# CHICKPEA BREEDING AND MANAGEMENT

Edited by

**S.S. Yadav**

*Pulse Research Laboratory, Division of Genetics, Indian Agricultural Research Institute, New Delhi, India*

**R.J. Redden**

*Australian Temperate Field Crops Collection, Department of Primary Industries, Victorian Institute for Dryland Agriculture, Horsham, Victoria, Australia*

**W. Chen**

*United States Department of Agriculture – Agricultural Research Service (USDA-ARS), Grain Legume Genetics and Physiology Research Unit, Washington State University, Pullman, Washington State, DC, USA*

**B. Sharma**

*Division of Genetics, Indian Agricultural Research Institute, New Delhi, India*

**CABI is a trading name of CAB International**

CABI Head Office
Nosworthy Way
Wallingford
Oxfordshire OX10 8DE
UK
Tel: +44 (0)1491 832111
Fax: +44 (0)1491 833508
E-mail: cabi@cabi.org
Website: www.cabi.org

CABI North American Office
875 Massachusetts Avenue
7th Floor
Cambridge, MA 02139
USA
Tel: +1 617 395 4056
Fax: +1 617 354 6875
E-mail: cabi-nao@cabi.org



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# 17 Biodiversity Management in Chickpea

R.J. Redden,[1] B.J. Furman,[2] H.D. Upadhyaya,[3] R.P.S. Pundir,[3] C.L.L. Gowda,[3] C.J. Coyne[4] and D. Enneking[1]

[1]*Australian Temperate Field Crops Collection, Department of Primary Industries, Victorian Institute for Dryland Agriculture, Horsham, Victoria 3401, Australia;* [2]*International Centre for Agricultural Research in Dry Areas (ICARDA), PO Box 5466, Aleppo, Syria;* [3]*Genetics Resources Divisions, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Asia Center, Hyderabad 502 324, India;* [4]*Plant Introduction Unit, 303 Johnson Hall, Washington State University, Pullman, WA 99164, USA*

## Morphological Diversity

Variation in cultivated chickpea is mostly noted in the separation of the kabuli large-seeded and the desi small-seeded gene pools, each with associated patterns of traits (Moreno and Cubero, 1978). The desi types have seed size generally in the range 10–25 g/100 seed, and are associated with small leaves or leaflets, and small pods with 1–3 seeds that are angular-shaped or beaked. Seeds vary in colour from cream to orange, dull green, various shades of brown to black, and flowers usually vary from pink to red, blue veined and purple. In the desi type, pod surface may be smooth, wrinkled or tuberculate, and anthocyanin occurrence on leaves and stems is associated with coloured flowers (van der Maesen, 1973).

Chickpea has an air-sac-inflated pod surrounding the seed, and pods and leaves have glandular pubescence.

There are small-seeded kabuli types of 25–35 g/100 seed, but the large-seeded kabuli range from 40 to 60 g/100 seed, with owl's head-shaped and generally cream coloured seeds and white flowers (Moreno and Cubero, 1978). Other seed colours of pink, red or black may occur at low frequencies. Leaves or leaflets and pods also tend to be large. Morphological diversity is narrower amongst the kabulis than amongst the desis from which they were derived in relatively recent millennia since there are few cytoplasmic differences (Moreno and Cubero, 1978).

Diversity analyses with randomly amplified polymorphic DNA (RAPD) and intersimple sequence repeat (ISSR) markers showed separate clustering of kabuli from desi types (Iruela *et al.*, 2002). This study showed that cultivated chickpea also had less polymorphism for molecular markers than wild species, consistent with other diversity analyses using protein and isozyme analyses.

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In a collection of more than 16,000 mainly desi landraces at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India, a core collection was identified. The most variable traits were: days to flowering and to maturity, plant height and width, number of pods per plant and yield (Upadhyaya *et al.*, 2001). Unimodal and bimodal distributions of traits for 150 accessions including desi and kabuli displayed: rachis length 3.5–7 cm; leaflets per leaf 11–16; leaflet length 10–17 mm; leaflet width 6–14 mm bimodal with peaks at 8 and 11 mm; pod length 17–30 mm with bimodal peaks at 20 and 26 mm; pod width 8–14 mm with bimodal peaks at 10 and 13 mm; pod thickness 8–14 mm with bimodal peaks at 9 and 13 mm; pods per plant from 10–150 with a mean of 75; seeds per pod 1–2 skewed towards 1; seed size 10–70 g/100 seed with bimodal peaks at 20 and 40 g; and number of branches 1–4 (Moreno and Cubero, 1978). They found high correlations between leaf rachis, leaflets, pods and seed size traits; these are reflected in the separation of the desi (*microsperma*) and kabuli (*macrosperma*) gene pools, which are also geographically separated.

Desi types are grown mainly in the Indian subcontinent, Asia, East and South Africa, while kabuli types are found in the Mediterranean and are imported to Chile (Malhotra *et al.*, 2000). The gene bank at the International Centre for Agricultural Research in the Dry Areas (ICARDA), Aleppo, Syria, has mainly kabuli germplasm, which has been assessed for phenological and growth diversity in winter and spring sowings, and diversity similarly assessed by the ICRISAT gene bank (Malhotra *et al.*, 2000). Earlier at ICRISAT, the range of phenological expression was wider than at ICARDA, and hence the ranges and maximum values for height and width were also greater. The geographic distribution of trait expressions largely follows the desi vs kabuli distributions, with intermediate seed types found in Ethiopia and Iran (Malhotra *et al.*, 2000). Fusarium wilt resistance is found in the Indian subcontinent and Ethiopia, dry root rot resistance in India and Iran, ascochyta blight resistance in India, Iran, Mexico and Turkey, grey mould resistance in Iran, helicoverpa resistance in India, and high seed protein in Pakistan and Sudan. Additionally a range of morphological mutants are also described by Malhotra *et al.* (2000).

## Germplasm Collections

The global chickpea germplasm collection is housed at ICRISAT, which has a total of 17,258 accessions in its gene bank, including 17,123 accessions of cultivated chickpea (*Cicer arietinum*) and 135 accessions comprising 18 wild *Cicer* spp., from 43 different countries. Of the entire cultivated chickpea accessions, 75.2% are of desi type, 21% kabuli type and 3.8% intermediate type (Upadhyaya, 2003). ICARDA has the Central and West Asia, and North Africa (CWANA) regional mandate for chickpea improvement and houses a total of 12,448 accessions in its gene bank, including 12,180 accessions of cultivated chickpea and 268 accessions, comprising 10 wild *Cicer* spp., from 60 different countries. The ICARDA collection focuses on kabuli types and, as such, has the largest global collection of this variety. The frequency of the ICRISAT and ICARDA collections by country

of origin of cultivated chickpea is given in Table 17.1; holdings by species are given in Table 17.2. A recent focus of ICARDA is the acquisition of material from Central Asia and the Caucasus (CAC), an area historically underrepresented.

In addition to the Consultative Group on International Agricultural Research (CGIAR) centres, other major chickpea collections are conserved at the Seed and Plant Improvement Institute (SPII), Iran (4925 accessions); the United States Department of Agriculture's (USDA) Western Regional Plant Introduction Station (WRPIS) (4662); the Centre for Legumes in Mediterranean Agriculture (CLIMA), Australia (4351); the National Bureau of Plant Genetic Resources (NBPGR), India (3830); and the N.I. Vavilov Institute of Plant Industry (VIR) in St Petersburg, Russia (2113).

**Table 17.1.** Frequency by country of origin in ICRISAT and ICARDA holdings.

| Country origin | ICRISAT | ICARDA |
|---|---|---|
| Afghanistan | 702 | 1,030 |
| Algeria | 16 | 60 |
| Armenia | – | 56 |
| Australia | 3 | 4 |
| Azerbaijan | – | 119 |
| Bangladesh | 170 | 1 |
| Bulgaria | 9 | 217 |
| Chile | 139 | 349 |
| China | 24 | 34 |
| Colombia | 1 | 9 |
| Cuba | – | 4 |
| Cyprus | 44 | 40 |
| Czech Republic | 8 | 7 |
| Ecuador | – | 2 |
| Egypt | 53 | 64 |
| Ethiopia | 933 | 110 |
| France | 2 | 21 |
| Georgia | – | 11 |
| Germany | 11 | 2 |
| Greece | 25 | 21 |
| Guatemala | – | 2 |
| Hungary | 4 | 3 |
| India | 7,081 | 439 |
| Iran | 4,856 | 1,782 |
| Iraq | 18 | 37 |
| Israel | 51 | – |
| Italy | 45 | 87 |
| Jordan | 25 | 156 |
| Kazakhstan | – | 14 |
| Kenya | 1 | 6 |
| Kyrgyzstan | – | 9 |
| Latvia | – | 3 |

*Continued*

**Table 17.1.** *Continued*

| Country origin | ICRISAT | ICARDA |
|---|---|---|
| Lebanon | 20 | 28 |
| Libyan Arab Jamahiriya | – | 5 |
| Malawi | 81 | 3 |
| Mexico | 397 | 160 |
| Moldova, Republic of | – | 21 |
| Morocco | 249 | 231 |
| Nepal | 80 | 8 |
| Nigeria | 3 | 1 |
| Pakistan | 484 | 270 |
| Palestine | – | 64 |
| Peru | 3 | 4 |
| Portugal | 84 | 179 |
| Romania | – | 4 |
| Russian Federation | 133 | 167 |
| Slovakia | – | 7 |
| Spain | 122 | 293 |
| Sri Lanka | 3 | 2 |
| Sudan | 12 | 14 |
| Syrian Arab Republic | 226 | 533 |
| Tajikistan | – | 170 |
| Tanzania | 97 | – |
| Tunisia | 33 | 271 |
| Turkey | 478 | 965 |
| Turkmenistan | – | 14 |
| Ukraine | – | 81 |
| Uganda | 1 | – |
| UK | – | 8 |
| USA | 82 | 124 |
| Uzbekistan | – | 304 |
| Venezuela | – | 1 |
| Yugoslavia | 6 | 6 |
| Unknown | 308 | 224 |
| Breeding lines | | 3,319 |
| Total | 17,123 | 12,180 |

At ICARDA, each sample in its gene bank is documented according to internationally agreed upon descriptor lists jointly published by the International Plant Genetic Resources Institute (IPGRI), ICRISAT and ICARDA, and made up of various categories of passport, characterization and evaluation data. Passport data are recorded in a database at the time of introduction of each accession, and characterization and evaluation information is added when available. The documentation system also assists the germplasm curators in controlling seed stock, seed viability and distribution of germplasm samples to users.

There are two main types of collections stored at the genetic resources unit (GRU): an active collection, which is available for distribution and includes

**Table 17.2.** *Cicer* spp. and accession numbers held at ICRISAT and ICARDA.

| Species | ICRISAT holdings | ICARDA holdings |
|---|---|---|
| *Cicer anatolicum* | 3 | 2 |
| *C. arietinum* | 17,123 | 12,180 |
| *C. bijugum* | 8 | 45 |
| *C. chorassanicum* | 3 | 3 |
| *C. cuneatum* | 1 | 5 |
| *C. echinospermum* | 4 | 15 |
| *C. flexuosum* | – | 1 |
| *C. floribundum* | 1 | – |
| *C. judaicum* | 22 | 77 |
| *C. macracanthum* | 5 | – |
| *C. microphyllum* | 52 | – |
| *C. montbretii* | 2 | – |
| *C. multijugum* | 1 | – |
| *C. nuristanicum* | 2 | – |
| *C. pinnatifidum* | 11 | 55 |
| *C. pungens* | 9 | – |
| *C. rechingeri* | 1 | – |
| *C. reticulatum* | 6 | 60 |
| *C. yamashitae* | 3 | 5 |
| *C. anariense* | 1 | – |
| Total | 17,258 | 12,448 |

all accessions; and a base collection, kept under conditions where the seeds remain viable for up to 100 years, containing ~86% of the total holdings. The active collection is stored in plastic containers in an atmosphere of 0°C and 15–20% relative humidity (RH); the base collection is stored in hermetically (vacuum) sealed aluminum foil packets and kept at –20°C. In addition, a duplicate collection, comprising 96% of the holdings, is housed at ICRISAT and other donor institutes for safety purposes.

## Core and Mini Core Collections and Their Use for Diversity Studies and New Breeding Goals

With the awareness of crop germplasm exploration and collection during the 1970s and later, numerous gene banks were established. At many such places, the numbers of collections are quite large and researchers have not been able to make good use of the germplasm resources. Such vast collections will not be of much use unless the individual accessions are characterized for relevant traits, and summarized and maintained in a user-friendly manner. Some of the traits of agronomic importance are influenced to a great extent by genotype × environments interactions, and require replicated multilocational evaluations.

This is a very costly and resource-demanding task owing to the large size of the germplasm collection. To overcome this, Frankel (1984) proposed sampling of the collection to a manageable sample or 'core collection'. A core collection contains a subset of accessions from the entire collection, which captures most of the available diversity of species (Brown, 1989). Following the concept, a chickpea core collection was developed at ICRISAT, which had 1956 accessions (about 10% of the entire collection), but represented almost the full diversity of ~17,000 accessions of the species (Upadhyaya *et al.*, 2001). Similarly, a chickpea core of 505 accessions was developed from 3350 accessions by the scientists at the USDA–Pullman, Washington (Hannan *et al.*, 1994).

When the size of the entire collection is large, even a core collection becomes unwieldy for evaluation by breeders. To overcome this, ICRISAT scientists developed a two-stage seminal strategy to develop a mini core collection, which consists of 10% accessions of the core collection (only 1% of the entire collection) (Upadhyaya and Ortiz, 2001) and represents the diversity of the entire core collection. The first stage involves developing a representative core subset (about 10%) from the entire collection using all the available information on origin, geographical distribution, and characterization and evaluation data of accessions. The second stage involves evaluation of the core subset for various morphological, agronomic and quality traits, as well as selecting a further subset of about 10% accessions from the core subset. At both stages standard clustering procedure should be used to separate groups of similar accessions. At ICRISAT, the scientists have already developed mini core collections of chickpea consisting of 211 accessions (Upadhyaya and Ortiz, 2001).

Diversity assessment in the core subset: the chickpea core consisting of 1956 accessions had 1465 desi, 433 kabuli and 58 intermediate seed types. This core collection was evaluated for seven morphological and 15 agronomic traits to estimate phenotypic diversity. The three groups differed significantly for flower and plant colour, dots on seed testa, seed testa texture, plant width, days to maturity, pods per plant, 100-seed weight and plot yield. The kabuli and intermediate types were not significantly different for growth habit and seed colour; however, they differed significantly from desi types for both the traits. Desi, kabuli and intermediate types were significantly different for plant width, days to maturity, pods per plant, 100-seed weight and plot yield. Kabuli plants had broader width, matured late, lowest number of pods, highest seed weight and lowest plot yield. The average phenotypic diversity index was highest in the intermediate types (0.2653) and lowest in the kabuli types (0.1490) (Upadhyaya *et al.*, 2002).

Identification of sources for highly useful traits: due to reduced size, the core collection can be evaluated extensively to identify the useful parents for crop improvement. By evaluating core collection of chickpea, we identified new sources of important traits, namely, early maturity (28 accessions) and large-seeded kabuli (16 accessions) types. The core collection was tested for agronomic traits through the yield trials conducted during two seasons (1999–2001) at ICRISAT along with two control cultivars – Annigeri and L 550. The controls were the released cultivars and were well adapted to the region's conditions. The scientists did not expect many germplasm accessions to be found

significantly superior-yielding compared to the controls. However, they found that seven chickpea accessions (ICCs 6122, 8324, 12197, 13124, 14230, 16862 and 16934) were superior in respect to the four important yield traits (days to flowering, pod number, grain yield and 100 seed weight) compared to control Annigeri. Similarly, nine kabuli accessions (ICCs 3410, 5644, 6160, 6246, 7200, 8042, 10755, 10783 and 15763) were superior in respect to the four yield traits mentioned earlier compared to the control L 550 (Table 17.3). The evaluation of chickpea core at Pullman, Washington, revealed high levels of resistance to ascochyta blight and pre-emergence damping-off diseases (Hannan *et al.*, 1994).

To gain benefits, the mini core collection of chickpea was evaluated to identify useful traits for use in crop improvement. From the chickpea mini core, 18 accessions having traits related to drought tolerance (Kashiwagi *et al.*, 2005) and 29 accessions having moderate to high tolerance to soil salinity (Serraj *et al.*, 2004) were identified. Similarly, Pande *et al.* (2005) screened the mini core collection for resistance to various diseases and identified 67 accessions

**Table 17.3.** Chickpea accessions found superior compared to respective desi and kabuli type controls in core collection of chickpea, mean of 1999/2000 and 2000/01 seasons, ICRISAT, Hyderabad, India.

| Accession[a] | Country of origin | Biological status | Days to 50% flowering | Pods per plant | Seed yield (kg/h) | 100-Seed weight (g) |
|---|---|---|---|---|---|---|
| *Desi* | | | | | | |
| ICC 6122 | India | Landrace | 40 | 64 | 1832 | 34.6 |
| ICC 8324 | India | Landrace | 46 | 72 | 2251 | 21.7 |
| ICC 12197 | India | Breeding line | 44 | 72 | 2178 | 28.6 |
| ICC 13124 | India | Landrace | 48 | 53 | 2188 | 33.8 |
| ICC 14230 | India | Landrace | 49 | 55 | 2166 | 33.6 |
| ICC 16862 | India | Landrace | 45 | 74 | 2288 | 25.2 |
| ICC 16934 | India | Landrace | 48 | 72 | 2212 | 23.1 |
| *Kabuli* | | | | | | |
| ICC 3410 | Iran | Landrace | 54 | 65 | 2138 | 21.8 |
| ICC 5644 | India | Landrace | 61 | 60 | 2138 | 23.3 |
| ICC 6160 | Syria | Landrace | 59 | 66 | 1996 | 40.5 |
| ICC 6246 | Tunisia | Landrace | 63 | 68 | 1898 | 21.8 |
| ICC 7200 | Egypt | Breeding line | 62 | 59 | 2171 | 21.5 |
| ICC 8042 | Iran | Landrace | 59 | 55 | 2075 | 30.8 |
| ICC 10755 | Turkey | Landrace | 61 | 58 | 2014 | 31.4 |
| ICC 10783 | Turkey | Landrace | 61 | 60 | 2167 | 35.6 |
| ICC 15763 | Morocco | Landrace | 59 | 69 | 1886 | 26.0 |
| *Control* | | | | | | |
| Annigeri (desi) | India | Cultivar | 50 | 70 | 2057 | 21.3 |
| L550 (kabuli) | India | Cultivar | 63 | 64 | 1858 | 19.9 |

[a]Accessions were significantly superior for yield in all classes except the early group.

resistant or highly resistant to fusarium wilt, 3, 55, and 6 accessions moderately resistant to ascochyta blight, botrytis grey mould and dry root rot, respectively. ICC 11284 was the only accession moderately resistant to both the foliar diseases (ascochyta blight and botrytis grey mould). Four accessions were found with combined resistance to dry root rot and fusarium wilt, and 15 accessions to fusarium wilt and botrytis grey mould. The evaluation of chickpea mini core at the Indian Institute of Pulses Research (IIPR), Kanpur, India during 2002/04 revealed 12 very promising accessions. Of these, six accessions, namely ICCs 14194, 14196, 14197, 14199, 12034 and EC 381882, were involved in hybridization to develop large-seeded kabuli types.

Researchers at the ICRISAT with those at the ICARDA have developed a global composite collection of 3000 accessions (Table 17.4) that will be molecular profiled using 50 polymorphic simple sequence repeat (SSR) markers (Upadhyaya *et al.*, 2006). The data generated will be used to define the genetic structure of the global composite collection and to select a reference sample of 300 accessions representing the maximum diversity for the isolation of allelic variants of candidate gene associated with beneficial traits. It is then expected that molecular biologists and plant breeders will have opportunities to use diverse lines in functional and comparative genomics, in mapping and

**Table 17.4.** Characteristics of germplasm included in global composite collection of chickpea.

| Germplasm/ traits | Number of accessions | Germplasm/ Traits | Number of accessions | Germplasm/ traits | Number of accessions |
|---|---|---|---|---|---|
| ICRISAT collection | | ICRISAT-collection | | ICRISAT collection | |
| Core collection | 1956 | Tolerance to leaf miner | 5 | Large seed size | 18 |
| Cultivars/ breeding lines | 39 | Resistance to nematode | 8 | Double pods | 8 |
| Resistance to ascochyta blight | 13 | Tolerance to cold | 12 | High seed protein | 10 |
| Black root rot | 8 | Heat | 4 | Morphological diversity | 35 |
| Botrytis grey mould | 8 | Drought | 10 | Wild *Cicer* spp. | 3 |
| Collar rot | 9 | Salinity | 4 | ICARDA collection | |
| Dry root rot | 6 | I Input responsive | 4 | Characterization and evaluation data | 212 |
| Fusarium wilt | 50 | High BNF | 8 | Random selection | 497 |
| Stunt | 8 | Early maturity | 25 | Wild *Cicer* spp. | 17 |
| Tolerance to pod borer | 16 | Multiseeded pods | 7 | Total | 3000 |

cloning gene(s), and in applied plant breeding to diversify the genetic base of the breeding populations, which will lead to the development of broad-based elite breeding lines/cultivars with superior yields and enhanced adaptation to diverse environments

## Conservation and Documentation

### Storage

Conservation of *Cicer* is almost wholly as seed, from annuals and also the wild perennials.

The principal conservers of diversity are as outlined earlier, the ICRISAT and ICARDA gene banks, and national gene banks in various countries from the Middle East centre of origin to Russia and the USA. However national breeding programmes in many countries have also associated working collections kept for short to medium term utility, in which storage conditions may not be as stringent for maintenance of viability as in major gene banks.

Viability will decline in all stored seed, as a function of initial viability, seed moisture and storage temperature (Roberts and Ellis, 1984). Seed harvest, drying, processing, and pre-storage temperature and humidity conditions may all affect the initial viability, which is usually close to 100% for freshly harvested seed from well-grown plants. Each seed lot has a viability constant, affected by both genotype and pre-storage conditions, which affects seed longevity. Seed survival curves conform to a negative cumulative normal distribution, which are transformed to straight line slopes with probit percentage viability plotted against time (Roberts and Ellis, 1984). They report that this slope is unaffected by either genotype within species or pre-storage conditions, but is affected by logarithmic constants for seed moisture, temperature and species. This enables seed longevity to be predicted for given storage conditions and initial viability, within a wide range of operational storage conditions from ambient to various levels of reduced temperature and seed moisture within biological limits (seeds will die if completely desiccated). With regular storage at 5 ± 1% seed moisture and within a temperature of –20°C and –30°C, the occurrence of mutations during storage appears to be a very minor concern (Roberts and Ellis, 1984).

The recommended storage facilities for gene banks (FAO/IPGRI, 1994), would contain a base collection of more than 100 seeds (FAO/IPGRI recommend more than 1000 seeds) in –18°C to –20°C, and an active collection of up to 1000 seed at 2–5°C, respectively for long-term conservation, and for immediate usage and distribution. Drying of seed before storage at 10–25°C and 10–15% RH is recommended. The base collection should aim to maintain the genetic integrity of the seed samples of accessions as originally received and enable long-term conservation of genetic diversity. It is also used to replenish seed stocks in the active collection in every fourth regeneration cycle (FAO/IPGRI, 1994). A duplicate collection kept in long-term storage is also recommended for safety purposes, also referred to as a back-up collection.

Further investigation of chickpea seed longevity is in progress at the Australian Temperate and Field Crops Collection (ATFCC) with storage trials of two genotypes at five different temperatures (40°C, 22°C, 15°C, 2°C and −18°C) and three seed moisture levels (6–7%, 10–11%, 12–13%) begun with seed harvest in December 2002, postharvest storage at 15°C, and initiation of treatments in February 2003 (Redden, Horsham, 2006, personal communication). An additional eight genotypes are being tested at 22°C. This study will examine whether the seed moisture and temperature storage constants for *Cicer* are invariant for genotype and conform to a logarithmic formula. Only the 40°C treatments have run the course from full viability to termination, and of themselves do not provide enough data to test the predictions, though initial indications are for genotypic variation and for greater longevity than predicted.

Such longevity studies are important to enable better planning of intervals between regeneration cycles and to reduce the staff as well as physical resources required to otherwise monitor seed viability with germination tests. Seed in the active collection may possibly retain high viability for at least 20 years, given high initial viability, seed desiccation and immediate deposit in active storage. Optimization of storage conditions is a cheap and efficient means of extending seed longevity, thereby lengthening the regeneration intervals and reducing the annual costs for maintenance of high levels of seed viability in the active collections.

Seeds should be stored in moisture-proof containers; heat sealing of plastic lined foil envelopes is one of the common gene banks procedures. Opening and resealing of these packets for seed removal and distribution is best carried out in a drying room, such as 15°C and 15% RH as described earlier.

A decision guide for seed regeneration, and precautions to maintain genetic integrity are outlined by Sackville Hamilton and Chorlton (1997).

## Documentation

There are three main activities, described in the IPGRI handbook for germplasm collections (Reed *et al.*, 2004):

**1.** Germplasm and site characterization (passport) for an accession collected as a traditional landrace *in situ*, for placement in an *ex situ* gene bank elsewhere;
**2.** Gene bank inventory with accession identifiers, taxonomic descriptors, country and site passport data, dates of accession, collector and donor details, synonyms for accessions acquired from other gene banks;
**3.** Accession characterization data in the case of chickpea standard trait descriptors are provided in IBPGR/ICRISAT and ICARDA, 1993.

Full records are very important for checking through synonyms for duplication of accessions, precise collection site data with referencing by latitude, longitude and altitude if possible, and for quality assurance on identity. This can be an issue in gene banks with multiple sources of accessions, and large numbers of accessions and species.

Equally important are characterization and evaluation data. Better targeted and more efficient utilization of germplasm by plant breeders and researchers can be achieved if the trait characteristics of accessions are known. This can include the agronomic, disease reaction, yield and quality data of accessions in a particular study, and over the different studies for each accession. These data can now be retrieved with International Crop Information Systems (ICIS) platforms for digital search and retrieval across relational databases for all relevant studies. An example is the ICIS evaluation database for chickpea, which combines databases of the ICARDA, ICRISAT, USDA and ATFCC enabling a more comprehensive search of genetic resources over large collections for multiple trait expressions, is available at: http://www.iris.irri.org/ranjanweb/SiteMain.jsp.

A number of gene banks provide well-documented and up-to-date taxonomic guides for the *Cicer* genus, e.g. the germplasm resources information network (GRIN) database of the USDA, available at: http://www.ars-grin.gov/cgi-bin/npgs/html/genform.pl

Taxonomic classifications may differ between gene banks; some may tend to split species into subspecies in comparison with GRIN, which describes alternative nomenclature.

## Germplasm Enhancement

Pre-breeding describes the transfer of desirable traits from exotic germplasm into elite breeding lines, whereas germplasm enhancement describes this activity as a process in the context of utility and sustainability of crops. In practice, germplasm enhancement is a long-term undertaking to utilize traits from unadapted and even wild germplasm sources to obtain traits that are not available in elite or domesticated lines. Most work in this area is carried out by public plant breeders and scientists because a private investment in the generation of enhanced germplasm is not profitable in the short term (Ortiz, 2002).

For chickpea, most germplasm enhancement has been carried out by the ICRISAT and ICARDA. Large-scale characterization and evaluation of chickpea germplasm collections (Singh and Malhotra, 1984a,b) has resulted in the publication of informative and detailed catalogues (Pundir *et al.*, 1988; Singh *et al.*, 1991; Robertson *et al.*, 1995). Much early work was focused on improving disease resistance, cold tolerance and the introgression of desi germplasm into the less diverse kabuli gene pool (Singh and Reddy, 1991; Singh, 1993). Germplasm developed from these activities is distributed annually through international nurseries to national breeding programmes. This has facilitated the use of enhanced germplasm in many countries. In fact, this material helped to revive the Australian kabuli industry after the devastating ascochyta blight epidemic of 2001, since resistant germplasm could be readily identified in the previous year's international nursery growing under epidemic conditions, near Horsham in 2001 (T. Bretag, Horsham, 2005, personal communication). International nurseries have become the predominant source of new germplasm in the Australian breeding programme for kabuli chickpea (K. Hobson, personal communication).

Since publication of the last monograph on chickpea (van der Maesen, 1973; Saxena and Singh, 1987), great advances have been made in the identification of chickpea germplasm with useful traits. Recent work has led to refinement of standardized methods for *Ascochyta* screening by development of differential tester sets (Chen *et al.*, 2004) and identification of tolerance to *Meloidogyne javanica* (Ansari *et al.*, 2004).

Molecular DNA marker technology is gaining quickly in resolution, much of it owing to syntenic genetic relationships with other crops for which genomic libraries are being developed. Genomic sequence resources facilitate the generation and testing of increasing numbers of DNA markers to map traits of interest with more precision (Winter *et al.*, 2003). The increasing availability of molecular markers promises to speed up the identification of useful traits during germplasm enhancement. For example, Sharma *et al.* (2004) identified DNA markers for *Fusarium oxysporum* f. sp. *ciceris* race 3 resistance. The establishment of sufficiently high throughput and cost-effective molecular breeding programmes still awaits realization. In anticipation of such future activity, several recent and current germplasm enhancement projects include a molecular marker component (Santra *et al.*, 2000).

Efforts are also being made to improve the utilization of the wild gene pool. Ever since useful disease and abiotic stress resistances were identified in the secondary and tertiary gene pool of chickpea, there has been a recognized need to transgress infertility barriers to facilitate the transfer of such traits to cultivated chickpea. Wild species are increasingly recognized as worthwhile sources of biotic and abiotic stress tolerance with recent releases of desi cultivars in India demonstrating that productive genotypes can be developed from wide crosses (Yadav *et al.*, 2006).

Following initial genetic characterization of wild species (Nguyen *et al.*, 2004) their exploitation for reproductive cold tolerance is a priority in Australia (H. Clarke, Perth, 2005, personal communication). While the availability of unique wild germplasm in *ex situ* collection is very limited (Berger *et al.*, 2003), existing resources are receiving attention as potential donors of useful traits such as resistance to *H. armigera* (Sharma *et al.*, 2005).

At present, a project in Horsham is aiming to identify tolerance to elevated levels of subsoil Boron and to develop enhanced germplasm for salinity tolerance utilizing accessions identified by Maliro *et al.* (2004), additional sources identified using eco-geographic principles and continued systematic screening of germplasm.

## References

Ansari, M.A., Patel, B.A., Mhase, N.L., Patel, D.J., Douaik, A. and Sharma, S.B. (2004) Tolerance of chickpea (*Cicer arietinum* L.) lines to root-knot nematode, *Meloidogyne javanica* (Treub) Chitwood. *Genetic Resources and Crop Evolution* 51, 449–453.

Brown, A.H.D. (1989) Core collections: a practical approach to genetic resources management. *Genome* 31, 818–824.

Berger, J., Abbo, S. and Turner, N.C. (2003) Ecogeography of annual wild *Cicer* species: the poor state of the world collection. *Crop Science* 43, 1076–1090.

Chen, W., Coyne, C.J., Peever, T.L. and Muehlbauer, F.J. (2004) Characterization of chickpea differentials for pathogenicity assay of Ascochyta blight and identification of chickpea accessions resistant to *Didymella rabiei*. *Plant Pathology* 53(6), 759–769.

FAO/IPGRI (1994) Genebank Standards. Food and Agriculture Organization of the United Nations, Rome, International Plant Genetic Resources Institute, Rome.

Frankel, O.H. (1984) Genetic perspectives of germplasm conservation. In: Arber, W., Llimensee, K., Peacock, W.J. and Starliger, P. (eds) *Genetic Manipulations: Impact of Man and Society*. Cambridge University Press, Cambridge, pp. 161–170.

Hannan, R.M., Kaiser, W.J. and Muehlbauer, F.J. (1994) Development and utilization of the USDA chickpea germplasm core collection. *1994 Agronomy Abstracts*. American Society of Agronomy, Madison, Wisconsin, p. 217.

IBPGR/ICRISAT and ICARDA (1993) Descriptors for chickpea (*Cicer arietinum* L.). International Board for Plant Genetic Resources, Rome, Italy.

Iruela, M., Rubio, J., Cubero, J.I., Gil, J. and Millan, T. (2002) Phylogenetic analysis in the genus *Cicer* and cultivated chickpea using RAPD and ISSR markers. *Theoretical and Applied Genetics* 104, 643–651.

Kashiwagi, J., Krishnamurthy, L., Upadhyaya, H.D., Krishna, H., Chandra, S., Vandez, V. and Serraj, R. (2005) Genetic variability of drought-avoidance root traits in the mini-core germplasm collection of chickpea (*Cicer arietinum* L.). *Euphytica* 146, 213–222.

Malhotra, R.S., Pundir, R.P.S. and Kaiser, W.J. (2000). *Cicer* species – conserved resources, priorities for collection and future prospects. In: Knight, R. (ed.) *Linking Research Marketing Opportunities for Pulses in the 21st Century*. Kluwer Academic, Dordrecht, The Netherlands, pp. 603–611.

Maliro, M.F.A., McNeil, D., Kollmorgen, J., Pittock, C. and Redden, R.J. (2004) Screening chickpea (*Cicer arietinum* L.) and wild relatives germplasm from diverse country sources for salt tolerance. In: *Proceedings of the 4th International Crop Science Congress*. 26 September–1 October 2004. Brisbane, Australia, p. 274.

Moreno, M. and Cubero, J.I. (1978) Variation in *Cicer arietinum* L. *Euphytica* 27, 465–485.

Nguyen, T.T., Taylor, P.W.J., Redden, R.J. and Ford, R. (2004) Genetic diversity estimates in *Cicer* using AFLP analysis. *Plant Breeding* 123, 173–179.

Ortiz, R. (2002) Germplasm enhancement to sustain genetic gains in crop improvement. In: Engels, J.M.M., Ramanatha Rao, V. and Jackson, M.T. (eds) *Managing Plant Genetic Diversity*. IPGRI, Rome, pp. 275–290.

Pande, S., Kishore, G.K., Upadhyaya, H.D. and Rao, J.N. (2005) Identification of sources of multiple fungal diseases resistance using mini-core collection in chickpea. *Plant Disease* 90, p. 1024.

Pundir, R.P.S., Reddy, K.N. and Mengesha, M.H. (1988) *ICRISAT Chickpea Germplasm Catalog: Evaluation and Analysis*. ICRISAT, Hyderabad, India.

Reed, B.M., Engelmann, F., Dulloo, M.E. and Engels, J.M.M. (2004) *Technical Guidelines for the Management of Field and In Vitro Germplasm Collections*. IPGRI Technical Handbook No 7.

Roberts, E.H. and Ellis, R.H. (1984) The implications of the deterioration of orthodox seeds during storage for genetic resources conservation. In: Holden, J.H.W. and Williams, J.T. (eds) *Crop Genetic Resources: Conservation and Evaluation*. Gheorge Allen & Unwin, London, pp. 18–37.

Robertson, L.D., Singh, K.B. and Ocampo, B. (1995) *A Catalog of Annual Wild Cicer Species*. ICARDA, Aleppo, Syria.

Sackville Hamilton, N.R. and Chorlton, K.K. (1997) Regeneration of accessions in seed collections: a decision guide. In: Engels, J. (ed.) *Handbook for Genebanks*, No 5. International Plant Genetic Resources Institute, Rome, Italy, pp. 1–72.

Santra, D.K., Takeoglu, M., Ratnaparkhe, M., Kaiser, W.J. and Muehlbauer, F.J. (2000) Identification and mapping of QTLs conferring resistance to Ascochyte blight in chickpea. *Crop Science* 40, 1606–1612.

Saxena, M.C. and Singh, K.B (1987) *The Chickpea*. CAB International, Wallingford, UK.

Serraj, R., Krishnamurthy, L. and Upadhyaya, H.D. (2004) Screening of chickpea mini-core germplasm for tolerance to soil salinity. *International Chickpea and Pigeonpea Newsletter* 11, 29–32.

Sharma, H.C., Pampapathy, G., Lanka, S.K. and Ridsdill-Smith, T.J. (2005) Antibiosis mechanism of resistance to pod borer, *Heliocoverpa armigera* in wild relatives of chickpea. *Euphytica* 142, 107–117.

Singh, K.B. (1993) Problems and prospects for stress resistance breeding in chickpea. In: Singh, K.B. and Saxena, M.C. (eds) *Breeding for Stress Tolerance in Cool-Season Food Legumes*. Wiley, Chichester, UK, pp. 17–35.

Singh, K.B. and Malhotra, R.S. (1984a) Collection and evaluation of chickpea genetic resources. In: Witcombe, J.R. and Erskine, W. (eds) *Genetic Resources and Their Exploitation – Chickpeas, Faba Beans and Lentils*. Martinus Nijhoff/Dr W. Junk Publishers (for ICARDA and IBPGR), The Hague, Boston, Lancaster, pp. 105–122.

Singh, K.B. and Malhotra, R.S. (1984b) Exploitation of chickpea genetic resources. In: Witcombe, J.R. and Erskine, W. (eds) *Genetic Resources and Their Exploitation – Chickpeas, Faba Beans and Lentils*. Martinus Nijhoff/Dr W. Junk Publishers (for ICARDA and IBPGR), The Hague, Boston, Lancaster, pp. 123–130.

Singh, K.B. and Reddy, M.V. (1991) Advance in disease-resistance breeding in chickpea. *Advances in Agronomy* 45, 191–222.

Singh, K.B., Holly, L. and Beijiga, G.A. (1991) A catalog of kabuli chickpea germplasm. ICARDA, Aleppo, Syria.

Sharma, K.D., Winter, P., Kahl, G. and Muehlbauer, F.J. (2004) Molecular mapping of *Fusarium oxysporum* f. sp. *Ciceri* race 3 resistance gene in chickpea. *Theoretical and Applied Genetics* 108, 1243–1248.

Upadhyaya, H.D. (2003) Geographical patterns of variation for morphological and agronomic characteristics in the chickpea germplasm collection. *Euphytica* 132, 343–352.

Upadhyaya, H.D. and Ortiz, R. (2001) A mini core subset for capturing diversity and promoting utilization of chickpea genetic resources. *Theoretical and Applied Genetics* 102, 1292–1298.

Upadhyaya, H.D., Bramel, P.J. and Singh, S. (2001) Development of a chickpea core subset using geographic distribution and quantitative traits. *Crop Science* 41, 206–210.

Upadhyaya, H.D., Furman, B.J., Dwivedi, S.L., Udupa, S.M., Gowda, C.L.L., Baum, M., Crouch, J.H., Buhariwalla, H.K. and Sube Singh (2006) Development of a composite collection for mining germplasm possessing allelic variation for beneficial traits in chickpea. *Plant Genetic Resources: Characterization and Utilization* 4(1), 13–19.

Upadhyaya, H.D., Ortiz, R., Bramel, P.J. and Sube Singh. (2002). Phenotypic diversity for morphological and agronomic characteristics in chickpea core collection. *Euphytica* 123, 333–342.

van der Maesen, L.J.G. (1973) *Cicer* L.: a monograph of the genus, with special reference to the chickpea (*Cicer arietinum* L.), its ecology and cultivation. Communication Agricultural University, Wageningen, The Netherlands, 72(10), 342 pp.

Yadav, S.S., Kumar, J., Turner, N.C., Berger, J., Redden, B., McNeil, D., Materne, M., Knights, T. and Bahl, P.N. (2006) Recent developments in breeding for wide adaptation and drought tolerance in grain legumes. *Plant Genetic Resources* 4(3) 181–187.

Winter, P., Staginnus, C., Sharma, P.C. and Kahl, G. (2003) Organisation and genetic mapping of the chickpea genome. In: Jaiwal, P.K. and Singh, R.P. (eds) *Improvement Strategies of Leguminosae Biotechnology – Focus on Biotechnology*, Vol. 10A. Springer, Berlin, pp. 303–352.