low latitude
100 regions in the Canary Islands, Morocco, south-east Spain, Israel (Snowball *et al.* 2008), Eritrea
101 (Snowball *et al.* 2012), Turkey, Greece and the Cyclades islands (Folegandros, Sikinos, Ios, Naxos and
102 Milos); *Melilotus siculus* and other salt tolerant species from Andalusia and Valencia (Nichols *et al.*
103 2010). Subsequently perennial pasture legumes were also targeted, including *Lotus* from Cape

104 Verde, Canary Islands and Azores (Sandral *et al.* 2006); and drought tolerant *Bituminaria bituminosa*
105 var. *albomarginata* (Albo Teder) from the Canary Islands. This most recent interest in Teder was
106 largely initiated as a result of the long standing relationship between Dr Francis and the Spanish
107 pasture legume specialist, Enrique Correal Castellanos, who forged a close friendship from the early
108 1970s onwards. These activities stimulated wider pasture collection outside of the Mediterranean
109 basin, such as drought tolerant perennial *Lessertia*, *Lebeckia* and *Lotononis* from South Africa and
110 *Syrmatium glabrum* from southern California. The Central Asian linkages were pivotal in the search
111 for germplasm which could reduce recharge and manage discharge for the control of dryland salinity
112 in southern Australia (Dear and Ewing 2008; Hughes *et al.* 2008). The Central Asian-Caucasian
113 collections included Armenia, Azerbaijan, Kazakhstan and Turkmenistan. Target species included
114 lucerne (*Medicago sativa* subsp. *sativa*) and its wild relatives (Auricht *et al.* 2010) and *Trifolium*
115 *tumens* (Hall *et al.* 2013). The Asian interests extended as far as the subcontinent. As a result of
116 associations developed in joint projects with the Nepal Agricultural Research Council (Table 2),
117 collections of the underutilised crop *G. abyssinica* were undertaken (Clements *et al.* 2002), leading
118 to the selection and release of a cultivar in Nepal. Indeed, Table 3 lists a wide range of pasture,
119 forage and crop cultivars aimed at different soil types, pH and rainfall ranges in southern Australia,
120 that were developed as a result of the genetic resource activities of Dr. Francis and colleagues.

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

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

167 **Mining germplasm collections**

168 It is in their utilization that genetic resource collections become valuable; a static collection
169 that is used neither for plant improvement, nor to enhance our understanding of adaptation and
170 evolution, consumes resources and has little intrinsic value. As collections grow ever larger there is

171 an increasing risk that much of the material remains filed away inside genebanks, playing no role in
172 plant improvement or scientific research. Typically the problem is one of scale. Improvements in
173 experimental design and analysis notwithstanding, it is often infeasible and potentially meaningless
174 to screen 1000s of accessions because of the difficulties of comparing traits over time (e.g. when
175 different accessions are evaluated over years) or space (e.g. when trials become very large, with
176 correspondingly increasing extraneous variation). In this context, the evaluation of smaller
177 germplasm subsets likely to contain the trait of interest is an attractive alternative. A common
178 approach to this problem is the evaluation of core collections that capture a high proportion of total
179 collection diversity, ideally >70% according to Brown (1989) in a subset of samples (often 10 to 20%
180 of the full collection) filtered by different criteria which increasingly include molecular data. The
181 underlying assumption here is that variation in the trait of interest is related to diversity *per se*, even
182 though there may not be a direct marker-trait link, especially for complex traits. This approach has
183 gained traction with the increasing genomic characterization of plant genetic resources, and has
184 been applied to a wide range of grain legumes (see references in Upadhyaya et al. (2011)). Indeed,
185 in collections which are particularly large these authors advocate the use of mini-cores that
186 subsample the primary core (Upadhyaya et al. 2011; Upadhyaya and Ortiz 2001).

187 Core collections based on ecogeographic, plant morphological and molecular data have been
188 developed for *Lupinus* spp (*L. angustifolius*, *L. albus*, *L. luteus*), Chinese field pea landraces (Zong et
189 al. 2009), *Trifolium subterraneum* (Ghamkhar et al. 2010), *T. spumosum* (Ghamkhar et al. 2008),
190 annual *Medicago* (Ellwood et al. 2006a; Skinner et al. 1999) and *Biserrula pelecinus* (Ghamkhar et al.
191 2012). In each case a maximisation strategy (Gouesnard et al. 2001) was employed to determine the
192 ideal size of each core and select multiple cores or iterations that were used to arrive at a final core
193 of lines or phenotypes. In the case of *T. subterraneum* the first subset of accessions was selected
194 using collecting site data, the second subset of phenotypes was selected using plant agro-
195 morphological characters, and the final core collection of phenotypes was selected using plant
196 molecular data from SSR markers. From the whole collection of 7,800 phenotypes (originating from
197 2,870 collecting sites) a core collection of 97 phenotypes was developed. Currently it is being
198 screened for methane production in sheep, soil phosphorus response, and acid soil tolerance at the
199 University of Western Australia. The development of annual *Medicago* cores has been instrumental
200 in the identification of discreet genotypes with disease and insect resistant traits (Ballard et al. 2012;
201 Ellwood et al. 2006b; Kamphuis et al. 2012) and the continued use of *M. truncatula* as the pre-
202 eminent model species for legume genetics research (Nair et al. 2006). The continued use of
203 molecular studies in phenotyping is providing a successful model for future work in the development

204 of core collections. Finally, the lupin core collection has been used to identify genetic variation and
205 phenotypic plasticity for a range of root traits in *L. angustifolius* (Chen *et al.* 2011).

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

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

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

237 site coordinates. Upadhyaya et al. (2011) outline a methodology for habitat characterization and
238 germplasm selection using a procedure to:

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

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

257 Thus in Mediterranean climates and beyond, winter cold and spring/summer terminal
258 drought are the twin climatic stresses that are negotiated by plants using appropriate phenology.
259 Terminal drought prone habitats select for early flowering and short lifecycles as a drought escape
260 mechanism, limiting biomass production and yield potential. Conversely, cool, high rainfall habitats
261 select for delayed phenology to minimize exposure of the sensitive reproductive phase to low
262 temperature stress, also facilitating increased biomass production, supporting a higher reproductive
263 effort. These trends have been reported widely in both wild and domesticated Mediterranean
264 annuals (Ehrman and Cocks 1996), including grasses (Volis 2007), crucifers (Petrů *et al.* 2006), yellow
265 lupin (*Lupinus luteus* L.) (Berger *et al.* 2008a), narrow-leafed lupin (Clements and Cowling 1994),
266 annual *Trifolium* from Sardinia (Bennett and Galwey 2002) and Turkey (Bennett 2000), *T. glomeratum*
267 L. (Bennett 1997), *T. subterraneum* L. (Piano *et al.* 1996), *T. tomentosum* (Bennett 1999), *Cicer*
268 *judaicum* Boiss (Ben-David *et al.* 2010) and chickpea (*C. arietinum* L.) (Berger *et al.* 2006; Berger *et al.*
269 2004).

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

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

303 drought stress using germplasm collected along rainfall gradients, at the present time it is difficult to
304 interpret this apparent contradiction.

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

312 The previous examples are illustrations of plant populations responding directly to climatic
313 selection pressure. However, climate can also indirectly impose selection pressure on plant
314 populations by influencing the incidence of pests and diseases. This approach has been used in
315 bread wheat to identify resistance to Sunn pest (*Eurygaster integriceps* Puton) (El Bouhssini *et al.*
316 2011; El Bouhssini *et al.* 2009), Russian wheat aphid (*Diuraphis noxia* Kurd) (Street *et al.* 2008),
317 powdery mildew (*Blumeria graminis* f. sp. *Tritici* D. C. Speer) (Bhullar *et al.* 2009), and stem rust
318 (*Puccinia graminis* f. sp. *tritici*) (Bari *et al.* 2012; Endresen *et al.* 2012). Germplasm collections were
319 filtered by country, latitude, agro-climatic zone, altitude, annual rain and winter temperatures
320 (Street *et al.* 2008). As a result, the size of the screening subsets were reduced to manageable
321 proportions (n~500), returning 10-12 resistant genotypes of Sunn pest and Russian wheat aphid,
322 respectively, a vast improvement on previous efforts where random screening of >2000 genotypes
323 did not uncover a single source of resistance (Street *et al.* 2008). In powdery mildew, a reverse
324 engineering approach was used to define the habitat characteristics of 400 known resistant
325 genotypes in the USDA-ARS National Small-Grains Collection, and this information used as a
326 multivariate filter to select 1,320 landraces from a total of 17,000 (Kaur *et al.* 2008), identifying new
327 sources of resistance leading to the isolation of 7 new resistance alleles (Bhullar *et al.* 2009).

328 **Conclusions and future priorities**

329 We preface these conclusions with the observation that to feed the projected population of
330 ~9 billion by the year 2050, global food supply will need to double (Parry and Hawkesford 2010), in a
331 diminishing resource base that is under threat due to land degradation, peak P and N supply,
332 reduced agricultural investment and climate change. Furthermore, productivity gains in crop yields
333 – positively correlated to research and development investment, have been declining over the last
334 30 years (Beintema and Elliott 2009; Fischer *et al.* 2009). There is therefore an urgent need to

335 increase food production per unit land area and per unit input, which will require the development
336 of better adapted, higher yielding, more resource efficient crop and pasture cultivars. To this end,
337 the effective utilization of plant genetic resources is essential to break current bottlenecks in plant
338 improvement.

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

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

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

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384 **Table headings**

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

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

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

391 **Fig headings**

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

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

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

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
oliaceum		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
hausknechtii	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
melchiorianum	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
fabas	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

610 Table 2: Dr. Clive Francis' interests in plant genetic resource collection, conservation and evaluation; summarized by project title, international and regional
 611 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	

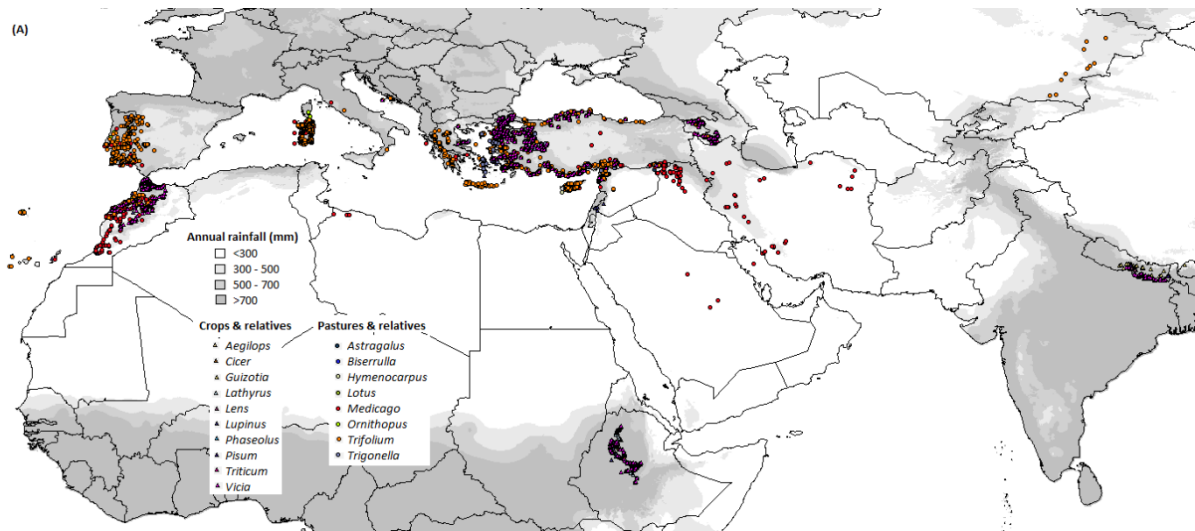
1996-1999	ACIAR	Improvement in drought and disease resistance in lentils in Nepal, Pakistan and Australia	Australia: CLIMA, DAFWA, VIDA	Nepal: NARC Pakistan: PARC
1997-1999	GRDC	Preservation & utilization of the unique pulse & cereal genetic resources of the Vavilov Institute	Australia: CLIMA Russia: 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 Industry (UZRIPI)
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
2001-2006	GRDC	Germplasm collection of <i>Trifolium</i> and other pasture legume species	Australia: CLIMA, DAFWA, NSW Ag, SARDI	Eritrea: Genetic Resource Centre of Eritrea, Hal Hale Research Centre Israel: Volcani Centre/Genebank, Hebrew University of Jerusalem,

		from short season, low latitude regions in the Mediterranean	Syria: ICARDA	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

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

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

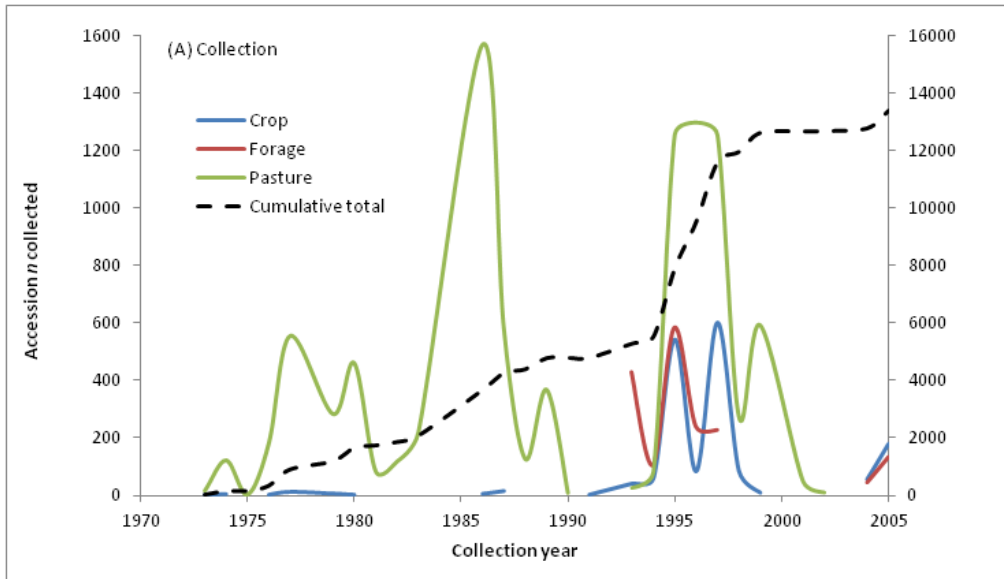
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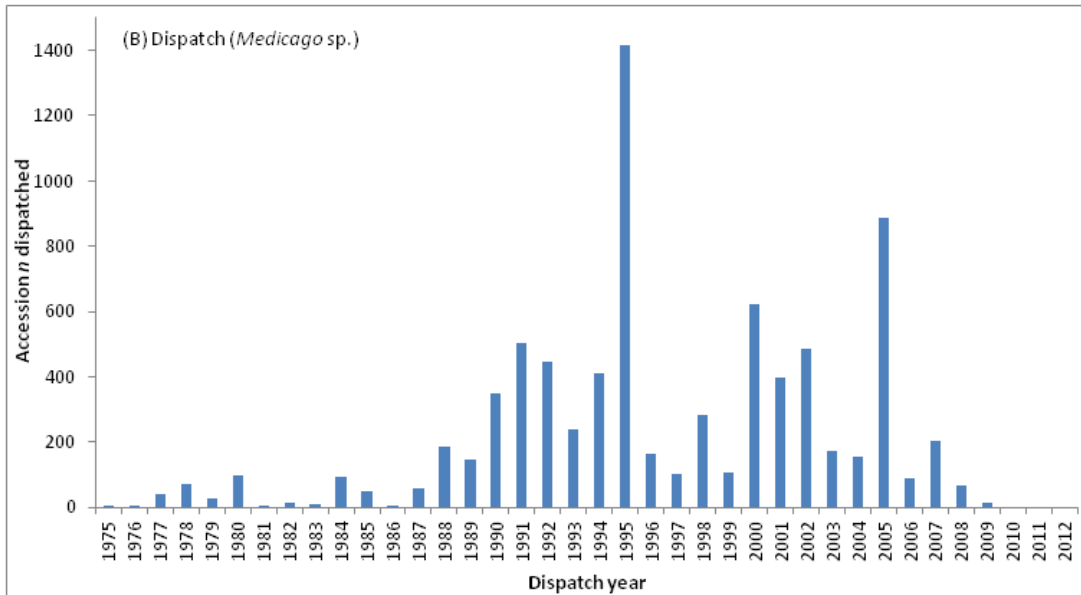
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Fig. 1

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618 Fig. 2a



619 Fig. 2b