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REVIEW

# Breeding for biotic stress resistance in chickpea: progress and prospects

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**Abstract** Chickpea (*Cicer arietinum* L.) is the third most economically important food legume in the world. Its yield potential is often limited by various biotic stresses, including fungal and viral diseases, insects, nematodes and parasitic weeds. Incorporating genetic resistance into cultivars is the most effective and economical way of controlling biotic stresses and this is a major objective in many breeding programs. Extensive searches for resistances have been conducted by screening commercial varieties, landraces and closely related species. Resistances to disease such as Ascochyta blight and Fusarium wilt have been identified and molecular tools are being used to increase the efficiency of gene transfer from wild species into chickpea elite genotypes. Quantitative trait loci for resistance genes have been located on linkage maps and molecular markers associated with these loci can potentially be used for efficient pyramiding of the traits. Significant chickpea genomic resources have been developed in order to investigate resistance genes. Such resources include an integrated genetic map, expressed sequence tag libraries, bacterial artificial chromosome libraries, microarrays and draft genome sequences. Although these resources have yet to be used to improve chickpea cultivars in the field, this is likely to change in the near future. These genomic resources, as well as high-resolution phenotyping tools and cutting-edge technologies such as next-generation sequencing, promise to increase efficiency as work to identify valuable candidate genes continues.

**Keywords** *Cicer arietinum* · Fungi · Virus · Insects · Nematodes · Molecular tools

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## Introduction

Chickpea is the world's third most important food legume after peas (*Pisum sativum* L.) and beans (*Phaseolus vulgaris* L.) (Saxena 1990). It is cultivated in over 50 countries, with a total area of 12.14 million hectares and annual production of 11.30 million tons (FAOSTAT 2012). It is often grown in rotation with other crops as a disease break and helps maintain soil fertility by fixing atmospheric nitrogen (Singh 1997). Chickpea is a highly nutritious grain with its seeds containing 20–30 % protein, 40 % carbohydrate and 3–6 % oil (Gil et al. 1996). It provides a high-quality protein source for people in both developed and developing countries (Deb and Khaleque 2009). The stover of chickpea is also fed to some animals as a nutrient-rich supplement to their major cereal fodder in lean seasons (Deb and Khaleque 2009).

Global chickpea production is affected by major biotic stresses, including fungal, bacterial and viral diseases, insect pests, nematodes and parasitic weeds. Incorporating genetic resistance into the crop is the most economically efficient way of controlling biotic stresses (Rubiales and Fondevilla 2012). Many of the major chickpea biotic stresses have been overcome by developing enhanced resistance in elite cultivars. However, there are still a number of biotic stresses for which no resistance has been identified. This review focuses on the progress that has been made to breed resistance to major biotic stresses and the future prospects of using molecular tools to assist chickpea breeding.

## Origin and genetic diversity

Chickpea is in the family Fabaceae (or Leguminosae) and the tribe Cicereae Alef (van der Maesen 1987) and is the only cultivated species of the *Cicer* genus. Domestication of chickpea, along with wheat, pea and lentils (Redden and Berger 2007), dates back 10,000–12,000 years in the Fertile Crescent of Iran, Turkey and Israel/Jordan. Three secondary centers of diversity are Ethiopia (plus the Mediterranean west from Greece/Crete), central Asia to the Indian subcontinent and Asia Minor to Iran and the Caucasus. Further distribution to the Americas and Australia occurred after European contact in these areas. The Desi type, with a small triangular seed, is the oldest type, with the larger round "rams head" Kabuli type being domesticated later in the Mediterranean region. The Kabuli type has narrower genetic diversity, geographic distribution and morphological variation (Redden and Berger 2007).

The domestic gene pool of chickpea is narrower than that of wheat, pea or lentil due to (i) the limited adaptive genetic variation of the wild progenitor *Cicer reticulatum* (only found in southeast Turkey), (ii) the genetic bottleneck of domestication, in which only a limited range of variants were selected, and (iii) a further selection for spring habit with loss of vernalization. As a result, chickpea has little genetic diversity for disease resistance (Abbo et al. 2007). However, the wild relatives of chickpea can increase the genetic diversity of this crop by providing a wider range of ecotypes that contain sources of pest and disease resistance (Redden and Berger 2007).

The wild relatives of chickpea have a wide geographic distribution, ranging from sea level (*C. judiacum*) to 5000 m (*C. microphyllum*), and from central Asia and India to the Canary Islands (Abbo et al. 2007). *C. pinnatifidum* is an annual with the widest distribution, being found from Armenia to the eastern Mediterranean, while other annuals are restricted to smaller areas. For example, *C. judiacum* is only found in Israel-Palestine, *C. cuneatum* at medium—high elevation in Ethiopia, Egypt and Saudi Arabia and *C. yamashitae* being restricted to Afghanistan (Van der Maesen et al. 2007).

The perennial wild relatives grow in terrain ranging from rocky slopes to forests, with *C. anatolicum*, *C. incisum*, *C. microphyllum* and *C. montbrettii* being widely distributed variously from the Balkans, to the eastern Mediterranean region and eastwards to Asia (Abbo et al. 2007; Van der Maesen et al. 2007). Although the tertiary gene pools of the perennial and annual species are genetically equally separated from the domestic gene pool (Nguyen et al. 2004), the annual wild relatives have been more widely studied as potential sources of disease resistance genes in comparison with the perennials (Singh et al. 2007).

A genetic diversity study in *Cicer* based on crossibility, karyotype, isozyme polymorphism, seed protein and RAPD analysis has demonstrated a close genetic relationship among *C. arietinum*, *C. reticulatum* and *C. echinospermum* which formed a primary crossibility group (Ahmad 1999). This was supported by an analysis of the external transcribed sequence

(ETS) of 18s rRNA sequences (Fig. 1). The ETS data also indicated a close association of the cultivated *C. arietinum* to *C. bijugum*, *C. judaicum* and *C. pinnatifidum*, which may infer that these species also played a role in the evolution of the cultivated species. This conclusion contradicted the previous finding of AFLP analysis (Nguyen et al. 2004), but is in agreement with a more recent study by van der Maesen et al. (2007). There has been limited success in crossing *C. bijugum*, *C. judaicum* and *C. pinnatifidum* with species in the primary crossibility group (Singh et al. 1994; ICARDA 1998), however, tissue culture methods such as embryo rescue techniques may provide the means to overcome crossability barriers to produce wide and interspecific hybridizations in the future (Badami et al. 1997). Furthermore *C. judaicum*, *C. bijugum* and particularly *C. pinnatifidum* possess very high levels of genetic diversity and were reported as sources of resistance or tolerance to biotic and abiotic stresses (Singh et al. 1998a, b) and therefore offer great potential as sources of resistance for the future of chickpea breeding.

## Genetic resources for resistance breeding

Most of the genetic resources for chickpea are in *ex situ* genebanks. The two main genebanks are the

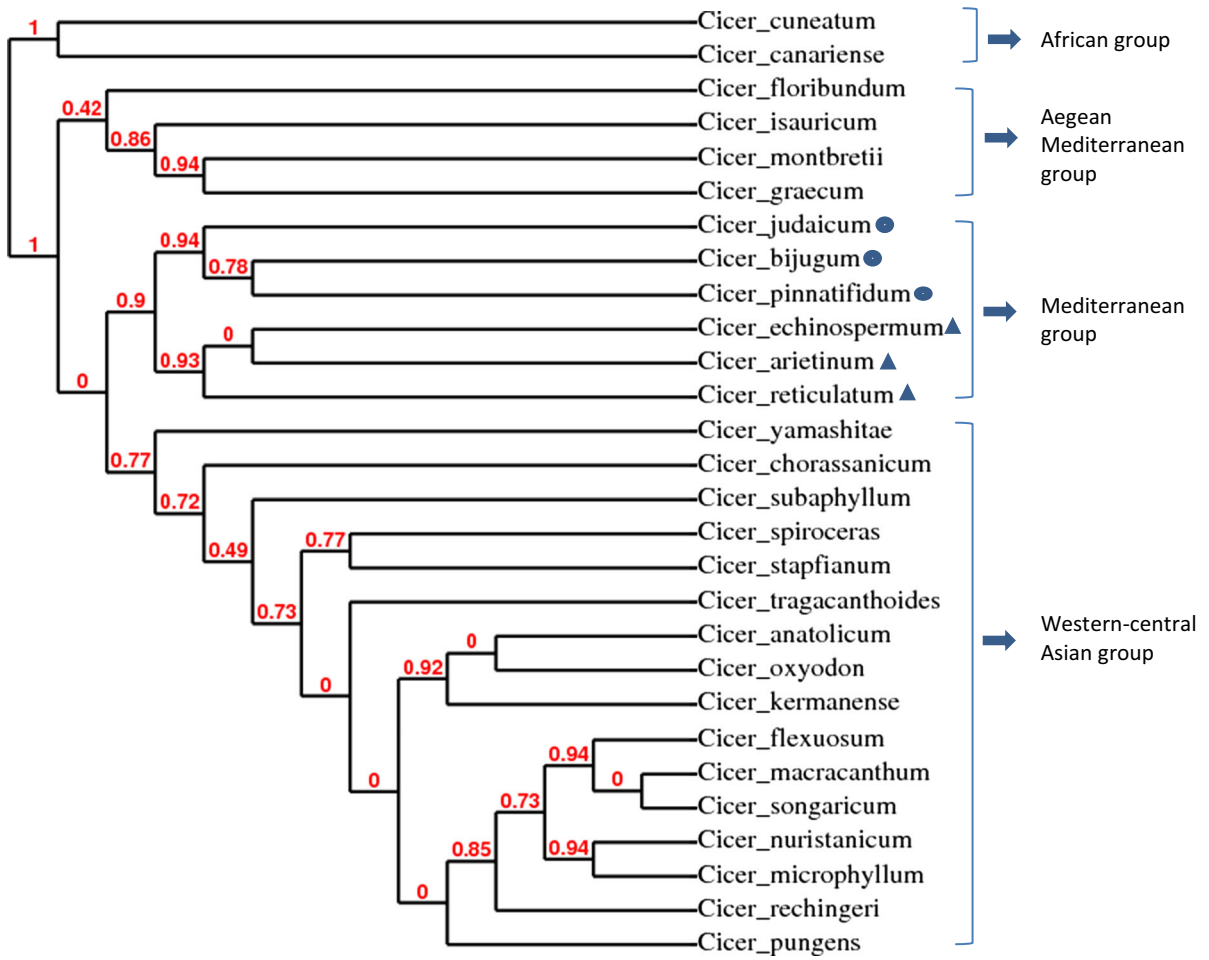


**Fig. 1** Distribution and phylogeny of 28 cicer species based on the partial sequence of 18s rRNA gene. *Filled triangle* represents the *Cicer* species with least distance to cultivated chickpea and composed the primary crossibility group; *filled circle* represents some annual species with close distance and potential crossibility to cultivated chickpea. The 18s rRNA sequences were sourced from NCBI data base and the dendrogram tree was generated using a robust phylogeny analysis method (Dereeper et al. 2008)

International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) in India with over 20,000, mainly Desi, accessions, and the International Center for Agricultural Research in the Dry Areas (ICARDA) in Syria with 13,800, mainly Kabuli, accessions. These collections are mainly traditional landraces, seed-lots derived from material that has evolved over centuries of selection in farmers fields. In addition to these genebanks, there are other important collections in India (16,000), the US Department of Agriculture (6200), Iran (5600), the Aegean Agricultural Research Institute in Turkey (2000), the Vavilov Institute in St. Petersburg (2600), and the Australian Grains Genebank in Horsham, Australia (9300 accessions). In addition, other collections exceeding 1000 accessions are in the Ukraine, Spain, Portugal, Ethiopia and Hungary (Guarino 2008). The majority of these collections consist of over 50 % landraces. Many countries around the Fertile Crescent and in central Asia have small collections with limited representation of both landraces and wild relatives (Guarino 2008).

Wild relatives of *C. arietinum* are generally under-represented in the genebank collections, even though they are genetically rich in comparison to the landrace collections. The level of duplication between collections is unclear, since many accessions have been shared between collections. For example, the world collection of annual wild *Cicer* species only consists of 593 entries held in nine genebanks around the world, with 285 being known as separate accessions of 8 wild species (Berger et al. 2003; Ahmad et al. 2005).

## Breeding for fungal disease resistance

Fungal diseases are the most important biotic stresses limiting grain production in chickpea. There are up to 172 pathogens that attack chickpea, of which 67 are fungal species. The most important diseases of chickpea are Ascochyta blight (AB), Botrytis grey mould (BGM), Fusarium wilt, Phytopthora root rot, dry root rot, Sclerotinia stem rot and rust (Singh et al. 2003a, b; Ahmad et al. 2005; Singh et al. 2007; Knights et al. 2008).

### Ascochyta blight

AB, caused by *Ascochyta rabiei* (Pass.) Labr. (teleomorph, *Didymella rabiei* (Kov.) v. Arx), is a severe disease in most chickpea-growing regions of the world. *A. rabiei* can infect all above-ground plant parts, and symptoms can appear any time after crop emergence. AB first appears as grey areas on the leaves, stems or pods that quickly turn into brown lesions with dark borders. As the disease progresses, small, circular, brown-black pycnidia develop in the center of the lesions. Concentric rings of pycnidia are the most diagnostic characteristic of the disease (Markell et al. 2008) (Fig. 2). Cool wet conditions (15–25 °C, 65–100 % RH) normally favour disease development and spread. The disease can significantly reduce seed quality and complete yield loss under heavy infection has been recorded (Davidson et al. 2004; Pande et al. 2005).

Considerable efforts have been made to develop screening methods to identify genetic resistance to AB in chickpea. Both controlled environment and field screening methods are being used to identify resistant genotypes. Temperature and relative humidity are critical factors in artificial disease establishment. A high level of relative humidity during the first 24 h post-inoculation is critical. Growth chambers where relative humidity can be controlled are useful, however additional steps, such as use of foggers or mist irrigation immediately after inoculation can help maintain relative humidity at high levels and ensure successful infection (Udupa and Baum 2003; Chen et al. 2005). Spore concentration in the inoculum is also a significant factor, with the ideal level being the lowest spore concentration that causes sufficient disease in a majority of host genotypes. This facilitates the greatest discrimination among the lines in a trial.

Field screening techniques for AB resistance in chickpea were initially developed by Singh et al. (1981). Screening was carried out in areas where the prevailing weather conditions were conducive to the development of disease and preferably where natural inoculum is abundant. The procedure consists of planting susceptible check plants every two or four tested entries, scattering infected plant debris collected in the previous season, maintaining high humidity through sprinkler irrigation, and, if needed, spraying the test entries with a spore suspension of a virulent isolate or mixture of isolates of *A. rabiei*. A resistant check was included in order to compare resistance of test entries with that of known resistant material.

Despite the availability of screening methods, variation in the reporting of races and pathotypes of


**Fig. 2** Typical symptoms of some fungal diseases in chickpea. **a** Ascochyta blight. Note symptoms of leaf and pod infection (Image courtesy Hollaway et al. 2012); **b** Botrytis grey mould. Note fluffy, grey spore mass on the infected pod (Image courtesy Hollaway et al. 2012); **c** Sclerotinia stem rot. Note white mycelial growth starting to develop on infected stem (Image courtesy Hollaway et al. 2012); **d** Chickpea rust. Note the small, round, brown pustules on infected leaves (Image provided by Dr Pedro Manjarrez-Sandoval from University of Arkansas); **e** Fusarium wilt. Note wilting of whole plant (Image courtesy Cunnington et al. 2007); **f** Phytophthora root rot. Note lack of lateral roots and discoloured root tissue (Image courtesy Hollaway et al. 2012); **g** Dry root rot. Note lack of lateral roots (Image provided by Professor Robert Harveson from University of Nebraska–Lincoln)

*A. rabiei* has made it difficult to compare results consistently across resistance studies (Vir and Grewal 1974; Qureshi and Alam 1984; Reddy and Kabbabeh 1985; Porta-Puglia et al. 1996; Udupa et al. 1998; Jamil et al. 2000; Chongo and Gossen 2003; Bayaa et al. 2004; Chongo et al. 2004). Classification of pathotypes is currently based on testing isolates against a set of host genotypes that have different resistance to the aggressiveness of the pathogen. Reddy and Kabbabeh (1985) reported six races of *A. rabiei* from Syria and Lebanon using six chickpea differentials, while 13 chickpea genotypes were used to cluster the 41 *A. rabiei* isolates into 3 pathogenic groups (Porta-Puglia et al. 1996). By using ILC1929 (susceptible), ILC 482 (moderately resistant) and ILC 3279 (highly resistant), Udupa et al. (1998) classified

53 Syrian isolates into three pathotypes: pathotype I (least aggressive), pathotype II (aggressive) and pathotype III (most aggressive). Jamil et al. (2000) investigated the response of 130 isolates using a similar classification system. A differential set of chickpeas (Sanford, CDC Frontier, Amit, ILC 3856, ICC 4200, ICC 4475 and UC 27) was used by Chongo et al. (2004) who identified 14 different pathotypes based on their responses to the differential set. Chen et al. (2004) further suggested that these could also be assigned to two classes: pathotype I (less aggressive) and pathotype II (aggressive). In short, the attempts to classify virulence in *A. rabiei* have been inconclusive because of the variable number of categories proposed by different studies, the lack of reproducibility of disease phenotypes among laboratories and the lack of comparable standard check cultivars or pathotypes (Peever et al. 2012). In addition, the number of pathotypes identified may be an artefact of the pathogen mating system or sampling (Caten 1987), as two mating types have been reported that enable sexual recombination in *A. rabiei*. It has been difficult to correlate the mating types with different pathogenic groups, and it is unclear what the differences in pathogenicity between locations actually mean (Pande et al. 2005).

Evaluation of chickpea germplasm has shown that only 2 out of 6594 Kabuli chickpeas and 3 out of 12,749 Desi chickpeas were identified as resistant to *Ascochyta rabiei*, none of the 19,343 germplasm accessions evaluated were found immune or highly resistant (Reddy and Singh 1984, 1992). However, some accessions of the wild *Cicer* species such as *C. bijugum*, *C. echinospermum*, *C. pinnatifidum*, *C. reticulatum* were classified as resistant to AB, especially two *C. echinospermum* accessions, having good resistance (Collard et al. 2001) and being cross-compatible with *C. arietinum*, could provide valuable sources of resistance (Singh and Reddy 1993; Ahmad and Slinkard 2004). Tertiary wild accessions also contain sources of resistance with the *C. judiacum* accession ATC 46934 showing resistance to AB 21 days after inoculation (Nguyen et al. 2004). Four other *C. judiacum* accessions and one *C. pinnatifidum* were also resistant 14 days after inoculation in this study. Two of the *C. judiacum* accessions were also resistant in a study by Haware et al. (1992). Screening of wild accessions at ICRISAT revealed five accessions of *C. judiacum* that were resistant (Pande et al. 2006a, b). Some new sources of resistance to AB have been identified in chickpea breeding lines at ICRISAT (Pande et al. 2010). The feasibility of introgression from the tertiary to the domestic gene pool is a research focus at ICRISAT, and access to these novel sources of resistance (Table 1) is an important priority for chickpea breeders (Singh and Ocampo 1993; Mallikarjuna 1999).

Classic genetic studies of AB resistance have shown it to be governed by single dominant genes in Desi cultivars (Hafiz and Ashraf 1953; Vir et al. 1975; Eser 1976; Taleei et al. 2009). A resistant Kabuli genotype had resistance conferred through the combination of a recessive and a dominant gene (Singh and Reddy 1983). Other studies have reported incomplete host plant resistance to AB, with a single dominant gene plus recessive genes, complementary genes, and various quantitative genes according to pathotype and host genotype (Ahmad et al. 1952; Tewari and Pandey 1986; Kusmenoglu 1990; Dey and Singh 1993; Tekeoglu et al. 2000a; Millán et al. 2006; Singh et al. 2007; Bhardwaj et al. 2010; Rubiales and Fondevilla 2010). Varieties with improved AB resistance (Table 1) have been released and widely adopted by growers in India, Pakistan, Syria, the United States, Canada and Australia (Ahmad et al. 2005). However, genetic changes in pathogen populations (Vail and Banniza 2009) and reports of fungicide resistance in the pathogen (Chang et al. 2007) provide continuing challenges for breeders.

## Botrytis grey mould

BGM, caused by *Botrytis cinerea* Pers., is the second most important disease of chickpea (Pande et al. 2006a, b) (Fig. 2). BGM can attack the chickpea plant at any stage of development (Hawthorne et al. 2012), but the disease usually appears around flowering time, when the canopy is fully developed and the weather is warm and humid (20–30 °C, 70–100 % RH). The flowers are more easily infected than other parts of the plant (Bakr and Ahmed 1992; Grewal et al. 1992; Haware and McDonald 1992; Haware 1998; Bakr et al. 2002; Pande et al. 2006a, b) and can subsequently abort. Botrytis can also infect pods and be carried into the next season through infected seed (Nene et al. 2012; Matthews et al. 2014). Relative humidity, leaf wetness and temperature are the most important factors for disease development (Tripathi and Rathi

**Table 1** The most widely used resistant sources for the related individual diseases in chickpea

| Diseases | Resistant sources | Level of resistance | References |
|---|---|---|---|
| Ascochyta blight | ILC72 | Resistant | Singh et al. (1984) |
| | ILC191 | Resistant | Singh et al. (1984) |
| | ILC3279 | Resistant | Singh et al. (1984) |
| | ILC3856 | Resistant | Singh et al. (1984) |
| | ICC4475 | Resistant | Singh and Reddy (1993) |
| | ICC6328 | Resistant | Singh and Reddy (1993) |
| | ICC12004 | Resistant | Singh and Reddy (1993) |
| | ILC200 | Resistant | Singh and Reddy (1993) |
| | ILC6482 | Resistant | Singh and Reddy (1993) |
| | Sanford | Resistant | Muehlbauer et al. (1998a) |
| | Dwelley | Resistant | Muehlbauer et al. (1998b) |
| | Myles | Resistant | Muehlbauer et al. (1998c) |
| | Ambar | Resistant | http://www.heritageseeds.com.au |
| | RIL58-ILC72/Cr5 | Resistant | Rubio et al. (2006) |
| Botrytis grey mould | CH-2007-22 | Resistant | Khan et al. (2010) |
| | ICC5035 | Medium resistant | Rewal and Grewal (1989c) |
| | ICC1069 | Medium resistant | Laha and Khatua (1988) |
| | GL84195 | Resistant | Singh and Kaur (1989) |
| | GL84212 | Resistant | Singh and Kaur (1989) |
| | GL86094 | Medium resistant | Singh and Kaur (1989) |
| | ICCL97322 | Resistant | Haware et al. (1997) |
| | *C. judaicum* 182 | Highly resistant | Singh et al. (1998a, b) |
| | *C. judaicum* ILWC 19-2 | Highly resistant | Singh et al. (1998a, b) |
| | *C. pinnatifidum* 188 | Highly resistant | Singh et al. (1998a, b) |
| Fusarium wilt | ICCV2 | Highly resistant | Ali et al. (2002) |
| | UC15 | Highly resistant | Ali et al. (2002) |
| | FLIP85-20C | Highly resistant | Ali et al. (2002) |
| | FLIP85-29C | Highly resistant | Ali et al. (2002) |
| | FLIP85-30C | Highly resistant | Ali et al. (2002) |
| | ICC14194 | Highly resistant | Gaur et al. (2006) |
| | ICC17109 | Highly resistant | Gaur et al. (2006) |
| | WR315 | Highly resistant | Gaur et al. (2006) |
| Sclerotinia stem rot | GL84012 | Partial resistant | Singh et al. (2007) |
| | GL88223 | Partial resistant | Singh et al. (2007) |
| | GLK8824 | Partial resistant | Singh et al. (2007) |
| | GF89-75 | Partial resistant | Singh et al. (2007) |
| Chickpea rust | RIL58-ILC72/Cr5 | Resistant | Rubio et al. (2006) |

1992; Butler 1993; Pande et al. 2002, 2006a, b). Chickpea genotypes with vigorous seedling growth, early canopy closure and early flowering are more likely to develop BGM than other cultivars (Nene et al. 2012; Matthews et al. 2014). Under favourable conditions, BGM can develop rapidly, spread widely and cause complete yield loss (Reddy et al. 1988; Pande et al. 2002, 2006a, b).

The *B. cinerea* pathogen is reported to be variable and adaptable to a wide range of environmental

conditions (Pande et al. 2006a, b). *B. cinerea* isolates collected from India and Nepal have been differentiated based on their morphocultural characters and effects on different chickpea genotypes (Singh and Bhan 1986; Rewal and Grewal 1989a, b; Kishore 2005). Nine simple sequence repeat markers were used on *B. cinerea* (Fournier et al. 2002) to study population structure of a total of 51 alleles were amplified among 146 *B. cinerea* isolates of chickpea from Bangladesh, India and Nepal, which revealed a high amount of within-population and overall genetic diversity (Isenegger et al. 2005, 2008).

Different methods have been applied to screen germplasm for BGM resistance under in vitro, greenhouse and field conditions (Pande et al. 2002, 2006a, b; Gurha et al. 2003). The cut-twig technique (Singh et al. 1998a, b) allows for non-destructive sampling of the plants and is particularly useful in wide hybridization programs (Pande et al. 2006a, b). High levels of resistance have not been found in cultivated chickpeas (Haware and Nene 1982; Haware and McDonald 1993), however Kabuli type chickpeas appear to be more susceptible to BGM than Desi types (MacLeod et al. 2005). Extensive screening of germplasm for BGM resistance at different locations has identified 9 sources of resistance to BGM (Pande et al. 2002), however these lines were found resistant at one location but may become susceptible at other locations because of pathogen variability (Singh and Bhan 1986).

Moderate levels of resistance to BGM (Table 1) have been found by screening over 13,000 lines and transgressive segregation among progeny of moderately resistant crosses has identified higher level of resistance that may be useful in breeding (Singh et al. 1982). Some domestic landraces with an erect habit appear to be less affected by BGM and maintained their yield even under conditions that highly favour disease development (Haware and McDonald 1993). The screening of a core collection of chickpea landraces revealed two accessions (IG 70037 and IG 70038) were found to be resistant to both AB and BGM (Pande et al. 2006a, b) whilst a breeding line (CH-2007-22) with a high level of resistance was identified by Khan et al. (2010). High levels of resistance have also been reported in wild relatives, including accessions of *C. judiacum*, *C. pinnatifidum*, *C. bijugum* and *C. echinospermum* (Singh et al. 1991).

The limited reports available on the genetics of BGM resistance in chickpea suggest that a few major genes control host resistance (Tewari et al. 1985; Rewal and Grewal 1989c; Chaturvedi et al. 1995; Pande et al. 2006a, b). Some of the resistant chickpea lines such as ICC1069, P349-2 and NEC2451 have been widely used in breeding (Haware et al. 1992; Chaturvedi et al. 1995) but higher levels of host resistance still need to be identified (Pande et al. 2005). Furthermore, these resistances are unlikely to hold in the longer term as pathogen diversity indicates likely breakdown of host resistance (Isenegger et al. 2008).

## Fusarium wilt

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *ciceris* (Padwick) Synd. & Hans, can severely limit chickpea production in most chickpea-growing areas of the world. Annual chickpea yield losses from Fusarium wilt vary from 10 to 15 % (Jalali and Chand 1992; Trapero-Casas and Jiménez-Díaz 1985), but can also result in the total loss of the crop under specific conditions (Halila and Strange 1996; Cachinero et al. 2002).

The fungus enters the vascular system of the plant via the roots. Cell wall degrading enzymes produced by the pathogen break down the host cell walls to form gels that block the plant's transport systems and cause wilting. Chlorosis will first appear on old leaves and gradually extends to the young ones so that at a late stage of the disease, all leaves are yellow (Fig. 2). The infected seedlings will have shrunken stems both above and below ground, which lead to the seedlings' collapse and death (Haware et al. 1986; Brayford 1998; Leslie and Summerell 2006).

Effective field screening and laboratory procedures have been developed, and genetic sources of resistance to Fusarium wilt have been identified at ICRISAT (Nene and Haware 1980). A significant proportion of the resistant chickpea accessions were Desi types rather than Kabuli (Haware et al. 1992) with some of these resistance sources also having resistance to dry root rot, Sclerotinia stem rot and AB (Haware 1990).

Eight pathogen races of Fusarium wilt have been documented, with races 2, 3 and 4 found only in India, races 0, 1B/C, 5 and 6 found mainly in the Mediterranean and the United States and race 1A reported in India, the United States, and the Mediterranean (Landa et al. 2006). Resistance to Fusarium wilt is race-specific and controlled by major resistance genes (Sharma et al. 2004; Sharma and Muehlbauer 2007).

Genetic studies have revealed that resistance to race 1 is controlled by at least three independent loci (h1, h2, and H3) (Upadhyaya et al. 1983a, b; Singh et al. 1987) while three independent genes (a, b, and C) conferred resistance to race 2 (Gumber et al. 1995; Kumar 1998). Resistance to race 0 and race 4 has been shown to be controlled by two genes (Tullu et al. 1999; Rubio et al. 2003) with resistance to race 3 and race 5 being controlled by a single gene (Tekeoglu et al. 2000b; Sharma et al. 2004). The genetic basis of resistance to races 1B/C and 6 is unknown. Markers linked to the genes governing resistance to six races (0, 1A, 2, 3, 4 and 5) of the pathogen have been identified and their position on chickpea linkage maps located. These genes lie in two separate clusters on LG2 and LG5 (Winter et al. 2000; Sharma and Muehlbauer 2007).

Fusarium wilt resistance has been incorporated into high-yielding Desi and Kabuli backgrounds (Kraft et al. 1994) using donors that were identified as highly resistant in wilt infected plots at ICRISAT. In a cooperative research effort between ICRISAT and ICARDA, wilt-resistant chickpea lines were developed in Tunisia. These lines may be exploited for the development of resistant cultivars against wilt (Halila and Strange 1997). Several chickpea varieties with durable and stable resistance to Fusarium wilt (Table 1) have been released in India and a number of other countries. Recent advances in the understanding of the genetics of resistance are likely to result in successful pyramiding of resistance genes (Singh et al. 2008). In countries where Fusarium wilt is not a major problem, such as Australia, pre-emptive breeding is underway to minimize the impact of this disease if it becomes a major production constraint.

## Chickpea rust

Chickpea rust, caused by *Uromyces cicerisarietini* (Grogon) Jacz. & Boyer, is a widespread and serious disease that causes considerable damage to this crop each year. It has been reported as a significant problem affecting chickpea production in the Mediterranean region, South Africa, Mexico, Australia, Italy and the United States (Ragazzi 1982; Jones 1983; Díaz-Franco and Pérez-García 1995; Sillero et al. 2006; Rubiales et al. 2011). Cool and moist weather conditions favour the build-up of rust. Symptoms first appear on the leaves as small, round or oval, cinnamon-brown, powdery pustules that tend to coalesce. Occasionally a ring of small pustules can be seen around larger pustules, which occur on both leaf surfaces but more frequently on the underside. If the crop is severely infected, pustules can be seen on stems and plants may dry up prematurely (Fig. 2).

No sources of resistance to rust have been identified in cultivated chickpea (Madrid et al. 2008), but a certain degree of slow-rusting (Table 1) has been reported recently and this tends to be more frequent in wild *Cicer* relatives (Rubiales et al. 2001; Sillero et al. 2012). Conventional breeding methods have facilitated the introgression of resistance from wild relatives such as *C. reticulatum* and *C. echinospermum* into *C. arietinum* (Ladizinsky and Adler 1976; Madrid et al. 2008). However, no successful crosses have been reported between cultivated chickpea and other wild relatives such as *C. pinnatifidus*, *C. judaicum*, and *C. bijugum* (Ahmad and Slinkard 2004; Madrid et al. 2008).

## Sclerotinia stem rot

Sclerotinia stem rot, caused mainly by *Sclerotinia sclerotiorum* (Lib.) de Bary, has been recorded as an important disease of chickpea in Australia (Bretag and Mebalds 1987; Fuhlbohm et al. 2003), Canada (Hilton 2000), Chile, India, Iran, Morocco, Syria (Haware, 1990), the United States (Matheron and Porchas, 2000; Chen et al. 2006) and elsewhere (Haware 1990; Boland and Hall 1994). *Sclerotinia minor* and *S. trifoliorum* have also been reported in chickpea fields in Australia (Bretag and Mebalds 1987; Fuhlbohm et al. 2003) and the United States (Matheron and Porchas 2000; Njambere et al. 2008).

This disease can occur at all stages of crop development and is favoured by excessive vegetative growth, high soil moisture, and cool weather (20 °C). Disease symptoms in the field include whitish or brownish mycelial strands on branches or inside the stem (Nene et al. 2012). Plants or branches turn yellow or droop while remaining green, then dry up and turn straw colored. Infections are typically not uniform within a field with chlorotic or drying branches or whole plants being scattered (Fig. 2). In order to screen for possible sources of resistance to Sclerotinia stem rot, Akem and Kabbabeh (1999) developed a detached shoot technique to determine the preliminary reaction of chickpea genotypes to *S. sclerotiorum*. By using this technique under controlled conditions in a

growth chamber, the authors identified five chickpea genotypes with some resistance to Sclerotinia stem rot. Resistance components included delayed initial infection, restricted lesion development and reduced sclerotial production (Akem and Kabbabeh 1999).

No complete resistance to Sclerotinia stem rot has been found in chickpea. However, some lines (GL84012, GL88223, GLK8824, and GF89-75) do show moderate resistance to the disease (Table 1). Some accessions in wild *Cicer* sp. (*C. reticulatum*, *C. pinnatifidus*, *C. judaicum*, and *C. yamashitae*) have shown good resistance to stem rot (Singh et al. 2007).

### Phytophthora root rot

Phytophthora root rot is a disease of chickpea caused by the oomycete *Phytophthora medicaginis* (Irwin and Dale 1982). It is most commonly observed in chickpea crops following alfalfa in the United States but is not a major yield-limiting disease. It is widespread in Australia, especially in the cracking clay soils of northern New South Wales and southern Queensland. Infection by *P. medicaginis* can occur at any growth stage causing seed decay, pre- and post-emergence damping off, loss of lower leaves, and yellowing, wilting and death of older plants (Moore et al. 2011) (Fig. 2). Symptoms are sometimes delayed if temperatures are cool and the soil is moist. *P. medicaginis*, in favorable environments, can cause up to 85 % of yield loss in susceptible varieties (Moore et al. 2015).

Screening can be performed directly in the field, in the greenhouse or in the laboratory. Effective screening for disease resistance requires accurate simulation of natural environmental conditions where plants are exposed to the inoculum (Porta-Puglia and Aragona 1997; Infantino et al. 2006). Genotypic differences in resistance to Phytophthora root rot have been identified (Brinsmead et al. 1985; Dale and Irwin 1991a, b) and cultivars that are less susceptible to the disease have been developed. The levels of resistance available in cultivated species are low compared to levels in wild species (Knights et al. 2003, 2008).

Higher levels of resistance to Phytophthora were found in *C. judiacum*, *C. reticulatum*, *C. bijugum* and *C. echinospermum*, with resistance in accessions of the last species being confirmed in greenhouse tests (Knights et al. 2008). Selections from inter-specific crosses with *C. echinospermum* were as resistant as the wild parent, indicating that these sources will be useful for breeders.

### Dry root rot

Dry root rot of chickpea, caused by *Rhizoctonia bataticola* Taub (Butler), is a serious disease under dry hot summer conditions, particularly in the semi-arid tropics of Ethiopia and in most of the chickpea-growing regions in India (Ali and Kumar 2001; Chen 2011). Disease generally appears around the flowering and podding stage. The first symptom is yellowing and sudden drying of the plants. Drooping of petioles and leaflets is confined to the top of the plant. Sometimes when the rest of the plant is dry, the leaves are chlorotic. The taproots become dark brown and quite brittle in dry soil and show extensive rotting, resulting in the loss of lateral roots. The lower portion of the taproot is often left in the soil when the plant is uprooted (Fig. 2).

*Rhizoctonia* survives in the soil as mycelium and sclerotia on debris. High daytime temperatures (25–30 °C) and dry soil conditions at flowering and podding increase the severity of the disease (Gurha et al. 2003). Previous studies have reported high levels of pathogenic and genetic variation in *R. bataticola* from different parts of the world (Tripathi and Sharma 1983; Trivedi and Gurha 2006; Aghakhani and Dubey 2009). The inheritance of resistance to dry root rot of chickpea was reported to be a dominant monogenic trait (Ananda Rao and Haware 1987).

Both pot culture and field screening techniques have been developed to screen chickpea resistance to dry root rot, and several sources that show resistance to dry root rot and fusarium wilt have been identified. These resistant sources have been utilized in chickpea breeding to develop varieties that are resistant or tolerant to multiple diseases (Gurha et al. 2003). Moderate resistance to dry root rot has also been identified at ICRISAT in chickpea germplasm and breeding lines (Pundir et al. 1988), leading to the development of moderately resistant varieties (Dua et al. 2001).

## Breeding for resistance to viruses

Viruses are a significant production constraint in chickpea (Bos et al. 1988; Kumar et al. 2008) and at

least 39 (Table 2) species of viruses are reported to infect this crop. On a worldwide scale, the major viruses affecting chickpea are *Alfalfa mosaic virus* (AMV), *Cucumber mosaic virus* (CMV), *Beet western yellows virus* (BWYV), *Bean leaf roll virus* (BLRV), *Chickpea chlorotic dwarf virus* (CpCDV), *Chickpea chlorotic stunt virus* (CpCSV) and *Faba bean necrotic yellows virus* (FBNYV). The viruses detected in Australian chickpea are AMV, CMV, BLRV and BWYV, with the latter being most important (van Leur et al. 2013). AMV and CMV are transmitted mechanically and non-persistently by aphids. The aphids carry the virus for only a few hours, but the virus can be transmitted in less than a minute of feeding. BLRV and BWYV are transmitted by aphids in a persistent manner, where the virus remains infective in the aphids for many weeks. None of the modern high-yielding chickpea varieties have adequate virus resistance. However, screening a wide range of chickpea germplasm for virus resistance revealed some potential sources of resistance that will be used in the Pulse Breeding Australia chickpea breeding program (van Leur et al. 2014).

BWYV (genus *Polerovirus*, family Luteoviridae) was first reported in North America (Duffus 1960) and has a global distribution with a wide host range. It is transmitted only by aphids and not through seed or mechanical means. It persists between seasons on alternative hosts such as perennial weeds. Infected Kabuli chickpea plants develop pale, chlorotic leaves and show stunting of the whole plant, while Desi chickpea plants develop purple leaves with mild stunting of the plant. In both types, plants that are infected early do not produce flowers and die. Common aphid species that spread this virus in chickpea include *Myzus persicae*, *Aphis craccivora*, *Acyrthosiphon kondoi* and *Acyrthosiphon pisum.* In recent years, BWYV has emerged as the most important virus of chickpea in Australia (Aftab and Freeman 2013). During late September 2012, unusually high BWYV incidence was observed in chickpea crops (88 %) in northern New South Wales (van Leur et al. 2013). In 2009, chickpea virus surveys were conducted in eastern Australia, and the percentage of plants infected by BWYV in individual chickpea paddocks ranged from 5–69, 1–19, 1–29 and 3–58 % in Victoria, South Australia, and northern and southern New South Wales, respectively (Aftab and Freeman 2013). Previous surveys in 2007 in Victoria and South Australia showed an incidence of 18–61 and 8–25 %, respectively. The chickpea variety Gully was developed through mass selection from an Iranian germplasm accession under high virus pressure and is resistant to BWYV (van Leur et al. 2014).

CMV (genus *Cucumovirus*, family Bromoviridae) was first found in cucumbers (*Cucumis sativus*) (Price 1934). It has a large host range that includes over 1000 plant species (Douine et al. 1979). It can be transmitted from plant to plant both mechanically by sap and by aphids in a stylet-borne fashion. It can also be transmitted in seeds and by parasitic weeds. Symptoms of CMV in Desi chickpea are leaf chlorosis, reddening, off shoots, reduced internode length and stunting. Kabuli chickpea symptoms are leaf chlorosis, reduced internode length, off shoots and stunting. In Australia, CMV is the second most important virus after BWYV. Chickpea surveys conducted in 2007 in Victoria and South Australia found that CMV occurred in 1–10 % of the chickpea plants. In 2009, surveys conducted in Victoria, South Australia and northern and southern New South Wales revealed that the incidence of CMV ranged from 1–63, 2–9, 1–17, and 2–16 %, respectively (Aftab and Freeman 2011).

AMV (genus *Alfamovirus*, family Bromoviridae) was first described in alfalfa (*Medicago sativa* L.) (Weimer 1931). It has a host range of at least 700 species belonging to 71 families (Edwardson and Christie 1997) and is widely distributed throughout the world. Transmission of the virus occurs mainly by some aphids or by seeds. Desi chickpeas show the symptoms of tip necrosis combined with chlorosis and reddening of the leaf margin. Infected Kabuli chickpeas show yellowing and necrosis of tips and stunting of plants. In Australia, this is the third important chickpea virus after BWYV and CMV. Australian surveys have shown incidence rates of AMV of 1–9 % in Victoria in 2007 and 2009, between 9–25 % in South Australia in 2006 and between 1–18 % in New South Wales in 2009 (Aftab and Freeman 2011).

CpCDV (genus *Mastrevirus*, family Geminiviridae) was first identified in 1993 in India. Infected Kabuli chickpea plants show yellowing of foliage whereas Desi plants show reddening. Other symptoms include phloem browning (revealed by a shallow cut at the collar), stunting and premature death (Nene and Reddy 1987; Nene et al. 1991; Horn et al. 1993). The vectors of CpCDV are two leafhopper species, *Neolimnus aegyptiacus* and *Orosius albicinctus* (Horn

**Table 2** Virus Diseases of Chickpeas

| Virus species | Genus | Family | Natural spread | Distribution | References |
|---|---|---|---|---|---|
| *Alfalfa mosaic virus* | Alfamovirus | Bromoviridae | Aphids, seed | Worldwide | Edwardson and Christie (1991) |
| *Bean common mosaic virus* | Potyvirus | Potyviridae | Aphids | Worldwide | Brunt et al. (1996) |
| *Bean leafroll virus* | Luteovirus | Luteoviridae | Aphids | Worldwide | Edwardson and Christie (1991) |
| *Bean yellow mosaic virus* | Potyvirus | Potyviridae | Aphids, seed | Worldwide | Edwardson and Christie (1991) |
| *Beet curly top virus* | Curtovirus | Geminiviridae | Leaf hopper | Worldwide | Brunt et al. (1996) |
| *Beet western yellows virus* | Polerovirus | Luteoviridae | Aphids | Worldwide | Edwardson and Christie (1991) |
| *Broad bean mottle virus* | Bromovirus | Bromoviridae | Beetles | Africa, Europe | Edwardson and Christie (1991) |
| *Broad bean stain virus* | Comovirus | Secoviridae | Weevils, seed | Europe, Africa, | Edwardson and Christie (1991) |
| *Broad bean true mosaic virus* | Comovirus | Comoviridae | Weevils, seed | Africa, Asia | Edwardson and Christie (1991) |
| *Broad bean wilt virus* | Fabavirus | Comoviridae | Aphids | Worldwide | Edwardson and Christie (1991) |
| *Cassia yellow blotch virus* | Bromovirus | Bromoviridae | Unknown | Australia | Brunt et al. (1996) |
| *Chickpea bushy dwarf virus* | Potyvirus | Potyviridae | Unknown | India | Brunt et al. (1996) |
| *Chickpea chlorosis virus* | Masterovirus | Geminiviridae | Leaf hopper | Australia | Thomas et al. (2010) |
| *Chickpea chlorotic stunt virus* | Polerovirus | Luteoviridae | Aphids | Africa, Asia | Abraham et al. (2006) |
| *Chickpea chlorotic dwarf virus* | Masterovirus | Geminiviridae | Leaf hopper | Asia | Horn et al. (1993) |
| *Chickpea distortion mosaic virus* | Potyvirus | Potyviridae | Aphid | India | Edwardson and Christie (1991) |
| *Chickpea filiform virus* | Potyvirus | Potyviridae | Aphid | USA | Edwardson and Christie (1991) |
| *Chickpea redleaf virus* | Masterovirus | Geminiviridae | Leaf hopper | Australia | Thomas et al. (2010) |
| *Clitoria yellow vein virus* | Tymovirus | Tymoviridae | Unknown | Kenya | Brunt et al. (1996) |
| *Cucumber mosaic virus* | Cucumovirus | Bromoviridae | Aphids, seed | Worldwide | Edwardson and Christie (1991) |
| *Epirus cherry virus* | Ourmiavirus | Unassigned | Seed | Greece | Brunt et al. (1996) |
| *Fababean necrotic yellows virus* | Nanovirus | Nanoviridae | Aphids | Asia | Katul et al. (1993) |
| *Glycine mosaic virus* | Comovirus | Comoviridae | Unknown | Australia | Brunt et al. (1996) |
| *Lettuce mosaic virus* | Potyvirus | Potyviridae | Aphids, seed | Worldwide | Edwardson and Christie (1991) |
| *Lettuce necrotic yellows virus* | Cytorhabdovirus | Rhabdoviridae | Aphids | Australia, Europe | Edwardson and Christie (1991) |
| *Lucerne Australian latent virus* | Nepovirus | Secoviridae | Seed | Australia | Brunt et al. (1996) |
| *Lucerne transient streak virus* | Sobemovirus | Unassigned | Unknown | Australia | Brunt et al. (1996) |
| *Pea enation mosaic virus* | Enamovirus | Luteoviridae | Aphids | Europe, USA | Edwardson and Christie (1991) |
| *Pea mild mosaic virus* | Comovirus | Comoviridae | Seed | New Zealand | Brunt et al. (1996) |
| *Pea seed-borne mosaic virus* | Potyvirus | Potyviridae | Aphids, seed | Worldwide | Brunt et al. (1996) |
| *Pea streak virus* | Carlavirus | Betaflexiviridae | Aphids | Europe, USA | Edwardson and Christie (1991) |

**Table 2** continued

| Virus species | Genus | Family | Natural spread | Distribution | References |
|---|---|---|---|---|---|
| *Peanut stunt virus* | Cucumovirus | Bromoviridae | Aphids, seed | USA, Japan | Brunt et al. (1996) |
| *Phasey bean virus* | Polerovirus | Luteoviridae | Aphids | Australia | Sharman et al. (2012) |
| *Soybean dwarf virus* | Luteovirus | Luteoviridae | Aphids | Worldwide | Edwardson and Christie (1991) |
| *Subterranean clover stunt virus* | Nanovirus | Nanoviridae | Aphids | Australia | Chu and Vetten (2003) |
| *Swordbean distortion mosaic virus* | Potyvirus | Potyviridae | Aphids | India | Brunt et al. (1996) |
| *Tomato spotted wilt virus* | Tospovirus | Bunyaviridae | Thrips | Australia | Thomas et al. (2004) |
| *Turnip mosaic virus* | Potyvirus | Potyviridae | Aphids | Worldwide | Brunt et al. (1996) |
| *Wisteria vein mosaic virus* | Potyvirus | Potyviridae | Aphids | Europe | Brunt et al. (1996) |

et al. 1993; Kumari et al. 2004). Significant yield losses due to CpCDV, of 60–100 %, have been reported in Sudan and India (Horn et al. 1995).

CpCSV (genus *Polerovirus*, family Luteoviridae) is a recently described virus that infects cool-season food legumes (Abraham et al. 2006, 2009; Asaad et al. 2009) and is a phloem-limited virus that is present in very low concentration and transmitted by aphids (*Aphis craccivora* Koch. and *Aphis pisum* Harris) in a persistent manner (Abraham et al. 2006; Asaad et al. 2009). CpCSV symptoms cannot be distinguished from those caused by other yellowing viruses like BLRV or BWYV.

FBNYV (genus *Nanovirus*, family Nanoviridae) was first reported in Syria. It is the causal agent of a destructive disease of chickpea in some arid regions, including countries in north Africa, west Asia and southern Europe (Katul et al. 1993; Franz et al. 1996). FBNYV is known to infect more than 50 legume species. Characteristic symptoms in chickpea include leaf rolling, yellowing and stunting. FBNYV is transmitted in a persistent manner by several aphid species, including *Aphis craccivora*, *A. fabae* and *A. pisum*, but it is confined to phloem tissues in the infected plants, rendering it non-transmissible by sap and through seed and pollen. No cultivars of chickpea with resistance to FBNYV are commercially available.

BLRV (genus *Luteovirus*, family Luteoviridae; Katul 1992) is a luteovirus transmitted by aphids in a persistent manner (Ashby 1984), with *A. pisum*, *A. craccivora* and *M. persicae* being the main vectors. This virus is not transmitted through seed or mechanically. Symptoms include phloem discoloration and foliage yellowing or reddening. This virus is limited to the Fabaceae family, and was first reported in Australia in 1999 (Schwinghamer et al. 1999). In Australia, this is the least important of the viruses affecting chickpea (data not shown).

Outside Australia other viruses infect chickpea and can cause significant yield loss. *Red clover vein mosaic virus* (RCVMV, genus *Carlavirus*, family Betaflexiviridae) causes mosaic symptoms, yellowing and bronzing of leaves, distortion of leaves, severe stunting and proliferation of auxiliary buds (rosetting). Yield loss can be 100 % if RCVMV infects chickpea at the pre-bloom stage (Larsen and Miklas 2001). *Pea streak virus* (PeSV, genus *Carlavirus*, family Betaflexiviridae) causes yellowing of foliage, wilting of the terminal tip, phloem discoloration and plant death, particularly when seedlings are infected. *Pea enation mosaic virus* (PEMV, genus *Enamovirus*, family Luteoviridae) causes a yellowing or reddening of the foliage, upward curling of the leaf margin, phloem discoloration, stunting and twisting of the seed pod.

Efforts have been made to identify sources of resistance and develop virus-resistant chickpea cultivars. For example, Chalam et al. (1986) identified two chickpea accessions that are resistant to CMV and nine that are resistant to BYMV. Kumar et al. (2005) found seven accessions that are resistant to CMV by screening 500 chickpea germplasm lines. In a recent study, 8 Desi type accessions were identified to be resistant to PEMV (Larsen and Porter 2010) and should make useful donors in virus resistance

breeding. A few chickpea varieties released in India have shown some level of resistance to viruses (Dua et al. 2001).

## Breeding for resistance to insects

Worldwide, nearly 60 insect species are known to feed on chickpea. Of these, the most important insect pests are the pod borers (*Helicoverpa* spp.), leaf miners (*Liriomyza cicerina*), bruchid weevils (*Callosobruchus* spp.), cowpea aphid (*Aphis craccivora*), cutworms (*Agrotis* spp., etc.), and leaf-feeding caterpillars such as armyworms (*Spodoptera* spp.) (Sharma et al. 2007).

### Pod borers

The pod borers *Helicoverpa armigera* and *H. punctigera* (the latter of which is an Australian migratory pest in early spring) are important insect pests of chickpea and are increasingly difficult to control (Sharma et al. 2007). The larvae feed directly on the seed pod, causing seed abortion and damage, thereby having the potential to cause major crop losses. Like field peas and faba beans, chickpeas are preferred by *Helicoverpa* over lupins, canola, Indian mustard and linseed (Sequeira et al. 2001). The spatial and temporal dynamics of this pest can be highly variable, so its control requires regular monitoring with the correct timing of chemical sprays (Evans et al. 2005). Host plant resistance has the potential to be a highly valuable part of an integrated pest management approach (Sharma et al. 2007).

Greenhouse and field-based screening methodologies have been used with conventional breeding techniques to select for *Helicoverpa* resistant cultivars (Sharma et al. 2005b). Open-field screening of 12,000 chickpea germplasm accessions at ICRISAT found some accessions had reduced susceptibility to *H. armigera* (Lateef 1985). Desi chickpeas appear to have variability in resistance to *H. armigera* (Cowgill and Lateef 1996).

Moderate resistance to *Helicoverpa* was found to be associated with increased acid exudate on the leaves, which can deter oviposition of moths and reduce larval damage on the plant (Lateef 1985). Oxalic acid production is important for *H. armigera* antibiosis, as this compound significantly inhibits the growth of larvae (Yoshida et al. 1995). Malic acid has no effect on larval growth, but it stimulates the oviposition of *Helicoverpa* moths (Yoshida et al. 1997).

Even stronger resistance to *H. armigera*, with high levels of antibiosis, has been found in wild *Cicer* spp. such as *C. pinnatifidum* and *C. judaicum* and in some perennial *Cicer* spp. (Sharma et al. 2005a, 2006). Commercial chickpea lines with genetically engineered resistance to *Helicoverpa* based on the Bt toxin are under development (Sanyal et al. 2005; Lawo et al. 2008; Acharjee et al. 2010). These lines have not yet been released, but evidence from cotton suggests that host plant resistance using the Bt toxin, coupled with effective management, will enable them to be used without triggering the development of significant insect resistance to the toxin in the field (Mahon et al. 2007).

Partial resistance to the pod borer *H. armigera* was found in breeding lines in a comparison of protected (netted) versus unprotected plants in a field trial during a pest infestation, and in another comparison between endosulfan-sprayed replicates versus unsprayed plants (Yadav et al. 2006). Susceptibility was greater in spreading types and in the Kabuli type. At ICRISAT, wild relatives of chickpea have shown low susceptibility to *H. armigera*, and wide crosses with elite lines are being used to study the genetics of this resistance and for breeding with the aid of MAS (Sharma 2006; Sharma et al. 2007).

### Leaf miners

The chickpea leaf miner (*Liriomyza cicerina*) is found throughout much of Europe, central and western Asia and north Africa (Naresh and Malik 1989; Kolesík and Pastucha 1992; CABI 2007; Martinez 2007). The larvae of this insect hatch from eggs oviposited under the leaf epidermis and feed inside the mesophyll, creating characteristic serpentine mines. Heavy infestations can cause leaf desiccation and premature leaf drop. In the Mediterranean region, leaf miners are the main insect pest of chickpea, causing up to 30 % yield loss (Weigand 1990). Spring-sown chickpea is more affected than winter-sown chickpea because of the insect's life cycle, which includes over-wintering diapause (El Bouhssini et al. 2008).

Chickpea germplasm with resistance to leaf miners, based on accessions of *C. echinospermum* and *C. reticulatum*, have been developed and released by

ICARDA for use in breeding programs (Singh and Weigand 1994, 1996). Leaf miner resistance is significantly correlated with leaf type and leaflet size, but not with leaf pigmentation. Genotypes with a large, simple leaf type were the most sensitive to leaf miner damage, whereas genotypes with multipinnate leaves composed of small/narrow leaflets were less sensitive (Toker et al. 2010).

### Bruchid weevils

Beetles of the genus *Callosobruchus* are major storage pests of chickpea and cause considerable economic losses (Erler et al. 2009). They can attack seed both in the field but more damage occurs during storage. Erler et al. (2009) studied chickpea resistance to bruchid feeding and found that Desi chickpeas were more resistant to *C. maculatus* than Kabuli chickpeas and one genotype exhibited complete resistance. Unfortunately, the most resistant Desi types had a rough (wrinkled), thick, green seed coat, making the product unacceptable to most consumers (Erler et al. 2009). Previous screens for resistance to *Callosobruchus* in 3000 Kabuli accessions at ICARDA revealed no resistant germplasm (Reed et al. 1987). However, a chickpea landrace with resistance to the seed beetle *C. maculates* F. has been identified (Erler et al. 2009).

### Aphids

Although virus transmission by aphids is the major concern caused by this insect (Weigand 1990; Sharma et al. 2007), they can also cause direct damage to the plant through feeding. The main aphid pest in chickpeas is the cowpea aphid, *Aphis craccivora*, a species that is widely distributed, especially in the tropics (CABI 1983). However, due to the exudation of organic acids from granular hairs covering the surface of chickpeas, direct damage by aphids is generally of little concern (Popelka et al. 2004). Work against direct aphid damage was conducted by Chakraborti et al. (2009) to produce transgenic chickpea plants expressing an antifeed compound from garlic (*Allium sativum*). The mannose-binding lectin was expressed with a phloem-specific promoter and caused potent antibiosis that reduced aphid populations on the plant.

## Breeding for resistance to nematodes and parasitic weeds

### Root-knot nematodes

The root-knot nematodes (RKN) are one of the most important groups of plant parasitic nematodes. The three species of RKN known to infest chickpea differ in their climatic distribution: *Meloidogyne artiella* is the main species of importance in the Mediterranean region, whereas *M. incognita* and *M. javanica* are more common in the subtropics of Asia, Africa and South America (Thompson et al. 2000). RKN reproduction is known to be higher during warmer seasons, therefore spring-sown crops around the Mediterranean are more affected than those sown in winter (Di Vito and Greco 1988; Thompson et al. 2000). Compared with other cool-season food legumes, chickpea is grown in warmer climates or at warmer times of the year and is consequently more exposed to RKN. By comparison, common and durum wheat are significantly better hosts for *M. artiella* than chickpea and produce higher rates of RKN multiplication (Di Vito and Greco 1988; Hernández Fernández et al. 2005).

Parasitism by RKNs involves the establishment of permanent feeding sites in the plant roots where the nemotodes stimulate the production of giant cells that act as sinks for plant photosynthates that the nematode preferentially access. Deformation and blockage of vascular tissues due to nematode feeding can limit translocation of water and nutrients, suppress plant growth and result in reduced seed yield. Affected plants are often stunted, with pale green to yellow leaves (Vovlas et al. 2005; Castillo et al. 2008).

A number of root-disease complexes are associated with RKN attack in plants. The fungal pathogens *Fusarium oxysporum* and *Macrophomina phaseolina* are known to cause root rot/wilt, which is exacerbated by the damage caused by RKN. Nematode attack can break down plant defenses and cause Fusarium wilt-resistant genotypes to become diseased (Siddiqui and Husain 1991; France and Abawi 1994; Maheshwari et al. 1995). In the Indian state of Karnataka, there was a 28 % incidence of wilt disease associated with the complex of *M. incognita* and *F. oxysporum* f. sp. *ciceri* in chickpea crops (Rao and Krishnappa 1995).

In screening more than 7000 accessions of chickpea and wild *Cicer* species, no resistance was found to *M.*

*javanica* (Ansari et al. 2004). However, some lines had good tolerance to RKN and achieve significantly greater yield and total dry matter in naturally infested fields (Sharma et al. 1993; Ansari et al. 2004). Resistance to *M. incognita* in chickpea is unknown, but there is some evidence that reduced susceptibility to RKN in some genotypes is associated with greater increases in root peroxidase activity in response to nematode infection (Siddiqui and Husain 1992). These peroxidases are associated with the initiation of the hypersensitive response, systemic defense mechanisms and lignification of cell walls, mechanisms that are commonly employed by plants in response to infection from a range of pathogens and parasites (Reuveni and Ferreira 1985; Bronner et al. 1991; Do et al. 2003; Montes et al. 2004; Choi et al. 2007; Oliveira et al. 2012).

### Root lesion nematodes

Root lesion nematodes (*Pratylenchus* spp.) are a major constraint to chickpea production and rank second after RKN in their global impact (Castillo et al. 2008). As their name indicates, they cause root lesions, which results in reduced growth and yield. They can also increase *F. oxysporum* infection (Castillo et al. 1998). After wheat, chickpea is one of the most susceptible crops to *Pratylenchus thornei* in rain-fed cropping systems (Taylor et al. 2000). *P. neglectus*, *P. mediterraneus* and possibly *P. penetrans* also infest chickpea (Thompson et al. 2000).

Chickpea genotypes vary in both their resistance and tolerance to *P. thornei* (Castillo et al. 1998). Nevertheless, few modern chickpea varieties show sufficient resistance to *P. thornei* or *P. neglectus* (Thompson et al. 2008, 2011). Consequently nematode numbers build up in the soil when chickpea is grown, reducing the usefulness of chickpea in a cropping rotation with wheat. Recently, chickpea lines that are resistant to root-lesion nematodes have been produced from hybrids of Desi chickpea cultivars with resistant accessions of *C. reticulatum* and *C. echinospermum* (Thompson et al. 2011). Levels of resistance identified in wild relatives were far superior to the levels identified in *C. arietinum.* Although many backcrosses are required to produce progeny that possess acceptable agronomic and seed quality parameters for commercial chickpea production, the quantum leap in resistance that is gained justifies the breeding effort.

### Cyst nematodes

The cyst nematode *Heterodera ciceri* is an aggressive parasite of chickpea found in the eastern Mediterranean region, particularly Syria and Turkey (Thompson et al. 2000; Sikora et al. 2005). Chickpea plants infested with cyst nematodes are stunted and chlorotic with reduced flowers and pods, along with poorly developed roots and reduced number of *Rhizobium* nodules, all of which lead to lower seed protein content (Greco et al. 1988).

Breeding for resistance to cyst nematodes presents the best option for control of nematode populations and reduction of yield loss (Greco et al. 2003). However, the cultivated chickpea species *C. arietinum* showed no resistance to *H. ciceri* in 9257 lines tested (Singh and Ocampo 1997). Fortunately, the accession Ladiz of the wild relative *C. reticulatum* had good resistance, and chickpea varieties based on hybrids of this line with a widely adapted and high-yielding Kabuli cultivar have been released (Malhotra et al. 2002).

### Parasitic weeds

Like other grain legumes, chickpeas are susceptible to parasitism by *Orobanche* spp. (broomrape) when they are grown in infested Mediterranean regions. Chickpea is a host of four different species of broomrape namely crenate broomrape (*Orobanche crenata* Forsk.), fetid broomrape (*O. foetida* Poir.), Egyptian broomrape (*Phelipanche aegyptiaca* Pers.) and *O. minor* (Rubiales et al. 2011). Among these *Orobanche* species, *O. crenata* is the most economically damaging parasitic plant on chickpea worldwide, while *O. minor*, *O. aegyptiaca and O. foetida* are only considered of importance in certain areas (Kharrat et al. 1992).

Fortunately, chickpea and wild *Cicer* relatives show good resistance to *Orobanche crenata* (Rubiales et al. 2003, 2004; Pérez-De-Luque et al. 2009). This resistance has been shown to lower broomrape seed germination and produce darker tissue at the site of radicle penetration, preventing parasite establishment or reducing development of established tubercles on the host roots (Rubiales et al. 2003, 2004). This

darkening host tissue is associated with the accumulation of secretions at the infection site that block neighbouring apoplastic vessels (xylem occlusions) in order to inhibit nutrient transfer to the parasite (Pérez-De-Luque et al. 2005).

## Prospect of chickpea biotic resistance breeding in the genomic era

Modern plant breeding has the capacity to use molecular tools to assist in the identification and selection of desirable characteristics (Moose and Mumm 2008). The ongoing development and application of molecular tools to plant breeding is likely to increase efficiencies and make recombining multiple traits possible in the absence of phenotypic selection.

## Molecular markers and marker assisted selection

DNA markers serve as powerful tools to improve the efficiency and precision of traditional plant breeding using marker-assisted selection (MAS). Marker loci tightly linked to major genes responsible for economically important traits such as disease resistance, male sterility, self-incompatibility and seed characteristics including shape, size, colour and texture, can be used for improving selection efficiently. Molecular research related to crop biotic stress has focused on locating and tagging genetic loci for resistance genes. As a result of the often simpler inheritance patterns, there has historically been a better understanding of the genetic basis of disease resistance, as compared to other traits such as insect and abiotic stress resistance. Therefore, the development and application of

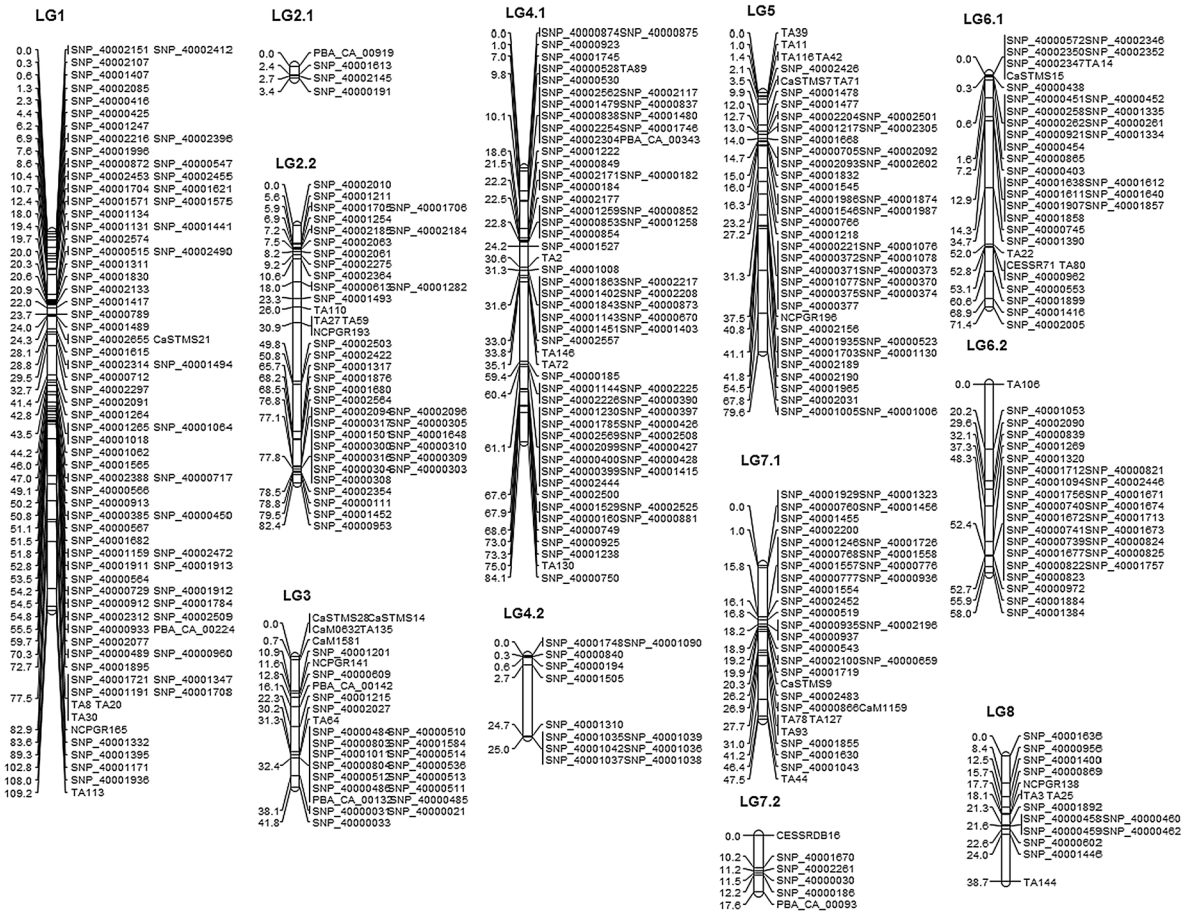


**Fig. 3** A genetic linkage map of chickpea from Lasseter × ICC3996 RIL mapping population (Map generated by Dr Sukhjiwan Kaur, part of this map was published in Stephens et al. 2014)

markers for disease resistance is more advanced and the most successful applications of MAS in plant breeding are diseases for which major resistance genes have been backcrossed into elite cultivars (Torres et al. 2010; Varshney et al. 2014).

A large number of inter- and intra-specific linkage maps (Fig. 3) have been generated and published for chickpea using different types of DNA markers (Kazan et al. 1993; Simon and Muehlbauer 1997; Hüttel et al. 1999; Winter et al. 1999, 2000; Lichtenzveig et al. 2005; Sethy et al. 2003, 2006a, b; Choudhary et al. 2006; Nayak et al. 2010; Thudi et al. 2011; Gaur et al. 2011, 2012; Stephens et al. 2014). Through the use of these linkage maps, linked markers/quantitative trait loci (QTLs) for resistance to various diseases in chickpea have been identified (Table 3).

*Ascochyta blight*

Resistance to AB has been increasingly considered a quantitative trait and many QTLs have been identified in different genomic regions (Santra et al. 2000; Flandez-Galvez et al. 2003a; Udupa and Baum 2003; Pande et al. 2005; Taran et al. 2007; Kanouni et al. 2009, 2011). Linkage group (LG) 4 has been reported by several researchers to contain QTLs for AB resistance (Santra et al. 2000; Tekeoglu et al. 2002; Cho et al. 2004; Taran et al. 2007; Stephens et al. 2014), while other reports highlight LG2 (Udupa and Baum 2003; Cho et al. 2004) and LG8 (Lichtenzveig et al. 2006). In an effort to provide more durable resistance, emphasis has shifted to developing molecular tools to allow successful pyramiding of resistance sources (Millán et al. 2006). These tools have significantly enhanced the capacity to breed chickpea for AB resistance, however only a limited number of gene-based markers capable of efficient implementation within a breeding program have been described in close linkage to AB resistance determinants segregating within cultivated germplasm (Madrid et al. 2013).

*Botrytis grey mould*

A limited number of reports are available on markers associated with BGM resistance in chickpea. However, a recent study identified three QTLs for resistance to BGM in chickpea, and associated markers provide an opportunity to pyramid different genes or QTLs to obtain higher levels of resistance (Anuradha et al. 2011). It is suggested that introgression of BGM resistance into elite material is practical, provided that donor parents with a high level of resistance are identified in the cultivated or cross-compatible wild species (Pande et al. 2006a, b).

*Fusarium wilt*

Molecular mapping studies have found that resistance genes to races 0, 1, 2, 3, 4, and 5 of the pathogen appear on LG2 of the chickpea map (Castro et al. 2010). The clustering of six resistance genes makes LG/2 a hotspot for fusarium wilt resistance (Millán et al. 2006; Sharma and Muehlbauer 2007). In order to apply MAS and better understand the molecular mechanism of resistance, closely linked markers have been identified for some of the genes and validated in different genetic backgrounds (Gowda et al. 2009; Ali et al. 2012). Near-isogenic lines have been developed for the resistance gene to race 5, which can be used for fine mapping and map-based cloning of this gene (Castro et al. 2010).

*Rust*

Recently, Madrid et al. (2008) identified a single dominant gene controlling resistance to chickpea rust in a recombinant inbred line population derived from an interspecific cross between *C. arietinum* (ILC72) × *C. reticulatum* (Cr5-10), the latter line being the resistance donor. This gene, *Uca1/uca1*, was located in an interval of 3.9 cM on LG7 (Madrid et al. 2008). Flanking markers should be able to facilitate a MAS program to incorporate this resistance into cultivated chickpea.

Experience with MAS in other crops has shown that molecular markers are most likely to succeed for traits with monogenic inheritance, or those in which the inheritance is controlled by few genes with large effect (William et al. 2007). In contrast to cereals (Koebner and Summers. 2007; Gupta et al. 2010) and corn (Ragot and Lee 2007), there are very few reports of MAS in legumes (Ragagnin et al. 2009; Torres et al. 2010). Several factors that limit the application of MAS in legume breeding include lack of marker studies, the need to validate the effect of MAS in

**Table 3** The QTLs or genes identified for chickpea host resistance to various biotic stresses

| Trait | Name of population | Locations | Markers associated with genes or QTL(s) | Genetic effects | References |
|---|---|---|---|---|---|
| Ascochyta blight | FLIP84-92C × PI 599072 | LG1, LG6 | UBC733b, UBC181a, *Dia4* | 50.3 and 45 % | Santra et al. (2000) |
| | Lasseter × ICC1 2004 | LG1, LG2, LG3 | TS45, TA146, TA130 | 76 % | Flandez-Galvez et al. (2003b) |
| | Lasseter × PI527930 | LG4 | CS5b650, GA2, OPB17c560 | N/A | Collard et al. (2003) |
| | ILC 1272 × ILC 3279 | LG2, LG4 | Ta20, TA72, ar1 | 35.9 % | Udupa and Baum (2003) |
| | PI 359075 × FLIP84-92C | LG2, LG4, LG6 | GA16, GA24, GAA47, Ta46 | 69.2 % | Cho et al. (2004) |
| | Cr5-10 × ILC72 | LG2 | OPAI09746, UBC881621 | 28.0 % | Cobos et al. (2006) |
| | LC3279 × WR315 | LG4 | TA194 | 55 % | Iruela et al. 2007) |
| | ICCV96029 × CDC Frontier | LG3, LG4, LG6 | TA64, TS54, TA176 | 56 % | Taran et al. (2007) |
| | ICCV 96029/CDC Luna, | LG2, LG4 | TR19, TS54 | 48 % | Anbessa et al. (2009) |
| | ICCV 96029/CDC Corinne, | LG4, LG8 | TA132, TS45 | 38 % | Anbessa et al. (2009) |
| | ICCV 96029/Amit | LG3 | TA64 | 14 % | Anbessa et al. (2009) |
| | ICC 12004 × Bivanij | LG3, LG4, LG6 | TA125, TA72, GA26 | 46.5 % | Kanouni et al. (2009) |
| | C 214 × ILC 3279 | LG4, LG5, LG6 | STMS11, Ta106, CaM0244 | 41.6 % | Sabbavarapu et al. (2003) |
| | Lasseter × ICC3996 | LG4 | SNP_40000185 | 45 % | Stephens et al. (2014) |
| | S95362 × Howzat | LG4 | TA146, TA72 | 59 % | Stephens et al. (2014) |
| Fusarium wilt | WR-315 × C-104 | N/A | CS-27, UBC170 | foc-1 | Mayer et al. (1997) |
| | ICC-4958 × PI 498777 | N/A | CS-27, UBC-855 | foc-4 | Ratnaparkhe et al. (1998) |
| | JG-62 × Surutato-77 | N/A | CS-27 | foc-1, foc-4 | Tullu et al. (1999) |
| | ICC-4958 × PI 498777 | LG2, LG3 | CS-27, UBC-170 | foc-0, foc-4, foc-5 | Tekeoglu et al. (2000b) |
| | ICC-4958 × PI 498777 | LG2 | CS27, TA96, TA27 | foc-1, foc-4, foc-5 | Winter et al. (2000) |
| | CA2156 × JG62 | LG3 | OPJ 20600 | foc-$0_1$ and foc-$0_2$ | Rubio et al. (2003) |
| | WR-315 × C-104 | LG2 | TA96, CS27A | foc-1, foc-3, foc-4 | Sharma et al. (2004) |
| | CA2139 × JG62 | LG3 | OPJ20(600), TR59 | 37.8 % | Cobos et al. (2005) |
| | JG62 × Vijay | LG2 | TA110, TA96, H1B06y | foc-1, foc-2, foc-3 | Gowda et al. (2009) |
| | C 214 × WR 315 | LG6 | CaM1402, CaM1125, TA22 | 29.2 % | Sabbavarapu et al. (2003) |
| Botrytis grey mould | JG62 × ICCV2 | LG3, LG6 | SA14, TA25, TA159 | 43.6 % | Anuradha et al. (2011) |
| Chickpea rust | ILC-72 × Cr5-10 | LG7 | TA18, TA180 | 31 % | Madrid et al. (2008) |

*RAPD* Random Amplified Polymorphic DNA, *SSR* Simple Sequence Repeats, *ISSR* Inter simple sequence repeat, *SNP* Single Nucleotide Polymorphism, *SCAR* Sequence Characterized Amplified Region, *STMS* Sequence-tagged microsatellite site markers, *RGA* Resistance Gene Analogs, *ASAP* Allele Specific Associated Primers, *LG* Linkage Group

different genetic backgrounds, and high genotype × environment interactions. However, a recent study by Varshney et al. (2014) reported successful introgression of Fusarium wilt and AB resistance into an elite cultivar of chickpea through the use of marker-assisted backcrossing. These success cases and some of the high-throughput marker technologies such as the SNP marker system may be able to accelerate the use of MAS in legume breeding.

## Genetic transformation

The efficiency of conventional breeding methods are sometimes limited in enhancing resistance to biotic stresses due to a lack of highly resistant sources in the available gene pool (Haware and McDonald 1992). Developing an efficient genetic transformation system for chickpea could add value to conventional breeding strategies. Two different transformation methods have been established in chickpea: the biolistic transformation technique (Kar et al. 1997) and the *Agrobacterium*-mediated method (Fontana et al. 1993; Kar et al. 1996; Krishnamurthy et al. 2000; Tewari-Singh et al. 2004). Due to its cost-effective nature, the latter has been optimized and used more widely in chickpea (Senthil et al. 2004; Mehrotra et al. 2011a, b).

The high efficiency of *Agrobacterium*-mediated transformation protocols has made this method an alternative approach of improving stress tolerance in elite chickpea cultivars by genetically modifying a genome with a gene conferring the desired tolerance. Significant achievements have been made at ICRISAT, including the development of transgenic plants carrying the *cry1Ac* and *P5CSF* genes (Jandhyala 2005; Sharma 2006). The *cry1Ac* gene, derived from the bacterium *Bacillus thuringiensis*, produces a toxin that kills the economically important chickpea pod borer (Jandhyala 2005). The *P5CSF129A* gene for proline accumulation stabilizes degrading proteins under osmotic stress (Mitra 2001; Munns 2005). Non-chimeric transgenic progeny plants with a high expression level of Bt-Cry protein have been created recently using embryogenic callus (Mehrotra et al. 2011).

Future work such as deploying antifungal genes like chitinase and glucanase for effective control of biotrophic fungal diseases in transgenic crop plants (Amian et al. 2011; Ceasar and Ignacimuthu 2012), or polygalacturonase-inhibitory proteins (PGIPs) to inhibit the activity of the fungal cell wall-degrading polygalacturonases and hence reduced disease symptoms due to necrotrophic pathogens like *B. cinerea* (Wally and Punja 2010) could make genetic transformation a potentially valuable and practical strategy for breeding resistance to biotic stresses in chickpea. A more efficient way of enhancing and broadening resistance of plants to different biotic stresses is to combine transgenes expressing several genes into a single line using different strategies such as crossing, single vector with multiple genes, co-transformation, sequential transformation and IRES elements. These genes or strategies should be utilized to develop more disease resistant plants and enhance chickpea breeding efficiency in future.

## Genomic technologies

Development of new genomic technologies has increased during the last decade, allowing the use of new strategies in crop breeding. For example, the study of complex biological processes in legumes has been facilitated by comparative genome analysis using model plants, such as *Medicago truncatula* and *Lotus japonicus*. These models allow us to better understand plant development, responses to biotic stresses, and evolution. Synteny among legume genomes, and specifically among chickpea and other legume species, has been investigated during the last 20 years. Comparative mapping among chickpea, pea, lentil and *Medicago* has suggested a high degree of synteny among legume crop species (Aubert et al. 2006).

*Medicago* is taxonomically the closest model species to chickpea (Kalo et al. 2004; Choi et al. 2006), and the extent of synteny between chickpea and *M. truncatula* has been assessed on the basis of the sequence from 11 bacterial artificial chromosome clones (Rajesh et al. 2007b). Coram and Pang (2005a) showed that levels of similarity between chickpea expressed sequence tag (EST) sequences and those in *Medicago* and *Lotus* were marginally superior to those observed for *Arabidopsis*. These studies provide evidence for macro-synteny between chickpea and the model crop species, although relatively little micro-synteny exists (Coram and Pang 2005a; Rajesh et al. 2007b). Thus, the use of the model crops to study

chickpea on a gene sequence level needs further assessment (Coram et al. 2007).

As the chickpea genome is the smallest (750 Mbp) among cool season food legumes, it is an attractive target for the development of saturated genetic linkage maps employing transcriptome and genome sequence information to identify important genes of interest. To date, several transcriptome sequencing studies for cultivated and non-domesticated chickpea accessions have been completed. The first EST study in chickpea was reported in 2005 (Coram and Pang 2005a). More than 500 unigenes were identified from the assembled transcriptome isolated from the stems and leaves of an AB resistant chickpea genotype after pathogen inoculation. As a result, potential defense related unigenes were identified by microarrays that were constructed using only defense related ESTs (Coram and Pang 2005b, 2006, 2007). A transcriptomics approach was also used to characterize the molecular interactions between chickpea and race 1 of *F. oxysporum* f. sp. *ciceris* (Nimbalkar et al. 2006). Investigation of the transcription difference in the root infection of some resistant and susceptible genotypes uncovered 19 differentially expressed sequences that were potentially involved in a defense response. Some of these expressed sequences were similar to previously characterized defense related proteins, including two transcription factors and three nucleotide binding site leucine-rich repeat-type gene sequences (Nimbalkar et al. 2006). In recent years, deep sequencing of the chickpea transcriptome using next-generation technologies has enabled the identification of new candidate genes and the development of functional molecular markers (Hiremath et al. 2011; Garg et al. 2011; Agarwal et al. 2012; Jhanwar et al. 2012).

Recently, the draft genome sequence of the genotype CDC Frontier, a Kabuli chickpea variety with resistance to AB and pod borer, has been released and was estimated to contain 28,269 candidate genes. Resequencing and analysis of 90 cultivated and wild genotypes resulted in the identification of candidate genes responsible for traits of interest including 187 disease resistance gene homologs (Varshney et al. 2013). These resistance genes still need to be characterized to understand their functional annotations and can be employed in MAS in near future. Jain et al. (2013) generated the draft sequence of a Desi chickpea genome with the assembly covering 70 % of the genome length, and more than 80 % of the gene space and predicted the presence of 27,571 genes. RNA-Seq analysis identified several tissue specific and stress responsive genes (Jain et al. 2013).

A series of reverse/forward genomic approaches to fully determine gene function, such as targeted induced local lesions in genomes (TILLING), insertional mutagenesis, and activation tagging have been applied in the model legumes (Coram et al. 2007). A chickpea TILLING mutant population has been constructed, and individuals carrying point mutations in the genes of interest can be phenotypically assessed to determine the function(s) of each gene (Rajesh et al. 2007a). This is a highly valuable chickpea genomic resource which may be used to screen for changes in the functions associated with previously identified candidate genes. Although these technologies have not yet directly led to the improvement of cultivars, the identification of candidate genes for stress resistance and tolerance will surely accelerate future breeding of elite chickpea cultivars.

## Conclusions

A major aim of chickpea breeding is to develop cultivars with a high level of resistance to yield reducing biotic stresses. Extensive searches for resistance to various biotic stresses have been conducted by screening germplasm, including cultivated varieties, landraces, and wild species. Resistance to some biotic stresses, such as AB and fusarium wilt, have been found in the chickpea and breeding for resistance to these diseases is making progress by identifying new resistance genes. To speed up the process of introgressing genes into chickpea elite genotypes, molecular tools can be integrated with conventional breeding approaches. Molecular markers associated with major QTLs conferring resistance to some biotic stresses have been located on linkage maps, and these markers can be used for efficient pyramiding of the traits of interest.

In an attempt to uncover important genes that are involved in resistance to biotic stresses, significant achievements have been made in chickpea genomics. Valuable resources, such as an integrated genetic map (Millán et al. 2010; Zatloukalová et al. 2011), a high resolution physical map (Zhang et al. 2010), EST libraries (Coram and Pang 2005a), bacterial artificial chromosomes (BAC) libraries (Rajesh et al. 2004,

2007b) and draft genome sequences (Varshney et al. 2013; Jain et al. 2013) have been generated. Although candidate genes identified from genomics have not yet been used directly to improve chickpea cultivars in the field, they may be used in this way in the near future.

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## References

Abbo S, Redden RJ, Yadav SS (2007) Ch 16: utilisation of wild relatives. In: Yadav SS, Redden R, Chen W, Sharma B (eds) Chickpea breeding and management. CAB International, Wallingford, pp 338–354

Abraham AD, Menzel W, Lesemann D-E, Varrelmann M, Vetten HJ (2006) *Chickpea chlorotic stunt virus*: a new polerovirus infecting cool-season food legumes in Ethiopia. Phytopathology 96:437–446

Abraham AD, Menzel W, Varrelmann M, Vetten HJ (2009) Molecular, serological and biological variation among *chickpea chlorotic stunt virus* isolates from five countries of North Africa and West Asia. Arch Virol 154:791–799

Acharjee S, Sarmah BK, Kumar PA, Olsen K, Mahon R, Moar WJ, Moore A, Higgins TJV (2010) Transgenic chickpeas (*Cicer arietinum* L.) expressing a sequence-modified *cry2Aa* gene. Plant Sci 178(3):333–339

Aftab M, Freeman A (2011) Temperate pulse viruses: *Alfalfa mosaic virus* Agnote No AG1206, *Cucumber mosaic virus* Agnote No AG1207, *Bean leafroll virus* Agnote No AG1252. Department of Environment and Primary Industries Victoria

Aftab M, Freeman A (2013) Temperate pulse viruses: *Beet western yellows virus* (BWYV). Department of Environment and Primary Industries (DEPI) Victoria Website Agnote No. AG1419

Agarwal G, Jhanwar S, Priya P, Singh VK, Saxena MS, Parida SK, Garg R, Tyagi AK, Jain M (2012) Comparative analysis of Kabuli chickpea transcriptome with Desi and wild chickpea provided a rich resource for development of functional markers. PLoS ONE 7:e52443

Aghakhani M, Dubey SC (2009) Determination of genetic diversity among Indian isolates of *Rhizoctonia bataticola* causing dry root rot of chickpea. Antonie Van Leeuwenhoek 96:607–619

Ahmad F (1999) Random amplified polymorphic DNA (RAPD) analysis reveals genetic relationships among the annual *Cicer* species. Theor Appl Genet 98:657–663

Ahmad F, Slinkard AE (2004) The extent of embryo and endosperm growth following interspecific hybridization between *Cicer arietinum* L. and related annual wild species. Genet Resour Crop Evol 51:765–772

Ahmad GD, Hafez A, Ashaf M (1952) Association of morphological characters with blight resistance. In: Proceedings of 4th Pakistan science conference, pp 17–19

Ahmad F, Gaur PM, Croser J (2005) Chickpea (*Cicer arietinum* L.). In: Singh RJ, Jauhar PP (eds) Genetic resources, chromosome engineering and crop improvement. Grain legumes, vol 1. CRC Press, Boca Raton, pp 187–217

Akem C, Kabbabeh S (1999) Screening for resistance to *Sclerotinia* stem rot in chickpea: a simple technique. Pak J Biol Sci 2:277–279

Ali M, Kumar S (2001) An overview of chickpea research in India. Indian J Pulse Res 14(2):81–89

Ali MEK, Inanga S, Sugimoto Y (2002) Soursce of resistance to Fusarium wilt of chickpea in Sudan. Phytopathol Mediterr 41:163–169

Ali H, Haq A, Shah T, Chen W (2012) Validation of molecular markers for resistance among Pakistani chickpea germplasm to races of *Fusarium oxysporum* f. sp. *ciceris*. Euro J Plant Pathol 132:237–244

Amian AA, Papenbrock J, Jacobsen HJ, Hassan F (2011) Enhancing transgenic pea *(Pisum sativum* L.) resistance against fungal diseases through stacking of two antifungal genes (chitinase and glucanase). GM. Crops 2(2):104–109

Ananda Rao PK, Haware MP (1987) Inheritance of dry root rot (*Rhizoctonia bataticola*) resistance in chickpea (*Cicer arietinum*). Plant Breed 98:349–352

Anbessa Y, Taran B, Warkentin TD, Tullu A, Vandenberg A (2009) Genetic analyses and conservation of QTL for ascochyta blight resistance in chickpea (*Cicer arietinum* L.). Theor Appl Genet 119:757–765

Ansari MA, Patel BA, Mhase NL, Patel DJ, Douaik A, Sharma SB (2004) Tolerance of chickpea (*Cicer arietinum* L.) lines to root-knot nematode, *Meloidogyne javanica* (Treub) Chitwood. Genet Resour Crop Evol 51(4):449–453

Anuradha C, Gaur P, Pande S, Kishore G, Ganesh M, Kumar J, Varshney R (2011) Mapping QTL for resistance to Botrytis grey mould in chickpea. Euphytica 182(1):1–9

Asaad N, Kumari SG, Haj-Kassem A, Shalaby AA, Al-Shaabi S, Malhotra RS (2009) Detection and characterization of chickpea chlorotic stunt in Syria. J Phytopathol 157:756–761

Ashby JW (1984) *Bean leaf roll virus*. CMI/AAB Descriptions of Plant Viruses, no. 286

Aubert G, Morin J, Jacquin F, Loridon K, Quillet MC, Petit A, Rameau C, Lejeune-Hénaut I, Huguet T, Burstin J (2006) Functional mapping in pea, as an aid to the candidate gene selection and for investigating synteny with the model legume *Medicago truncatula*. Theor Appl Genet 112:1024–1041

Badami PS, Nallikarjuna N, Moss JP (1997) Interspecific hybridization between *Cicer arietinum* and *C. pinnatifidum*. Plant Breed 116:393–395

Bakr MA, Ahmed F (1992) Botrytis gray mold of chickpea in Bangladesh. In: Haware MP, Faris DG, Gowda CLL (eds) Botrytis gray mold of chickpea. Summary proceedings of the BARI/ICRISAT Working Group meeting. ICRISAT, Patancheru, pp 10–12

Bakr MA, Rahman ML, Ahmed AU (2002) Manifestation of Botrytis grey mould in chickpea in Bangladesh. In: Bakr MA, Siddique KHM, Johansen C (eds) Integrated management of Botrytis grey mould of chickpea in Bangladesh

and Australia. Bangladesh Research Institute, Joydebour, pp 63–69
Bayaa B, Udupa SM, Baum M, Malhotra RS, Kabbabeh S (2004) Pathogenic variability in Syrian isolates of *Ascochyta rabiei*. In: Proceedings of the 5th European conference of grain legumes and 2nd international conference on legume genomics and genetics, June 7–11, Dijon, France, p 306
Berger JD, Abbo S, Turner NC (2003) Ecogeography of annual wild *Cicer* species: the poor state of the world collection. Crop Sci 43:1076–1090
Bhardwaj R, Sandu JS, Kaur L, Gupta SK, Gaur PM, Varshney R (2010) Genetics of aschochyta blight resistance in chickpea. Euphytica 171:337–343
Boland G, Hall R (1994) Index of plant hosts of *Sclerotinia sclerotiorum*. Can J Plant Pathol 16:93–108
Bos L, Hampton RO, Makkouk KM (1988) Viruses and virus diseases of pea, lentil faba bean and chickpea. In: Summerfield RJ (ed) World Crops: cool season food legumes. Kluwer Academic Publishers, Dordrecht, pp 591–615
Brayford D (1998) *Fusarium oxysporum* f. sp. *ciceris*. IMI Descriptions of Fungi and Bacteria No. 1113
Bretag TW, Mebalds MI (1987) Pathogenicity of fungi isolated from *Cicer arietinum* (chickpea) grown in northwestern Victoria. Aust J Exp Agric 27:141–148
Brinsmead RB, Rettke ML, Irwin JAG, Ryley MJ, Langdon PW (1985) Resistance in chickpea to *Phytophthora megasperma* f. sp. medicaginis. Plant Dis 69:504–506
Bronner R, Westphal E, Dreger F (1991) Enhanced peroxidase activity associated with the hypersensitive response of *Solanum dulcamara* to the gall mite *Aceria cladophthirus* (Acari: Eriophyoidea). Can J Bot 69(10):2192–2196
Brunt A, Crabtree K, Dallwitz M, Gibbs A, Watson L (1996) Viruses of plants: descriptions and lists from VIDE database. CAB International, Wallingford
Butler DR (1993) How important is crop microclimate in chickpea Botrytis gray mold? In: Haware MP, Gowda CLL, McDonald D (eds) Recent advances in research on Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 7–9
CABI (1983) Distribution maps of plant pests: *Aphis craccivora*. http://www.cabi.org/dmpp/?loadmodule=review&page=4049&reviewid=80108&site=164. Accessed 15 Nov 2011
CABI (2007) Crop Protection Compendium, 2007 Edition. CAB International, Wallingford (Online version). http://www.cabi.org/compendia/cpc/. Accessed May 2014
Cachinero JM, Hervas A, Jimenez-Diaz RM, Tena M (2002) Plant defence reactions against Fusarium wilt in chickpea induced by incompatible race 0 of *Fusarium oxysporum* f. sp. *ciceri* and non-host isolates of *F. oxysporum*. Plant Pathol 51:765–776
Castillo P, Vovlas N, Jiménez-Díaz RM (1998) Pathogenicity and histopathology of *Pratylenchus thornei* populations on selected chickpea genotypes. Plant Pathol 47(3):370–376
Castillo P, Navas-Cortés JA, Landa BB, Jiménez-Díaz RM, Vovlas N (2008) Plant-parasitic nematodes attacking chickpea and their in planta interactions with rhizobia and phytopathogenic fungi. Plant Dis 92(6):840–853
Castro P, Piston F, Madrid E, Millan T, Gil J, Rubio J (2010) Development of chickpea near-isogenic lines for fusarium wilt. Theor Appl Genet 121:1519–1526
Caten CE (1987) The concept of race in plant pathology. In: Wolfe MS, Caten CE (eds) Populations of plant pathogens: Their dynamics and genetics. Blackwell Scientific Publications, Oxford
Ceasar SA, Ignacimuthu S (2012) Genetic engineering of crop plants for fungal resistance: role of antifungal genes. Biotechnol Lett 34(6):995–1002
Chakraborti D, Sarkar A, Mondal H, Das S (2009) Tissue specific expression of potent insecticidal *Allium sativum* leaf agglutinin (ASAL) in important pulse crop chickpea (*Cicer arietinum* L) to resist the phloem feeding *Aphis craccivora*. Transgen Res 18(4):529–544
Chalam TV, Reddy MV, Nene YL, Beniwal SPS, Subbayya J (1986) Some properties of a strain of *Cucumber mosaic virus* isolated from chickpea in India. Plant Dis 70:128–130
Chang KF, Ahmed HU, Hwang SF, Gossen BD, Strellkov SE, Blade SF, Turnbull GD (2007) Sensitivity of field populations of *Ascochyta rabiei* to chlorothalonil, mancozeb and pyraclostrobin fungicides and effect of strobilurin fungicides on the progress of ascochyta blight of chickpea. Can J Plant Sci 87:937–944
Chaturvedi R, Singh IS, Gupta AK (1995) Inheritance of resistance to Botrytis grey mould in chickpea (*Cicer arietinum* L.). Legume Res 18:1–4
Chen W (2011) Dry root rot of chickpea. Compendium of chickpea and lentil diseases and pests, pp 15–16
Chen W, Coyne CJ, Peever TL, Muhlbauer FJ (2004) Characterization of chickpea differentials for pathogenicity assay of ascochyta blight and identification of chickpea accessions resistant to *Didymella rabiei*. Plant Pathol 53:759–769
Chen W, Mcphee KE, Muehlbauer FJ (2005) Use of a mini-dome bioassay and grafting to study resistance of chickpea to ascochyta blight. J Phytopathol 153:579–587
Chen W, Schatz B, Henson B, McPhee KE, Muehlbauer FJ (2006) First report of *Sclerotinia* stem rot of chickpea caused by *Sclerotinia sclerotiorum* in North Dakota and Washington. Plant Dis 90:114–114
Cho S, Chen W, Muehlbauer FJ (2004) Pathotype-specific genetic factors in chickpea (*Cicer arietinum* L.) for quantitative resistance to ascochyta blight. Theor Appl Genet 109:733–739
Choi HK, Luckow MA, Doyle J, Cook DR (2006) Development of nuclear gene-derived molecular markers linked to legume genetic maps. Mol Genet Gen 276:56–70
Choi HW, Kim YJ, Lee SC, Hong JK, Hwang BK (2007) Hydrogen peroxide generation by the pepper extracellular peroxidase $CaPO_2$ activates local and systemic cell death and defense response to bacterial pathogens. Plant Physiol 145(3):890–904
Chongo G, Gossen BD (2003) Diseases of Chickpea. In: Bailey KL, Gossen BD, Gugel R, Morrall RAA (eds) Diseases of field crops in Canada. Canadian Phytopathological Society, Saskatoon, pp 185–190
Chongo G, Gossen BD, Buchwaldt L, Adhikari T, Rimmer SR (2004) Genetic diversity of *Ascochyta rabiei* in Canada. Plant Dis 88:4–10
Choudhary S, Sethy NK, Shokeen B, Bhatia S (2006) Development of sequence-tagged microsatellite site markers for chickpea (*Cicer arietinum* L.). Mol Ecol Notes 6:3–95
Chu PWG, Vetten HJ (2003) *Subterranean clover stunt virus*. AAB Descr Plant Viruses 396:16

Cobos MJ, Fernandez MJ, Rubio J, Kharrat M, Moreno MT, Gil J, Millan T (2005) A linkage map of chickpea (*Cicer arietinum* L.) based on populations from Kabuli × Desi crosses: location of genes for resistance to fusarium wilt race 0. Theor Appl Genet 110:1347–1353

Cobos M, Rubio J, Strange R, Moreno M, Gil J, Millan T (2006) A new QTL for Ascochyta blight resistance in a RIL population derived from an interspecific cross in chickpea. Euphytica 149:105–111

Collard B, Ades P, Pang E, Brouwer J, Taylor P (2001) Prospecting for sources of resistance to ascochyta blight in wild *Cicer* species. Australas Plant Pathol 30:271–276

Collard BCY, Pang ECK, Ades PK, Taylor PWJ (2003) Preliminary investigation of QTLs associated with seedling resistance to ascochyta blight from *Cicer echinospermum*, a wild relative of chickpea. Theor Appl Genet 107:719–729

Coram T, Pang E (2005a) Isolation and analysis of candidate ascochyta blight defence genes in chickpea. Part I. Generation and analysis of an expressed sequence tag (EST) library. Physiol Mol Plant Pathol 66:192–200

Coram T, Pang E (2005b) Isolation and analysis of candidate ascochyta blight defence genes in chickpea. Part II. Microarray expression analysis of putative defence-related ESTs. Physiol Mol Plant Pathol 66:201–210

Coram T, Pang E (2006) Expression profiling of chickpea genes differentially regulated during a resistance response to *Ascochyta rabiei*. Plant Biotechnol J 4:647–666

Coram TE, Mantri NL, Ford R, Pang ECK (2007) Evans Review No. 4: functional genomics in chickpea: an emerging frontier for molecular-assisted breeding. Funct Plant Biol 34:861–873

Cowgill SE, Lateef SS (1996) Identification of antibiotic and antixenotic resistance to *Helicoverpa armigera* (Lepidoptera: Noctuidae) in chickpea. J Econ Entomol 89(1):224–229

Cunnington J, Lindbeck K, Jones RH (2007) National Diagnostic Protocol for the detection of Fusarium Wilt of Chickpea (*Fusarium oxysporum* f. sp. *ciceris*. Developed and published by Plant Health Australia. http://www.planthealthaustralia.com.au/wp-content/uploads/2013/03/Fusarium-wilt-of-chickpea-DP-2007.pdf

Dale ML, Irwin JAG (1991a) Stomata as an infection court for *Phytophthora megasperma* f. sp. *medicaginis* in chickpea and a histological study of infection. Phytopathology 81:375–379

Dale ML, Irwin JAG (1991b) Glasshouse and field screening of chickpea cultivars for resistance to *Phytophthora megasperma* f. sp. *medicaginis*. Aust J Exp Agric 31:663

Davidson JA, Pande S, Bretag TW, Lindbeck KD, Kishore GK (2004) In: Elad Y, William B, Tudzynski P, Delen N (eds) Biology, pathology and control. Kluwer Academic Publishers, Dordrecht

Deb AC, Khaleque MA (2009) Nature of gene action of some quantitative traits in Chickpea (*Cicer arietinum* L). World J Agric Sci 5(3):361–368

Dereeper A, Guignon V, Blanc G, Audic S, Buffet S, Chevenet F, Dufayard JF, Guindon S, Lefort V, Lescot M, Claverie JM, Gascuel O (2008) Phylogeny.fr: robust phylogenetic analysis for the non-specialist. Nucleic Acids Res 36:465–469

Dey SK, Singh G (1993) Resistance to ascochyta blight in chickpea genetic basis. Euphytica 68:147–153

Di Vito M, Greco N (1988) The relationship between initial population densities of M*eloidogyne artiellia* and yield of winter and spring chickpea. Nematol Mediterr 16:163–166

Díaz-Franco A, Pérez-García P (1995) Control químico de la roya y la rabia del garbanzo y su influencia en el rendimiento de grano. Rev Mex Fitopatol 13:123–125

Do HM, Hong JK, Jung HW, Kim SH, Ham JH, Hwang BK (2003) Expression of peroxidase-like genes, $H_2O_2$ production, and peroxidase activity during the hypersensitive response to *Xanthomonas campestris* pv. *vesicatoria* in *Capsicum annuum*. Mol Plant Microbe Interact 16:196–205

Douine L, Quiot JB, Marchoux G, Archange P (1979) Index of plants susceptible to *Cucumber mosaic virus* (CMV): bibliographical study. Ann Phytopathol 11:439–475

Dua RP, Chaturvedi SK, Sewak Shiv (2001) Reference varieties of chickpea for IPR regime. Indian Institute of Pulses Research, Kanpur, p **34**

Duffus JE (1960) Radish yellows, a disease of radish, sugar beet and other crops. Phytopathology 50:389–394

Edwardson JR, Christie RG (1991) CRC Handbook of viruses infecting Legumes. CRC Press, Boca Raton

Edwardson JR, Christie RG (1997) Viruses infecting peppers and other Solanaceous crops. Monograph 18-1, vol 1. University of Florida Agricultural Experiment Station

El Bouhssini M, Mardini K, Malhotra RS, Joubi A, Kagka N (2008) Effects of planting date, varieties and insecticides on chickpea leaf miner (*Liriomyza cicerina* R.) infestation and the parasitoid *Opius monilicornis* F. Crop Prot 27(6):915–919

Erler F, Ceylan F, Erdemir T, Toker C (2009) Preliminary results on evaluation of chickpea, *Cicer arietinum*, genotypes for resistance to the pulse beetle, *Callosobruchus maculatus*. J Insect Sci 9(58):1–7

Eser D (1976) Heritability of some important plant characters, their relationships with plant yield and inheritance of Ascochyta blight resistance in chickpea (*Cicer arietinum* L.). Ankara University, Faculty of Agriculture Publications No. 620, Ankara

Evans K, White P, Mangano P (2005) Insects pests of pulses. In: White P, Seymour M, Burgess P, Harries M (eds) Producing pulses in the southern agricultural region. Department of Agriculture, Perth, Western Australia, pp 104–111

Food and Agriculture Organization of the United Nations (2012) FAO statistics. Food and Agriculture Organization of the United Nations, Rome

Flandez-Galvez H, Ford R, Pang ECK, Taylor PWJ (2003a) An intraspecific linkage map of the chickpea (*Cicer arietinum* L.) genome based on sequence-tagged microsatellite site and resistance gene analog markers. Theor Appl Genet 106:1447–1456

Flandez-Galvez H, Ades R, Ford R, Pang E, Taylor P (2003b) QTL analysis for ascochyta blight resistance in an intraspecific population of chickpea (*Cicer arietinum* L.). Theor Appl Genet 107:1257–1265

Fontana GS, Santini L, Caretto S, Frugis G, Mariotti D (1993) Genetic transformation in the grain legume *Cicer arietinum* L. Plant Cell Rep 12:194–198

Fournier E, Giraud T, Loiseau A, Vautrin D, Estoup A, Solignac M, Cornuet JM, Brygoo Y (2002) Characterization of nine polymorphic microsatellite loci in the fungus *Botrytis cinerea* (Ascomycota). Mol Ecol Notes 2:253–255

France RA, Abawi GS (1994) Interaction between *Meloidogyne incognita* and *Fusarium oxysporum* f. sp. *phaseoli* on selected bean genotypes. J Nematol 26(4):467–474

Franz A, Makkouk KM, Katul L, Vetten HJ (1996) Monoclonal antibodies for the detection and differentiation of *Faba bean necrotic yellows virus isolates*. Ann Appl Biol 128:255–268

Fuhlbohm MJ, Tatnell JR, Ryley MJ (2003) First report of stem rot and wilt of chickpea caused by *Sclerotinia minor* in Queensland, Australia. Aust Plant Pathol 32:323–324

Garg R, Patel RK, Tyagi AK, Jain M (2011) *De novo* assembly of chickpea transcriptome using short reads for gene discovery and marker identification. DNA Res 18:53–63

Gaur PM, Pande S, Upadhyaya HD, Rao BV (2006) Extra-large Kabuli chickpea with high resistance to Fusarium wilt. SAT eJ 2(1):1–2. http://www.ejournal.icrisat.org

Gaur R, Sethy NK, Choudhary S, Shokeen B, Gupta V, Bhatia S (2011) Advancing the STMS genomic resources for defining new locations on the intraspecific genetic linkage map of chickpea (*Cicer arietinum* L.). BMC Genom 12:117

Gaur R, Azam S, Jeena G, Khan AW, Choudhary S, Jain M, Yadav G, Tyagi AK, Chattopadhyay D, Bhatia S (2012) High-throughput SNP discovery and genotyping for constructing a saturated linkage map of chickpea (*Cicer arietinum* L.). DNA Res 19(5):357–373

Gil J, Nadal S, Luna D, Moreno M, de Haro A (1996) Variability of some physicochemical characters in Desi and Kabuli chickpea types. J Sci Food Agric 71:179–184

Gowda SJM, Radhika P, Kadoo NY, Mhase LB, Gupta VS (2009) Molecular mapping of wilt resistance genes in chickpea. Mol Breed 24:177–183

Greco N, Di Vito M, Saxena MC, Reddy MV (1988) Effect of *Heterodera ciceri* on yield of chickpea and lentil and development of this nematode on chickpea in Syria. Nematologica 34(1):98–114

Greco N, Di Vito M, Malhotra RS, Saxena MC, Zaccheo G, Catalano F, Hajjar S (2003) Effect of population densities of *Heterodera ciceri* on new resistant lines of chickpea. Nematol Mediterr 31(2):173–180

Grewal JS, Pal M, Rewal N (1992) Botrytis gray mold of chickpea in India. In: Haware MP, Faris DG, Gowda CLL (eds) Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 6–8

Guarino L (ed) Global Diversity Trust Rome (2008) global strategy for the ex situ conservation of chickpea (*Cicer arietinum* L.), p 55. http://www.croptrust.org/documents/web/CicerStrategy_FINAL_2Dec08.pdf. Accessed 24 July 2014

Gumber RK, Kumar J, Haware MP (1995) Inheritance of resistance to fusarium wilt in chickpea. Plant Breed 114:277–279

Gupta PK, Kumar J, Mir RR, Kumar A (2010) Marker-assisted selection as a component of conventional plant breeding. Plant breeding reviews. Wiley, New York, pp 145–217

Gurha SN, Singh G, Sharma YR (2003) Diseases of chickpea and their management. In: Ali M, Kumar S, Singh NB (eds) Chickpea research in India. Army Printing Press, Lucknow, pp 195–227

Hafiz A, Ashraf M (1953) Studies on inheritance of resistance to Mycosphaerella blight in gram. Phytopathology 43:580–581

Halila MH, Strange RN (1996) Identification of the causal agent of wilt of chickpea in Tunisia as *Fusarium oxysporum* f. sp. *ciceris* race 0. Phytopathol Mediterr 35:67–74

Halila MH, Strange RN (1997) Screening of Kabuli chickpea germplasm for resistance to Fusarium wilt. Euphytica 96:273–279

Haware MP (1990) Fusarium wilt and other important diseases of chickpea in the Mediterranean area. Opt Méditerr Sér Sémin 9:61–64

Haware MP (1998) Diseases of chickpea. In: Allen DJ, Lenne JM (eds) The pathology of food and pasture legumes. ICARDA. CAB International, Wallingford, pp 473–516

Haware MP, McDonald D (1992) Integrated management of Botrytis gray mold of chickpea. In: Haware MP, Faris DG, Gowda CLL (eds) Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 3–6

Haware MP, McDonald D (1993) Botrytis gray mold of chickpea. In: Haware MP, Gowda CLL, McDonald D (eds) Recent advances in research on Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 3–6

Haware MP, Nene YL (1982) Screening chickpea for resistance to Botrytis gray mold. Int Chick News 6:17–18

Haware MP, Nene YL, Mathur SB (1986) Seed-borne diseases of chickpea. Technical Bulletin, Danish Government Institute of Seed Pathology for Developing Countries

Haware MP, Narayana JR, Pundir RPS (1992) Evaluation of wild *Cicer* species for resistance to four chickpea diseases. Int Chick News 27:16–18

Haware MP, Tripathi HS, Rathi YPS, Lenne JM, Janthi S (1997) Integrated management of Botrytis gray mold of chickpea: cultural, chemical, biological and resistance options. In: Haware MP, Lenne JM, Gowda CLL (eds) Recent advances in research on Botrytis Gray mold of chickpea. ICRISAT, Patancheru, pp 9–12

Hawthorne W, Davidson J, McMurray L, Hobson K, Lindbeck K, Brand J (2012) Chickpea disease management strategy (southern region). Southern pulse bulletin, PA 2012#8

Hernández Fernández V, Martín Barbarroja J, Jiménez Díaz RM, Castillo P (2005) Reproductive fitness of *Meloidogyne artiellia* populations on chickpea and durum wheat. Nematology 7(2):243–247

Hilton SA (2000) Canadian plant disease survey. Agriculture and Agri-Food Canada 80:1–151. http://www.cps-scp.ca/download/cpds_v80.pdf. Accessed 5 May 2014

Hiremath PJ, Farmer A, Cannon SB, Woodward J, Kudapa H, Tuteja R, Kumar A, Bhanuprakash A, Mulaosmanovic B, Gujaria N, Krishnamurthy L, Gaur PM, Kavikishor PB, Shah T, Srinivasan R, Lohse M, Xiao Y, Town CD, Cook DR, May GD, Varshney RK (2011) Large-scale transcriptome analysis in chickpea (*Cicer arietinum* L.), an orphan legume crop of the semi-arid tropics of Asia and Africa. Plant Biotechnol J 9:922–931

Hollaway G, Freeman A, McLean M, Richardson H, Henry F, Aftab M, Spackmann M, Marcroft S, Elliott V, Rodda M, Li H, McQueen V, Kant P (2012) Identification and management of field crop diseases in Victoria. Department of

Primary Industries, Melbourne. ISBN 978-1-74217-752-6 (print). http://www.croppro.com.au/crop_disease_manual.php

Horn NM, Reddy SV, Roberts IM, Reddy DVR (1993) *Chickpea chlorotic dwarf virus*, a new leafhopper- transmitted Geminivirus of chickpea in India. Ann Appl Biol 122:467–479

Horn NM, Reddy SV, Reddy DVR (1995) Assessment of yield losses caused by *chickpea chlorotic dwarf geminivirus* in chickpea (*Cicer arietinum* L.) in India. Eur J Plant Pathol 101:221–224

Hüttel B, Winter P, Weising K, Choumane W, Weigand F (1999) Sequence-tagged microsatellite site markers for chickpea (*Cicer arietinum* L.). Genome 42:210–217

ICARDA (1998) Germplasm program: legumes annual report for 1998. ICARDA, Aleppo

Infantino A, Kharrat M, Riccioni L, Coyne CJ, McPhee KE, Grunwald NJ (2006) Screening techniques and sources of resistance to root diseases in cool season food legumes. Euphytica 147:201–221

Iruela M, Castro P, Rubio J, Cubero JI, Jacinto C, Millan T, Gil J (2007) Validation of a QTL for resistance to ascochyta blight linked to resistance to fusarium wilt race 5 in chickpea (*Cicer arietinum* L.). Eur J Plant Pathol 119:29–37

Irwin JAG, Dale JL (1982) Relationships between *Phytophthora megasperma* isolates from chickpea, lucerne and soybean. Aust J Bot 30:199–210

Isenegger DA, MacLeod WJ, Ford R, Pande S, Abu Bakr M, Taylor PWJ (2005) Genetic structure of *Botrytis cinerea* that causes Botrytis grey mould disease of chickpea in Bangladesh. In: Innovations for sustainable plant health—15th Australian Plant Pathological Society handbook, p 224

Isenegger DA, Macleod WJ, Ford R, Taylor PWJ (2008) Genotypic diversity and migration of clonal lineages of *Botrytis cinerea* from chickpea fields of Bangladesh inferred by microsatellite markers. Plant Pathol 57:967–973

Jain M, Misra G, Patel RK, Priya P, Jhanwar S, Khan AW, Shah N, Singh VK, Garg R, Jeena G, Yadav M, Kant C, Sharma P, Yadav G, Bhatia S, Tyagi AK, Chattopadhyay D (2013) A draft genome sequence of the pulse crop chickpea (*Cicer arietinum* L.). Plant J 74(5):715–729

Jalali BL, Chand H (1992) Chickpea wilt. In: Singh US, Mukhopadhayay AN, Kumar J, Chaube HS (eds) Plant diseases of international importance. Diseases of cereals and pulses, vol 1. Prentice Hall, Englewood Cliffs, pp 429–444

Jamil FF, Sarwar N, Sarwar M, Khan JA, Geistlinger J, Kahl G (2000) Genetic and pathogenic diversity within *Ascochyta rabiei* (Pass.) Lab. populations in Pakistan causing blight of chickpea (*Cicer arietinum* L.). Physiol Mol Plant Pathol 57:243–254

Jandhyala P (2005) ICRISAT plans to start open field trials for transgenic groundnut. In: Business standard. http://www.seedquest.com/News/releases/2005/February/11365.htm. Accessed 5 July 2014

Jhanwar S, Priya P, Garg R, Parida SK, Tyagi AK, Jain M (2012) Transcriptome sequencing of wild chickpea as a rich resource for marker development. Plant Biotechnol J 10(6):690–702

Jones DR (1983) Chickpea rust—a disease new to Australia. Queensland Dep of Primary Industry Farm Note AGDEX 168/637

Kalo A, Seres A, Taylor SA, Jaka J, Kevei ZA, Kereszt GE, Ellis THN, Kiss GB (2004) Comparative mapping between *Medicago sativa* and *Pisum sativum*. Mol Genet Gen 272:235–246

Kanouni H, Taleei A, Peyghambari SA, Okhovat SM, Baum M, Abang M (2009) QTL analysis for ascochyta blight resistance in chickpea (*Cicer arietinum* L.) using microsatellite markers. J Agric Res 25:109–127

Kanouni H, Taleei A, Okhovat M (2011) Aschochyta blight (*Aschochyta rabei* (Pass.) Lab.) of chickpea (*Cicer arietinum* L). Strategies for resistance. Int J Plant Breed Genet 5:1–22

Kar S, Johnson TM, Nayak P, Sen SK (1996) Efficient transgenic plant regeneration through *Agrobacterium*-mediated transformation of Chickpea (*Cicer arietinum* L). Plant Cell Rep 16:32–37

Kar S, Basu D, Das S, Ramakrishnan NA, Mukherjee P, Nayak P, Sen SK (1997) Expression of *cry1A(c)* gene of *Bacillus thuringiensis* in transgenic chickpea plants inhibits development of podborer (*Heliothis armigera*) larvae. Transgen Res 6:177–185

Katul L (1992) Characterization by serology and molecular biology of *Bean leafroll virus* and *Faba bean necrotic yellows virus*. PhD Thesis, University of Gottingen, Germany

Katul L, Vetten HJ, Maiss E, Makkouk KM, Lesemann DE, Caster R (1993) Characterisation and serology of virus-like particles associated with *Faba bean necrotic yellows*. Ann Appl Biol 123:629–647

Kazan K, Muehlbauer FJ, Weeden NF, Ladizinsky G (1993) Inheritance and linkage relationships of morphological and isozyme loci in chickpea (*Cicer arietinum* L.). Theor Appl Genet 86:417–426

Khan MR, Ashraf S, Shahid S, Anwer MA (2010) Response of some chickpea cultivars to foliar, seed and soil inoculations with *Botrytis cinerea*. Phytopathol Mediterr 49:275–286

Kharrat M, Halila MH, Linke KH, Haddar T (1992) First report of *Orobanche foetida* Poiret on faba bean in Tunisia. Fabis Newsl 30:46–47

Kishore GK (2005) Cultural, morphological, pathogenic and genetic variation in *Botrytis cinerea*, causal agent of gray mold in chickpea. PhD Thesis, Jawaharlal Nehru Technological University, Hyderabad

Knights EJ, Southwell RJ, Schwinghamer MW (2003) Evaluation of wild *Cicer* species for resistance to phytophthora root rot. In: Sharma RN, Shrivastava GK, Rathore AL, Sharma ML, Khan MA (eds) Chickpea research for the millennium; proceedings of the international chickpea conference. Indira Gandhi Agricultural University, Raipur, p 54

Knights EJ, Southwell RJ, Schwinghamer MW, Harden S (2008) Resistance to *Phytophthora medicaginis* Hansen and Maxwell in wild *Cicer* species and its use in breeding root rot resistant chickpea (*Cicer arietinum* L.). Aust J Agric Res 59:383–387

Koebner R, Summers R (2007) Marker-assisted selection in wheat: evolution, not revolution. In: Guimarães E, Ruane J, Scherf B, Sonnino A, Dargie J (eds) Marker-assisted selection. Current status and future perspectives in crops,

livestock, forestry and fish. Food and Agriculture Organization of the United Nations, Rome, pp 51–58

Kolesík P, Pastucha L (1992) Chickpea leafminer *Liriomyza cicerina* (Rondani, 1875) [Diptera, Agromyzidae] - a new species of Czecho-Slovak fauna. Biológia (Bratislava) 47:439–440

Kraft JM, Haware MP, Jimenez-Diaz RM, Bayaa B, Harrab M (1994) Screening techniques and sources of resistance to root rots and wilt in cool season food legumes. In: Muehlbauer FJ, Kaiser WJ (eds) Expanding the production and use of cool season food legums. Kluwer Academic Publishers, Dordrecht, pp 268–289

Krishnamurthy KV, Suhasani K, Sagare AP, Meixner M, de Kathen A, Pickardt T, Schieder O (2000) *Agrobacterium* mediated transformation of chickpea (*Cicer arietinum* L.) embryo axes. Plant Cell Rep 19:235–240

Kumar S (1998) Inheritance of resistance to Fusarium wilt (race 2) in chickpea. Plant Breed 117:139–142

Kumar J, Yadav SS, Kumar R, Hegde V, Singh AK, Singh N (2005) Evaluation of chickpea (*Cicer arietinum* L.) germplasm for stunt virus and phonological traits. In: Abstract of 4th international food legume research conference, pp 18–22

Kumar PL, Kumari SG, Waliyar F (2008) Virus diseases of chickpea. In: Rao GP, Kumar PL, Penna RJH (eds) Characterization, diagnosis and management of plant viruses, vol 3., Vegetable and Pulse Crops Studium Press LLC, Texas, pp 213–234

Kumari SG, Makkouk KM, Attar N, Ghulam W, Lesemann DE (2004) First report of *Chickpea chlorotic dwarf virus* infecting spring chickpea in Syria. Plant Dis 88:424

Kusmenoglu I (1990) Ascochyta blight of chickpea: inheritance and relationship to seed size, morphological traits and isozyme variation. MSc Thesis, Washington State University

Ladizinsky G, Adler A (1976) Genetic relationships among the annual species of *Cicer* L. Theor Appl Genet 48:197–203

Laha SK, Khatua DC (1988) Sources of resistance against gray mold and stemphylium blight of gram. Environ Ecol 6(3):656–659

Landa BB, Navas-Cortes JA, del mar Jiminez-Gasco M, Katan J, Retig B, Jimenez-Diaz RM (2006) Temperature response of chickpea cultivars to races of *Fusarium oxysporum* f. sp. *ciceris*, causal agent of fusarium wilt. Plant Dis 90:365–374

Larsen RC, Miklas PN (2001) Effect of *Red clover vein mosaic carlavirus* infection on seed production and biomass yield in chickpea. Phytopathology 91(6 Supplement):S45

Larsen RC, Porter LD (2010) Identification of novel sources of resistance to *Pea enation mosaic virus* in chickpea germplasm. Plant Pathol 59:42–47

Lateef SS (1985) Gram pod borer (*Heliothis armigera*) (Hub.) resistance in chickpeas. Agric Ecosyst Environ 14(1–2):95–102

Lawo NC, Mahon RJ, Milner RJ, Sarmah BK, Higgins TJV, Romeis J (2008) Effectiveness of Bt chickpeas and the entomopathogenic fungus *Metarhizium anisopliae* to control *Helicoverpa armigera* (Lepidoptera: Noctuidae). Appl Environ Microbiol 74(14):4381–4389

Leslie JF, Summerell BA (2006) The *Fusarium* laboratory manual. Blackwell Publishing Asia, Richmond

Lichtenzveig J, Scheuring C, Dodge J, Abbo S, Zhang HB (2005) Construction of BAC and BIBAC libraries and their applications for generation of SSR markers for genome analysis of chickpea (*Cicer arietinum* L.). Theor Appl Genet 110:492–510

Lichtenzveig J, Bonfil DJ, Zhang HB, Shtienberg D, Abbo S (2006) Mapping quantitative trait loci in chickpea associated with time to flowering and resistance to *Didymella rabiei* the causal agent of Ascochyta blight. Theor Appl Genet 113:1357–1369

MacLeod B, Vanstone V, Jones R, Galloway J (2005) Producing pulses in the northern agricultural region—diseases of pulses. Bulletin 4656, Western Australian Government

Madrid E, Rubiales D, Moral A, Moreno MT, Millán T, Gil J, Rubio J (2008) Mechanism and molecular markers associated with rust resistance in a chickpea interspecific cross (*Cicer arietinum* × *Cicer reticulatum*). Eur J Plant Pathol 121:43–53

Madrid E, Chen W, Rajesh PN, Castro P, Millan T, Gil J (2013) Allele-specific amplification for the detection of ascochyta blight resistance in chickpea. Euphytica 189:183–190

Maheshwari TU, Sharma SB, Reddy DD, Haware MP (1995) Co-infection of wilt-resistant chickpeas by *Fusarium oxysporum* f. sp. *ciceri* and *Meloidogyne javanica*. J Nematol 27(4S):649–653

Mahon RJ, Olsen KM, Garsia KA, Young SR (2007) Resistance to *Bacillus thuringiensis* toxin Cry2aB in a strain of *Helicoverpa armigera* (Lepidoptera: Noctuidae) in Australia. J Econ Entomol 100:894–902

Malhotra RS, Singh KB, Di Vito M, Greco N, Saxena MC (2002) Registration of ILC 10765 and ILC 10766 chickpea germplasm lines resistant to cyst nematode. Crop Sci 42(5):1756

Mallikarjuna N (1999) Ovule and embryo culture to obtain hybrids from interspecific incompatible pollinations in chickpea. Euphytica 110:1–6

Markell S, Wise K, McKay K, Goswami R, Gudmestad N (2008) Plant disease management. NDSU Extension Service. North Dakota State University, Fargo

Martinez M (2007) Agromyzidae. In: Page T (ed) Fauna Europaea: Diptera: Brachycera. Fauna Europaea version 1.3. Fauna Europaea, Amsterdam http://www.faunaeur.org. Accessed 3 July 2014

Matheron ME, Porchas M (2000) First report of stem and crown rot of garbanzo caused by *Sclerotinia minor* in the United States and by *Sclerotinia sclerotiorum* in Arizona. Plant Dis 84:1250

Matthews P, McCaffery D, Jenkins L (2014) Winter crop variety sowing guide 2014. Department of Primary Industries, NSW Government

Mayer MS, Tullu A, Simon CJ, Kumar J, Kaiser WJ, Kramer JM, Kraft JM, Muehlbauer FJ (1997) Development of a DNA marker for Fusarium wilt resistance in chickpea. Crop Sci 37:1625–1629

Mehrotra M, Sanyal I, Amla DV (2011a) High-efficiency *Agrobacterium* mediated transformation of chickpea (*Cicer arietinum* L.) and regeneration of insect-resistant transgenic plants. Plant Cell Rep 30:1603–1616

Mehrotra M, Singh AK, Sanyal I, Altosaar I, Amla DV (2011b) Pyramiding of modified *cry1Ab* and *cry1Ac* genes of *Bacillus thuringiensis* in transgenic chickpea (*Cicer*

*arietinum* L.) for improved resistance to pod borer insect *Helicoverpa armigera*. Euphytica 182:87–102
Millán T, Clarke HJ, Siddique KHM, Buhariwalla HK, Gaur PM, Kumar J, Gil J, Kahl G, Winter P (2006) Chickpea molecular breeding: new tools and concepts. Euphytica 147:81–103
Millán T, Winter P, Jüngling R, Gil J, Rubio J, Cho S, Cobos M, Iruela M, Rajesh P, Tekeoglu M, Kahl G, Muehlbauer F (2010) A consensus genetic map of chickpea (*Cicer arietinum* L.) based on 10 mapping populations. Euphytica 175:175–189
Mitra J (2001) Genetics and genetic improvement of drought resistance in crop plants. Curr Sci 80:758–763
Montes MJ, Lopez-Brana I, Delibes A (2004) Root enzyme activities associated with resistance to *Heterodera avenae* conferred by gene *Cre7* in a wheat/*Aegilops triuncialis* introgression line. J Plant Physiol 161(4):493–495
Moore K, Ryley M, Schwinghamer M, Cumming G, Jenkins L (2011) Chickpea: Phytophthora root rot management. Northern Pulse Bulletin. PA 2011#11
Moore K, Kelly L, Ryley M, Hobson K, Knights T, Harden S, Martin W, King K, Nash P, Chiplin G, Bithell S (2015) Phytophthora in chickpea varieties - resistance rankings and yield loss. GRDC updated papers. http://www.grdc.com.au/Research-and-Development/GRDC-Update-Papers/2015/02/Phytophthora-in-chickpea-varieties-resistance-rankings-and-yield-loss
Moose SP, Mumm RH (2008) Molecular plant breeding as the foundation for 21st century crop improvement. Plant Physiol 147:969–977
Muehlbauer FJ, Kaiser WJ, Kusmenoglu I (1998a) Registration of 'Sanford' Chickpea. Crop Sci 38:282
Muehlbauer FJ, Kaiser WJ, Kusmenoglu I (1998b) Registration of 'Dwelley' Chickpea. Crop Sci 38:282–283
Muehlbauer FJ, Kaiser WJ, Kusmenoglu I (1998c) Registration of 'Myles' Chickpea. Crop Sci 38:283
Munns R (2005) Genes and salt tolerance: bringing them together. New Phytol 167:645–663
Naresh J, Malik V (1989) Observations on the insect pests of chickpea (*Cicer arietinum* L.) in Haryana. Bullet Entomol New Delhi 27:75–77
Nayak S, Zhu H, Varghese N, Datta S, Choi H-K, Horres R, Jüngling R, Singh J, Kavi Kishor P, Sivaramakrishnan S, Hoisington D, Kahl G, Winter P, Cook D, Varshney R (2010) Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with *Medicago truncatula* genome. Theor Appl Genet 120:1415–1441
Nene YL, Haware MP (1980) Screening chickpea for resistance to wilt. Plant Dis 64:379–380
Nene YL, Reddy MV (1987) Chickpea diseases and their control. In: Saxena MC, Singh RS (eds) The Chickpea. CAB International, Wallingford, pp 233–270
Nene YL, Reddy MV, Haware MP, Ghanekar AM, Amin KS (1991) Field diagnosis of chickpea disease and their control. Information Bulletin No 28, ICRISAT, Andhra Pradesh
Nene YL, Reddy MV, Haware MP, Ghanekar AM, Amin KS, Pande S, Sharma M (2012) Field diagnosis of chickpea diseases and their control. Information bulletin No. 28 (revised). International Crops Research Institute for the Semi-arid Tropics, Patancheru, p 60
Nguyen TT, Taylor PWJ, Redden RJ, Ford R (2004) Genetic diversity in *Cicer* using AFLP analysis. Plant Breed 123:173–179
Nimbalkar S, Harsulkar A, Giri A, Sainani M, Franceschi V, Gupta V (2006) Differentially expressed gene transcripts in roots of resistant and susceptible chickpea plant (*Cicer arietinum* L.) upon *Fusarium oxysporum* infection. Physio Mol Plant Pathol 68:176–188
Njambere EN, Chen W, Frate C, Wu B-M, Temple SR, Muehlbauer FJ (2008) Stem and crown rot of chickpea in California caused by *Sclerotinia trifoliorum*. Plant Dis 92:917–922
Oliveira JTA, Andrade NC, Martins-Miranda AS, Soares AA, Gondim DMF, Araj-Filho JH, Freire-Filho FR, Vasconcelos IM (2012) Differential expression of antioxidant enzymes and PR-proteins in compatible and incompatible interactions of cowpea (*Vigna unguiculata*) and the root-knot nematode *Meloidogyne incognita*. Plant Physiol Biochem 51:145–152
Pande S, Singh G, Rao JN, Bakr MA, Chaurasia PCP, Joshi S, Johansen C, Singh SD, Kumar J, Rahman MM, Gowda CLL (2002) Integrated management of Botrytis gray mold of chickpea. Information Bulletin No. 61, ICRISAT, Andhra Pradesh, India
Pande S, Siddique KHM, Kishore GK, Bayaa B, Gaur PM, Gowda CLL, Bretag TW, Crouch JH (2005) Ascochyta blight of chickpea (*Cicer arietinum* L.): a review of biology, pathogenicity, and disease management. Aust J Agric Res 56:317–332
Pande S, Krishna Kishore G, Upadhyaya HD, Narayana Rao J (2006a) Identification of sources of multiple disease resistance in mini-core collection of chickpea. Plant Dis 90:1214–1218
Pande S, Ramgopal D, Kishore GK, Mallikarjuna N, Sharma M, Pathak M, Narayana Rao J (2006b) Evaluation of wild *Cicer* species for resistance to Ascochyta blight and Botrytis grey mold in controlled environment at ICRISAT, Patancheru, India. J Sat Agric Res 2(1):1–3
Pande S, Sharma M, Gaur PM and Gowda CLL (2010) Host Plant Resistance to Ascochyta Blight of Chickpea. Information Bulletin No 82. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, p 40
Peever TL, Chen W, Abdo Z, Kaiser WJ (2012) Genetics of virulence in *Ascochyta rabiei*. Plant Pathol 61:754–760
Pérez-De-Luque A, Rubiales D, Cubero JI, Press MC, Scholes J, Yoneyama K, Takeuchi Y, Plakhine D, Joel DM (2005) Interaction between *Orobanche crenata* and its host legumes: unsuccessful haustorial penetration and necrosis of the developing parasite. Ann Bot 95(6):935–942
Pérez-De-Luque A, Fondevilla S, Pérez-Vich B, Aly R, Thoiron S, Simier P, Castillejo MA, Fernández-Martinez JM, Jorrín J, Rubiales D, Delavault P (2009) Understanding *Orobanche* and *Phelipanche*–host plant interactions and developing resistance. Weed Res 49:8–22
Popelka JC, Terryn N, Higgins TJV (2004) Gene technology for grain legumes: can it contribute to the food challenge in developing countries? Plant Sci 167(2):195–206
Porta-Puglia A, Aragona M (1997) Improvement of grain legumes general part: diseases. Field Crop Res 53:17–30
Porta-Puglia A, Crino P, Mosconi C (1996) Variability in virulence to chickpea of an Italian population of *Ascochyta rabiei*. Plant Dis 80:39–41

Price WC (1934) Isolation and study of some yellow strains of cucumber mosaic. Phytopathology 24:743–761

Pundir RPS, Reddy KN, Mengesha MH (1988) ICRISAT germplasm catalogue: evaluation and analysis. ICRISAT, Patancheru

Qureshi SH, Alam SS (1984) Pathogenic behavior of *Ascochyta rabiei* isolates on different cultivars of chickpea in Pakistan. Int Chick News 10:29–31

Ragagnin VA, Souza TLPO, Sanglard DA, Arruda KMA, Costa MR, Alzate-Marin AL, Carneiro JES, Moreira MA, Barros EG (2009) Development and agronomic performance of common bean lines simultaneously resistant to anthracnose, angular leaf spot and rust. Plant Breed 128:156–163

Ragazzi A (1982) Un grave attacco di ruggine su foglie di cese. (A serious attack of rust on *Cicer arietinum* leaves). Inform Fitopatol 2:41–43

Ragot M, Lee M (2007) Marker-assisted selection in maize: current status, potential, limitations and perspectives from the private and public sectors. In: Guimarães E, Ruane J, Scherf B, Sonnino A, Dargie J (eds) Marker-assisted selection. Current status and future perspectives in crops, livestock, forestry and fish. Food and Agriculture Organization of the United Nations, Rome, pp 117–150

Rajesh PN, Coyne C, Meksem K, DerSharma K, Gupta V, Muehlbauer FJ (2004) Construction of a Hind III bacterial artificial chromosome library and its use in identification of clones associated with disease resistance in chickpea. Theor Appl Genet 108:663–669

Rajesh P, Darlow M, Till B, Muehlbauer F (2007a) Estimation of mutation frequency in chickpea genome using TILLING. In: Lazo G, Grant D, Blake V (eds) Plant and animal genome XV conference, San Diego, p 47

Rajesh P, O'Bleness M, Main D, Roe B, Muehlbauer F (2007b) Analysis of genome organization and composition using 500 Kb BAC sequences in chickpea. In: Lazo G, Grant D, Blake V (eds) Plant and animal genome XV conference, San Diego

Rao VK, Krishnappa K (1995) Integrated management of *Meloidogyne incognita-Fusarium oxysporum* f. sp. *ciceri* wilt disease complex in chickpea. Int J Pest Manag 41(4):234–237

Ratnaparkhe MB, Santra DK, Tullu A, Muehlbauer FJ (1998) Inheritance of inter-simple sequence-repeat polymorphisms and linkage with a Fusarium wilt resistance gene in chickpea. Theor Appl Genet 96:348–353

Redden RJ, Berger JD (2007) History and origin of chickpea. In: Yadav SS, Redden R, Chen W and Sharma B (eds) Chickpea Breeding & Management, Chap 1. CAB International, Wallingford, pp 1–13

Reddy MV, Kabbabeh S (1985) Pathogenic variability in *Ascochyta rabiei* (Pass.) Labr. in Syria and Lebanon. Phytopathol Mediterr 24:265–266

Reddy MV, Singh KB (1984) Evaluation of a world collection of chickpea germplasm lines for resistance to ascochyta blight. Plant Dis 68:900–901

Reddy MV, Singh KB (1992) Registration of five chickpea germplasm lines resistant to ascochyta blight. Crop Sci 32:1079–1080

Reddy MV, Singh O, Bharati MP, Sah RP, Joshi S (1988) Botrytis grey mold epiphytotic of chickpea in Nepal. Int Chick News 19:15

Reed W, Cardona C, Sithanantham S, Lateff SS (1987) The chickpea pest insect and their control. In: Saxena MC, Singh KB (eds) The chickpea. CAB International, Wallingford, pp 283–318

Reuveni R, Ferreira JF (1985) The relationship between peroxidase activity and the resistance of tomatoes (*Lycopersicum esculentum*) to *Verticillium dahliae*. J Phytopathol 112(3):193–197

Rewal N, Grewal JS (1989a) Effect of temperature, light and relative humidity on conidial germination of three strains of *Botrytis cinerea* infecting chickpea. Int Phytopathol 42:79–83

Rewal N, Grewal JS (1989b) Differential response of chickpea to grey mould. Indian Phytopathol 42(2):265–268

Rewal N, Grewal JS (1989c) Inheritance of resistance to *Botrytis cinerea* Pers. *Cicer arietinum*. Euphytica 44: 61–63

Rubiales D, Fondevilla S (2010) Resistance of cool season food legumes to Aschochyta blight. Field Veg Crop Res 47:439–442

Rubiales D, Fondevilla S (2012) Future prospects for ascochyta blight resistance breeding in cool season food legumes. Front Plant Sci 3:27

Rubiales D, Moreno I, Moreno MT, Sillero JC (2001) Identification of partial resistance to chickpea rust (*Uromyces ciceris-arietini*). In: Proceedings of the 4th European conference on grain legumes, Cracow, pp 194–195

Rubiales D, Pérez-de-Luque A, Joel DM, Alcántara C, Sillero JC (2003) Characterization of resistance in chickpea to crenate broomrape (*Orobanche crenata*). Weed Sci 51(5):702–707

Rubiales D, Alcántara C, Sillero JC (2004) Variation in resistance to *Orobanche crenata* in species of *Cicer*. Weed Res 44(1):27–32

Rubiales D, Castillejo MA, Madrid E, Barilli E, Rispail N (2011) Legume breeding for rust resistance: lessons to learn from the model *Medicago truncatula*. Euphytica 180:89–98

Rubio J, Moussa E, Kharrat M, Moreno MT, Millan NT, Gil J (2003) Two genes and linked RAPD markers involved in resistance to *Fusarium oxysporum* f. sp. *ciceris* race 0 in chickpea. Plant Breed 122:188–191

Rubio J, Moreno MT, Moral A, Rubiales D, Gil J (2006) Registration of RIL58-ILC72/Cr5, a chickpea germplasm line with rust and Ascochyta blight resistance. Crop Sci 46:2331–2332

Sabbavarapu MM, Sharma M, Chamarthi SK, Swapna N, Rathore A, Thudi M, Gaur PM, Pande S, Singh S, Kaur L, Varshneyet RK (2003) Molecular mapping of QTLs for resistance to Fusarium wilt (race 1) and Ascochyta blight in chickpea (*Cicer arietinum* L.). Euphytica 193:121–133

Santra DK, Tekeoglu M, Ratnaparkhe M, Kaiser WJ, Muehlbauer FJ (2000) Identification and mapping of QTLs conferring resistance to ascochyta blight in chickpea. Crop Sci 40:1606–1612

Sanyal I, Singh AK, Kaushik M, Amla DV (2005) Agrobacterium-mediated transformation of chickpea (*Cicer arietinum* L.) with *Bacillus thuringiensis cry1Ac* gene for resistance against pod borer insect *Helicoverpa armigera*. Plant Sci 168(4):1135–1146

Saxena NP (1990) Status of chickpea in the Mediterranean basin. In: Sexana MC, Cubro JI, Wery J (eds) Present status

and future prospects of chickpea crop production and improvement in the Mediterranean countries. Options Méditerraneennes, (CIHEAM) Series A No. 9, pp 17–24
Schwinghamer MW, Johnstone GR, Lord-Johnston CF (1999) First report of *Bean leafroll virus* Luteovirus in Australia. Aust Plant Pathol 28:260–267
Senthil G, Williamson B, Dinkins R, Ramsay G (2004) An efficient transformation system for chickpea (*Cicer arietinum* L.). Plant Cell Rep 23:297–303
Sequeira RV, McDonald JL, Moore AD, Wright GA, Wright LC (2001) Host plant selection by Helicoverpa spp in chickpea-companion cropping systems. Entomol Exp Appl 101(1):1–7
Sethy NK, Shokeen B, Bhatia S (2003) Isolation and characterization of sequence-tagged microsatellite sites markers in chickpea (*Cicer arietinum* L.). Mol Ecol Notes 3:428–430
Sethy NK, Choudhary S, Shokeen B, Bhatia S (2006a) Identification of microsatellite markers from *Cicer reticulatum*: molecular variation and phylogenetic analysis. Theor Appl Genet 112:347–357
Sethy NK, Shokeen B, Edwards KJ, Bhatia S (2006b) Development of microsatellite markers and analysis of intraspecific genetic variability in chickpea (*Cicer arietinum* L.). Theor Appl Genet 112:1416–1428
Sharma HC (2006) Integrated pest management at ICRISAT: present status and future priorities. International Crops Research Institute for the semi-Arid Tropics, Patancheru, p 48
Sharma KD, Muehlbauer FJ (2007) Fusarium wilt of chickpea: physiological specialization, genetics of resistance and resistance gene tagging. Euphytica 157:1–14
Sharma SB, Singh O, Pundir RPS, McDonald D (1993) Screening of *Cicer* species and chickpea genotypes for resistance to *Meloidogyne javanica*. Nematol Mediterr 21(2):165–167
Sharma KD, Winter P, Kah G, Muehlbauer FJ (2004) Molecular mapping of *Fusarium oxysporum* f. sp. *ciceris* race 3 resistance gene in chickpea. Theor Appl Genet 108:1243–1248
Sharma HC, Pampapathy G, Lanka S, Ridsdill-Smith T (2005a) Antibiosis mechanism of resistance to pod borer, *Helicoverpa armigera* in wild relatives of chickpea. Euphytica 142(1):107–117
Sharma HC, Pampapathy G, Kumar R (2005b) Standardization of cage techniques to screen chickpeas for resistance to *Helicoverpa armigera* (Lepidoptera: Noctuidae) in greenhouse and field conditions. J Econ Entomol 98(1):210–216
Sharma HC, Bhagwat M, Pampapathy G, Sharma J, Ridsdill-Smith T (2006) Perennial wild relatives of chickpea as potential sources of resistance to *Helicoverpa armigera*. Genet Resour Crop Evol 53(1):131–138
Sharma HC, Gowda CL, Stevenson PC, Ridsdill-Smith TJ, Clement SL, Ranga Rao GV, Romies J, Miles M, Bouhssini M (2007) Host plant resistance and insect pest management in chickpea. In: Yadav SS, Redden RJ, Chen W, Sharma B (eds) Chickpea breeding and management. CAB International, Wallingford, pp 520–537
Sharman M, Wilson C, Thomas J (2012) A distinct polerovirus infecting crop and weed legumes from eastern Australia is transmitted by cowpea aphid (Abstract). In: 10th Australian plant virology workshop, Hanmer Springs, New Zealand, 19–22 November 2012, p 28
Siddiqui ZA, Husain SI (1991) Interaction of *Meloidogyne incognita* race 3 and *Macrophomina phaseolina* in root-rot disease complex of chickpea. Nematol Mediterr 19:237–239
Siddiqui ZA, Husain SI (1992) Response of twenty chickpea cultivars to *Meloidogyne incognita* race 3. Nematol Mediterr 20(1):33–36
Sikora RA, Greco N, Silva JFV (2005) Nematode parasites of food legumes. In: Luc M, Sikora RA, Bridge J (eds) Plant parasitic nematodes in subtropical and tropical agriculture. Oxfordshire, GBR, CABI Publishing, Wallingford, pp 259–318
Sillero JC, Fondevilla S, Davidson J, Vaz Patto MC, Warkentin TD, Thomas J, Rubiales D (2006) Screening techniques and sources of resistance to rusts and mildews in grain legumes. Euphytica 147(1–2):255–272
Sillero JC, Moreno-Alias I, Rubiales D (2012) Identification and characterization of resistance to rust (*Uromyces ciceris-arietini* (Grognot) Jacz. & Boyd) in a germplasm collection of *Cicer* spp. Euphytica 188(2):229–238
Simon CJ, Muehlbauer FJ (1997) Construction of a chickpea linkage map and its comparison with maps of pea and lentil. J Hered 88:115–119
Singh KB (1997) Chickpea (*Cicer arietinum* L.). Field Crops Res 53:161–170
Singh G, Bhan LK (1986) Physiological races of *Botrytis cinerea* causing grey mould of chickpea. Plant Dis Res 1:69–74
Singh G, Kaur L (1989) Genetic variability studies and scope for improvement in chickpea, Punjab, India. Int Chickpea Mewsl 20:7
Singh KB, Ocampo B (1993) Interspecific hybridization in annual *Cicer* species. J Genet Breed 47:199–204
Singh KB, Ocampo B (1997) Exploitation of wild *Cicer* species for yield improvement in chickpea. Theor Appl Genet 95:418–423
Singh KB, Reddy MV (1983) Inheritance of resistance to ascochyta blight in chickpea. Crop Sci 23:9–10
Singh KB, Reddy MV (1993) Sources of resistance to Aschochyta blight in wild *Cicer* species. Neth J Plant Pathol 99:163–167
Singh KB, Weigand S (1994) Identification of resistant sources in *Cicer* species to *Liriomyza cicerina*. Genet Resour Crop Evol 41(2):75–79
Singh KB, Weigand S (1996) Registration of three leaf miner-resistant chickpea germplasm lines: ILC 3800, ILC 5901, and ILC 7738. Crop Sci 36(2):472
Singh KB, Hawtin GC, Nene YL, Reddy MV (1981) Resistance in chickpeas to Ascochyta blight. Plant Dis 65:586–587
Singh G, Singh K, Kapoor S (1982) Screening for sources of resistance to Ascochyta blight of chickpea. Int Chick News 6:15–17
Singh G, Kapoor S, Singh K, Gill AS (1984) Screening for resistance to gram wilt. Indian Phytopathol 37:393–394
Singh H, Kumar J, Smithson JB, Haware MP (1987) Complementation between genes for resistance to race 1 of *Fusarium oxysporum* f. sp. *ciceri* in chickpea. Plant Pathol 36:539–543
Singh G, Kaur L, Sharma YR (1991) Ascochyta blight and gray mold resistance in wild species of *Cicer*. Crop Improv 18:150–151

Singh KB, Malhotra RS, Halila MH, Knights EJ, Verma MM (1994) Current status and future strategy in breeding chickpea for resistance to biotic and abiotic stresses. Euphytica 73:137–149

Singh G, Sharma YR, Bains TS (1998a) Status of Botrytis gray mold of chickpea research in Punjab, India. In: Pande S, Bakr MA, Johansen C (eds) Recent advances in research and management of Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 7–14

Singh K, Ocampo B, Robertson LD (1998b) Diversity for abiotic and biotic stress resistance in the wild annual *Cicer* species. Genet Res Crop Evol 45:9–17

Singh BK, Srivastava M, Narain U (2003a) Evaluation of biogents *Rhizoctonia bataticola* causing chickpea dry root rot. Farm Sci J 12:48–49

Singh R, Durga Prasad C, Singhal V, Randhawa GJ (2003b) Assessment of genetic diversity in chickpea cultivars using RAPD, AFLP and STMS markers. J Genet Breed 57:165–174

Singh G, Chen W, Rubiales D, Moore K, Sharma YR, Gan Y (2007) Chapter 24: diseases and their management. In: Yadav SS, Redden R, Chen W, Sharma B (eds) Chickpea breeding and management. CAB International, Wallingford, pp 497–519

Singh R, Sharma P, Varshney RK, Sharma SK, Singh NK (2008) Chickpea improvement: role of wild species and genetic markers. Biotechnol Genet Eng Rev 25:267–313

Stephens A, Lombardi M, Cogan NOI, Forster JW, Hobson K, Materne M, Kaur S (2014) Genetic marker discovery, interspecific linkage map construction and quantitative trait locus analysis of ascochyta blight resistance in chickpea (*Cicer arietinum* L.). Mol Breed 33:297–313

Taleei A, Kanouni H, Baum M (2009) Genetical analysis of ascochyta blight resistance in chickpea. In: Slezak D, Arsalan T, Fang WC, Song X, Kim T (eds) Bioscience and biotechnology, communications in computer and information science. Springer-Verlag, Berlin

Taran B, Warkentin TD, Tullu A, Vandenberg A (2007) Genetic mapping of aschochyta blight resistance in chickpea using a simple sequence repeat linkage map. Genome 50:26–34

Taylor SP, Hollaway GJ, Hunt CH (2000) Effect of field crops on population densities of *Pratylenchus neglectus* and *P. thornei* in southeastern Australia; Part 1: *P. neglectus*. J Nematol 32(4S):591–599

Tekeoglu M, Santra DK, Kaiser WJ, Muehlbauer FJ (2000a) Ascochyta blight resistance inheritance in three chickpea recombinant inbred line populations. Crop Sci 40:1251–1256

Tekeoglu M, Tullu A, Kaiser WJ, Muehlbauer FJ (2000b) Inheritance and linkage of two genes that confer resistance to fusarium wilt in chickpea. Crop Sci 40:1247–1251

Tekeoglu M, Rajesh PN, Muehlbauer FJ (2002) Integration of sequence tagged microsatellite sites to the chickpea genetic map. Theor Appl Genet 105:847–854

Tewari SK, Pandey MP (1986) Genetics of resistance to Ascochyta blight in chickpea (*Cicer arietinum* L.). Euphytica 35:211–215

Tewari SK, Pandey MP, Pandya BP, Chaube HS, Tripathi HS (1985) Inheritance of resistance to Botrytis grey mould in chickpea. Int Chick News 12:11–12

Tewari-Singh N, Sen J, Kiesecker H, Reddy VS, Jacobsen HJ, Mukherjee SG (2004) Use of herbicide or lysine plus threonine for non-antibotic selection of transgenic chickpea. Plant Cell Rep 22:576–583

Thomas JE, Schwinghamer M, Parry JN, Sharman M, Schilg MA, Dann EK (2004) First report of *Tomato spotted wilt virus* in chickpea (*Cicer arietinum* L.) in Australia. Australas Plant Pathol 33:597–599

Thomas JE, Perry JN, Schwinghamer MW, Dann EK (2010) Two novel masteroviruses from chickpea (*Cicer arietinum* L.) in Australia. Arch Virol 155(11):1777–1788

Thompson JP, Greco N, Eastwood R, Sharma SB, Scurrah M (2000) Integrated control of nematodes of cool season food legumes—linking research and marketing opportunities for pulses in the 21st century. Proceedings of the third international food legumes research conference. Kluwer Academic Publishers, Dordrecht, pp 491–506

Thompson JP, Owen KJ, Stirling GR, Bell MJ (2008) Root-lesion nematodes (*Pratylenchus thornei* and *P. neglectus*): a review of recent progress in managing a significant pest of grain crops in northern Australia. Australas Plant Pathol 37:235–242

Thompson J, Reen R, Clewett T, Sheedy J, Kelly A, Gogel B, Knights E (2011) Hybridisation of Australian chickpea cultivars with wild *Cicer* spp. increases resistance to root-lesion nematodes (*Pratylenchus thornei* and *P. neglectus*). Aust Plant Pathol 40(6):601–611

Thudi M, Bohra A, Nayak SN, Varghese N, Shah TM, Penmetsa RV, Thirunavukkarasu N, Gudipati S, Gaur PM, Kulwal PL, Upadhyaya HD, Kavikishor PB, Winter P, Kahl G, Town CD, Kilian A, Cook DR, Varshney RK (2011) Novel SSR markers from BAC-end sequences, DArT arrays and a comprehensive genetic map with 1291 marker loci for chickpea (*Cicer arietinum* L.). PLoS ONE 6:e27275

Toker C, Erler F, Ceylan FO, Canci H (2010) Severity of leaf miner [*Liriomyza cicerina* (Rondani, 1875) Diptera: Agromyzidae] damage in relation to leaf type in chickpea. Turk J Entomol 34:211–226

Torres AM, Jain SM, Brar DS (2010) Application of molecular markers for breeding disease resistant varieties in crop plants. In: Jain SM, Brar DS (eds) Molecular techniques in crop improvement. Springer, Netherlands, pp 185–205

Trapero-Casas A, Jiménez-Díaz RM (1985) Fungal wilt and root rot diseases of chickpea in southern Spain. Phytopathology 75:1146–1151

Tripathi HS, Rathi YPS (1992) Epidemiology of Botrytis gray mold of chickpea. In: Haware MP, Faris DG, Gowda CLL (eds) Botrytis gray mold of chickpea. ICRISAT, Patancheru, pp 8–9

Tripathi NN, Sharma BK (1983) Incidence of chickpea dry root rot (*Rhizoctonia bataticola*) in Southern Haryana. Int Chick News 8:22–23

Trivedi S, Gurha SN (2006) Status of some soil borne pathogens infecting chickpea in Bundelkhand region of Uttar Pradesh. Indian J Pulses Res 19:88–90

Tullu A, Kaiser WJ, Kraft JM, Muehlbauer FJ (1999) A second gene for resistance to race 4 of Fusarium wilt in chickpea and linkage with a RAPD marker. Euphytica 109:43–50

Udupa SM, Baum M (2003) Genetic dissection of pathotype-specific resistance to ascochyta blight disease in chickpea

(*Cicer arietinum* L.) using microsatellite markers. Theor Appl Genet 106:1196–1202

Udupa SM, Weigand F, Saxena MC, Kahl G (1998) Genotyping with microsatellite markers resolves pathotype diversity in aschochta blight pathogen of chickpea. Theor Appl Genet 97:299–307

Upadhyaya HD, Haware MP, Kumar J, Smithson JB (1983a) Resistance to wilt in chickpea. I. Inheritance of late wilting in response to race 1. Euphytica 32:447–452

Upadhyaya HD, Smithson JB, Haware MP, Kumar J (1983b) Resistance to wilt in chickpea. II. Further evidence for two genes for resistance to race 1. Euphytica 32:749–755

Vail S, Banniza S (2009) Molecular variability and mating-type of *Ascochyta rabiei* of chickpea from Saskatchewan, Canada. Aust Plant Pathol 38:392–398

Van der Maesen LJG (1987) Origin, history and taxonomy of chickpea. In: Chickpea The (ed) Saxena MC and Singh KB. CAB Int Publ, Wallingford, pp 11–34

Van der Maesen LJG, Maxted N, Javadi F, Coles S, Davies AMR (2007) Taxonomy of the genus *Cicer* revisited. In: Yada SS (ed) Chickpea breeding and management. CAB International, Wallingford, pp 14–30

Van Leur JAG, Aftab M, Manning W, Bowring A, Riley MJ (2013) A severe outbreak of chickpea viruses in northern New South Wales Australia. Australas Plant Dis Notes. doi:10.1007/s13314-013-0093-y **(published online)**

Van Leur JAG, Aftab M, Sharman M, Lindbeck K (2014) Viral diseases in canola and winter pulses—impacts and management. Grains Research and Development Corporation (GRDC) updates, Goodiwindi, Queensland

Varshney RK, Song C, Saxena RK, Azam S, Yu S, Sharpe AG, Cannon S, Baek J, Rosen BD, Tar'an B, Millan T, Zhang X, Ramsay LD, Iwata A, Wang Y, Nelson W, Farmer AD, Gaur PM, Soderlund C, Penmetsa RV, Xu C, Bharti AK, He W, Winter P, Zhao S, Hane JK, Carrasquilla-Garcia N, Condie JA, Upadhyaya HD, Luo MC, Thudi M, Gowda CL, Singh NP, Lichtenzveig J, Gali KK, Rubio J, Nadarajan N, Dolezel J, Bansal KC, Xu X, Edwards D, Zhang G, Kahl G, Gil J, Singh KB, Datta SK, Jackson SA, Wang J, Cook DR (2013) Draft genome sequence of chickpea (*Cicer arietinum* L.) provides a resource for trait improvement. Nat Biotechnol 31:240–246

Varshney RK, Mohan SM, Gaur PM, Chamarthi SK, Singh VK, Srinivasan S, Swapna N, Sharma M, Singh S, Kaur L, Pande S (2014) Marker assisted backcrossing to introgress resistance to fusarium wilt race 1 and ascochyta blight in C 214, an elite cultivar of chickpea. Plant Genome 7:1–11

Vir S, Grewal JS (1974) Physiologic specialization in *Ascochyta rabiei* the causal organism of gram blight. Indian Phytopathol 27:355–360

Vir S, Grewal JS, Gupta VP (1975) Inheritance of resistance to Ascochyta blight in chickpea. Euphytica 24:209–211

Vovlas N, Rapoport HF, Jiménez Díaz RM, Castillo P (2005) Differences in feeding sites induced by root-knot nematodes *Meloidogyne* spp in chickpea. Phytopathology 95(4):368–375

Wally O, Punja ZK (2010) Genetic engineering for increasing fungal and bacterial disease resistance in crop plants. GM Crops 1(4):199–206

Weigand S (1990) Insect pests of chickpea in the Mediterranean area and possibilities for resistance. In: Saxena MC, Cubero JI, Wery J (eds) Present status and future prospects of chickpea crop production and improvement in the Mediterranean countries. Options Méditerranéennes–Série Séminaires 9, pp 73–76

Weimer JL (1931) Alfalfa mosaic. Phytopathology 21:122–123

William HM, Morris M, Warburton M, Hoisington DA (2007) Technical, economic and policy considerations on marker-assisted selection in crops: lessons from the experience at an international agricultural research centre. In: Guimarães E, Ruane J, Scherf B, Sonnino A, Dargie J (eds) Marker-assisted selection. Current status and future perspectives in crops, livestock, forestry and fish. Food and Agriculture Organization of the United Nations, Rome, pp 381–404

Winter P, Paff T, Udupa SM, Huttel B, Sharma PC et al (1999) Characterization and mapping of sequence-tagged microsatellite sites in the chickpea (*Cicer arietinum* L.) genome. Mol Gen Genet 262:90–101

Winter P, Benko-Iseppon AM, H-ttel B, Ratnaparkhe M, Tullu A et al (2000) A linkage map of the chickpea (*Cicer arietinum* L.) genome based on recombinant inbred lines from a *C. arietinum*, *C. reticulatum* cross: localization of resistance genes for fusarium wilt races 4 and 5. Theor Appl Genet 101:1155–1163

Yadav SS, Kumar J, Yadav SK, Singh S, Yadav VS, Turner NC, Redden R (2006) Evaluation of *Helicoverpa* and drought resistance in Desi and Kabuli chickpea. Plant Genet Resour C 4(3):198–203

Yoshida M, Cowgill SE, Wightman JA (1995) Mechanism of resistance to *Helicoverpa armigera* (Lepidoptera: Noctuidae) in chickpea: role of oxalic acid in leaf exudate as an antibiotic Factor. J Econ Entomol 88(6):1783–1786

Yoshida M, Cowgill SE, Wightman JA (1997) Roles of oxalic and malic acids in chickpea trichome exudate in host-plant resistance to *Helicoverpa armigera*. J Chem Ecol 23(4):1195–1210

Zatloukalová P, Hřibová E, Kubaláková M, Suchánková P, Šimková H, Adoración C, Kahl G, Millán T, Doležel J (2011) Integration of genetic and physical maps of the chickpea (*Cicer arietinum* L.) genome using flow-sorted chromosomes. Chromosome Res 19:729–739

Zhang XJ, Scheuring CF, Zhang MP, Dong JJ, Zhang Y, Huang JJ, Lee M-K, Abbo S, Sherman A, Shtienberg D, Chen WD, Muehlbauer F, Zhang H-B (2010) A BAC/BIBAC-based physical map of chickpea (*Cicer arietinum* L.). BMC Genom 11:501