Damping-off Resistance in Chickpeas

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ABSTRACT

Kumar, J., Kaiser, W. J., and Hannan, R. M. 1991. Damping-off resistance in chickpeas. Plant Dis. 75:1244-1245.

Association of resistance to preemergence damping-off caused by *Pythium ultimum* and gene *P* for flower and seed coat color was studied in two crosses of chickpeas (*Cicer arietinum*), kabuli line C 104, and desi lines T3(GW) and P 436-2 made at ICRISAT, Patancheru, India. Evaluations were performed under greenhouse conditions. Resistance was found to be inherited polygenically. Gene *P* appeared to be closely linked to the resistance. Kabuli segregants with reduced susceptibility were identified in both crosses, which indicates that linkage between gene *P* and genes for resistance to *P. ultimum* can be broken.

Additional keywords: anthocyanin, garbanzo beans, gram

Chickpeas (*Cicer arietinum* L.) (garbanzo beans, gram) are classified into desi and kabuli types based on color, size, and shape of seeds (9). Desi types usually have pink flowers and small, brown, angularly shaped seeds. Kabuli types have white flowers and large, cream-colored, owl's head-shaped seeds. Flower color is governed by at least three genes. The inheritance of seed coat color and seed shape in chickpeas is not well understood (9). Kabuli types have thin seed coats and are more susceptible than desi types to preemergence damping-off caused by *Pythium ultimum* Trow (3). We do not know of any kabuli germ plasm line resistant to *P. ultimum* (3). Resistance in pea (*Pisum sativum* L.) to *P. ultimum* is associated primarily with seed coat color, but other traits are also involved (5,6,8,10). Ewing (1) attributed this resistance to the presence of the *A* gene for production of anthocyanin in the testa. Muehlbauer and Kraft (6) reported that four other genes cumulatively increased the resistance of the *A* gene to preemergence damping-off. Our study was undertaken to determine the inheritance of resistance in crosses of desi × kabuli chickpeas to preemergence damping-off and its association with gene(s) that control anthocyanin pigmentation of flowers, plants, and seeds.

This study was jointly conducted at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, A.P. 502 324, India, and USDA-ARS Regional Plant Introduction Station, Pullman, WA 99164-6402.

Approved as ICRISAT JA 788.

Accepted for publication 5 April 1991.

MATERIALS AND METHODS

A susceptible kabuli chickpea line, C 104 (ICC [ICRISAT chickpea] 4928), and two resistant desi-type lines, T3(GW) (ICC 5864) and P 436-2 (ICC 554), were crossed in a diallel fashion. The F_1 and F_2 generations were grown in the field under disease-free conditions in 1982 (summer) and in 1982–1983 (postrainy) seasons at the ICRISAT Center, Patancheru, India. For each cross, individual F_2 plants (140–152) were classified for flower and seed coat color. Before conducting these studies, the seeds were kept in cold storage and were of very good quality with very good germination. Seeds of different generations were planted in soils infested with the *P. ultimum* pathogen at Pullman, WA, in March 1984. Two control lines, PI 458870 (kabuli) and PI 273879 (desi), were also included.

Raised soil beds (1.3 m wide × 3.4 m long × 0.34 m deep) containing Spofford silt loam soil (pH approximately 6.6, conductivity 0.6 mmhos/cm) obtained from Central Ferry, WA, were used for this study. The soil was composed of 27% sand, 53.8% coarse silt, 2.8% fine silt, 16.4% clay, and 1.6% organic matter. Soil temperatures ranged between 16 and 18 C in all studies. Greenhouse temperature was maintained at 22 ± 5 C. From past studies (3), we know that the propagule density of *P. ultimum* is greater than 100 propagules per gram of soil used in this study. More than 95% of the plants of the untreated PI 458870 will suffer preemergence or postemergence damping-off, whereas untreated PI 273879 will suffer little damage and have more than 90% emergence in these soils.

Up to 33 seeds of each parental line, F_1, and F_2 progeny were planted in the infested soils and up to 15 in sterile soils (as control) in two or three replications in a randomized complete block design. First emergence counts were taken when the seedlings began to break through the soil after 5–7 days. Additional stand counts were made every 3–4 days for 14 days. The same field soil used in the ground beds was steam-treated for 16 hr in two 8-hr intervals. This soil was then amended with sterile peat moss (10–15%, v/v) to improve friability and reduce soil compaction. Control screening was conducted in plastic pots, 15 cm in diameter and 15 cm deep. Pots were watered to saturation after planting and every 2–4 days. Emergence counts were made as in the ground beds. The percent data were transformed (arcsine) for statistical analyses.

Isolations were made from seeds that did not germinate. Such seeds were removed from the soil, placed in running tap water for 15–30 min, and surface-disinfested in 0.25% NaOCl for 5 min. Seed pieces were plated on 2% water agar. Plates were incubated at 24–26 C and observed after 5–7 days for growth of *Pythium* spp. and other fungi.

RESULTS AND DISCUSSION

F_1 plants of the three crosses had pink flowers and individual plants in F_2 of the two desi × kabuli crosses segregated in a 3:1 pink/white ratio. There was no segregation for flower color in F_2 of the T3(GW) × P 436-2 cross. This indicated that the pink-flowered parents were homozygous dominant for gene *P* for pink flower color (7). The white-flowered parent, C 104, was apparently homozygous recessive for this gene.

Because seed coat color is a maternal trait, F_3 phenotypes were used to determine F_2 genotypes. Inheritance of this trait was complex as has been reported in other studies (9). We classified F_3 progenies according to seed coat color into three categories—brown (parental), light brown (nonparental), and cream (parental)—and related these to the parental (F_2 individual plant) flower colors. In addition to the *P* gene, other loci also influenced the seed coat color. Because it was easy to classify flower color of plants, we related this trait with reaction to *P. ultimum*.

P. ultimum was present in all isolations. Other fungi isolated occasionally

Table 1. Reaction of parents and progenies of individual plants of F_2 derived F_3 progenies of chickpeas and two PI lines used as controls to *Pythium ultimum* in the greenhouse

Cross and chickpea parent	Flower color[a]	Number of progenies in emergence (class interval) (%)										Infested soil		Noninfested soil	
		0-10	10-20	20-30	30-40	40-50	50-60	60-70	70-80	80-90	90-100	Mean emergence (%)	Total seeds tested	Mean emergence (%)	Total seeds tested
T_3 (GW) × C 104															
T_3 (GW)	P											63.6	33	100	14
C 104	W											0.0	33	100	12
F_2 progenies (F_3)	P	3	2	5	5	11	6	11	11	16	32	70.4 ± 1.99	3,061	94.0 ± 1.42	1,076
F_2 progenies (F_3)	W	27	8	5	0	1	0	0	0	0	0	8.0 ± 1.96	1,194	94.0 ± 2.41	421
	P+W[b]	30	10	10	5	12	6	11	11	16	32	52.9 ± 2.34	4,255		
P 436-2 × C 104															
P 436-2												81.8	33	91.7	12
C 104												3.0	33	85.7	14
F_1												100	19	100	6
F_2 progenies (F_3)	P	1	2	3	2	7	9	9	21	11	50	78.9 ± 1.65	3,261	88.4 ± 1.58	1,133
F_2 progenies (F_3)	W	32	4	0	1	0	0	0	0	0	0	7.1 ± 1.82	1,019	90.2 ± 2.34	356
	P+W	33	6	3	3	7	9	9	21	11	50	61.8 ± 2.41	4,280		
Controls															
PI 458870												7.3	213	94.4	67
PI 273879												95.8	213	98.3	59

[a] Flower color of the mother plant was either pink (P) or white (W).
[b] Represents the totals of the two preceding populations.

included *Pythium* spp., *Fusarium* spp., and *Rhizoctonia solani* Kühn. Emergence of control cultivars PI 458870 and PI 273879 was 7.3 and 95.8% in the infested soil compared with 94.4 and 98.3%, respectively, in the noninfested soil (Table 1).

Mean percent emergence and standard errors for progenies of pink-flowered F_2 (*P* genotype) plants were 70.4 ± 1.99 for the T3(GW) × C 104 cross and 78.9 ± 1.65 for P 436-2 × C 104 (Table 1). The comparative values for progenies of white-flowered (*pp* genotype) F_2 plants for the two crosses were 8.0 ± 1.96 and 7.1 ± 1.82. In the noninfested soil, mean emergence of parents and F_3 progenies ranged from 85.7 to 94.0%. Emergence of one white-flowered F_2 progeny in the T3(GW) × C 104 cross was 42.4% and one in P 436-2 × C 104 was 35.5%. In addition, a number of white-flowered F_2 progenies in both the crosses had more than 20% emergence.

Resistance was generally associated with the pink flower color of the mother plant, but not all progenies of pink-flowered F_2s were resistant. Some of these were as susceptible as the kabuli parent C 104. These probably had no genes for resistance. No progeny in the white-flowered group was as resistant as those from the pink-flowered plants.

The complexity of inheritance of resistance in chickpeas to *P. ultimum* is shown by the lack of segregation for a specific genetic ratio in any of the two crosses studied (Table 1). The data indicate that the trait is governed by several genes if it is not under polygenic control. Similar conclusions were drawn for snap bean (11). Our study indicates that genes for resistance to *P. ultimum* are located close to the *P* gene, possibly in a gene cluster. The gene *P* has also been reported to affect seed coat color in chickpeas (9). In peas, the major *A* gene for pigmentation influences resistance to *P. ultimum* (1,5).

The conclusion that resistance is polygenic emphasizes the importance of testing F_3 progenies rather than single F_2 plants, especially where lethal screening was employed. It was easier to identify resistant segregants by testing F_3 progenies. In each cross, when segregation for reaction to *P. ultimum* is considered, there was a biomodal distribution of the F_3 progenies. This is because the progenies of white-flowered plants were generally susceptible and had emergence of less than 50%.

All white-flowered progenies are not kabuli types. Only eight of 143 progenies in T3(GW) × C 104 and 12 of 152 progenies in P 436-2 × C 104 were kabuli types. One way of developing resistance to *P. ultimum* in kabuli types is to make selections for kabuli types among segregating populations of desi × kabuli crosses. In the present study, emergence of kabuli type F_3 progenies in the infested soil ranged from 0 to 42.4% in the first and 0 to 35.5% in the second cross, which suggests that some genes for resistance have been transferred to these progenies. We were unable to recover any kabuli lines with high resistance. Thus, there may be a close linkage between the *P* gene and those for resistance to *P. ultimum*. The linkage apparently can be broken because desi segregants, as susceptible as the kabuli check, were obtained. Kabuli segregants with higher levels of resistance may be recovered if a larger number of F_3 progenies were screened. It may be safe to screen only white-flowered F_3 progenies in such crosses, thus reducing the work load.

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