Identification of recessive *er* gene for powdery mildew resistance in a landrace of *Pisum sativum*

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A sample of seed was collected by the author in January 2000 from the field of a farmer in Dharwad district of Karnataka in South India. The plant had features typical of a primitive cultivar, such as tall and thin stems, red flowers (A), small leaves, flowers and pods, small seeds with black mottling on green testa, and dehiscent pods. The seeds are round (R) with mild rectangular configuration. The leaflets have red color at the margin, and the stipules lack an anthocyanin ring at the base (presumably a result of the d allele). It flowers in about 45 days under Delhi conditions.

A germplasm accession identified as P. *arvense* (P 1890) with similar (but not identical) features was received from the National Bureau of Plant Genetic Resources, Delhi, as NIC 11184. It was collected as a landrace from village Kanwa in the Kota district of Rajasthan in western India in 1992 (collector's record NKD/TSA/1275 dated 27.1.1992).

Both these genotypes turned out to be resistant to powdery mildew (PMR) at Delhi as well as in the Lahaul Valley of Himachal Pradesh in high Himalayas (elevation approximately 4000 m). The Lahaul Valley is known for its intense powdery mildew pressure, where even confirmed PMR genotypes can display dense fungal growth on the leaves and stipules (but never on the stem, peduncles, and pods). The Dharwad and Kanwa accessions give a similar reaction in Lahaul.

To confirm the nature of resistance and define allelism, the Dharwad accession was crossed with a powdery mildew susceptible (PMS) strain, Pusa 10, and the PMR variety P 1542. The major gene constellations and features of the three parents are as follows:

Dharwad:	A, I, Le, R, PMR, small pod, small seed, opaque mottled testa
Pusa 10:	a, I, le, R, Er, very large and thick pod, bold seed, translucent spotless testa
P 1542:	a, i, le, r, er, long and slender pod, bold seed, translucent spotless testa

The observations recorded in the F_1 and F_2 generations are given below:

Cross	Fj	F_2
Pusa 10 x Dharwad	A Le PMS mottled testa	Segregation for all traits except I and R
P 1542 x Dharwad	A Le PMR mottled testa	Segregation for all traits except PMR

These observations confirm that the Dharwad accession and P 1542 carry a common recessive gene for powdery mildew resistance (absence of segregation). The PMS phenotype in the F_1 and a 3:1 (susceptible:resistant) segregation in the F_2 of the cross Pusa 10 x Dharwad also confirmed the monogenic recessive nature of the PMR trait in Dharwad.

The materials derived from the two crosses were advanced as single plant progenies (single seed descent), and are now at an F_6 stage. Over the years, all possible gene combinations have been evolved. The PMR nature of the P 1542 x Dharwad derivatives has been confirmed repeatedly at Delhi and Lahaul. These results provide compelling evidence for a common PMR gene operating in Dharwad accession and the common P. *sativum* genotypes that are being used in breeding for powdery mildew resistance.

The results also suggests that only a single locus controlling powdery mildew resistance exists in the genus *Pisum*. This locus was discovered by Harland (1), recognized as Er1, and mapped on chromosome 6 (2). The putative gene Er2 has never been mapped.

1. Harland, S.C. 1948. Heredity 2: 263-269.

2. Sarala, K. 1993. Ph. D. Thesis. Indian Agric. Res. Inst., Delhi, India: 109+xi.

Pisum fulvum carries a recessive gene for powdery mildew resistance

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A new source of powdery mildew resistance in pea has been identified in the genetic line Wt 11256 which was received from Prof. W.K. Swiecicki as a donor of genes *Adi Umb Astr Le R*. It belongs to *Pisum fulvum*, which is still considered to be a separate species. The seeds received were very small with dark red testa. The plants had spreading growth habit. The strain was very late in winter at Delhi, produced flowers 97 days after sowing, and did not produce seed due to high temperatures during flowering period. The genotype was also resistant to powdery mildew. It had no trace of fungal infection even though the plants remained green till early May. By this time most of the pea materials had been harvested. The disease appeared toward the end of February, and all susceptible genotypes were laden with fungus by mid-March when all plant parts, including leaves, stipules, stem, peduncles and pods, were covered with thick mycelial coat. The pods of early susceptible genotypes turned black by March end. Isolated patches of fungal growth could be seen on foliage in the upper green part of the resistant genotypes, although the infestation did not spread to stem and reproductive parts. This question has been examined separately (3). The plants of Wt 11256 remained absolutely free from infection through the entire period of growth. Patches of fungal growth did not appear even on foliage until the end of plant life. Resistance to powdery mildew was unmistakable.

We have concluded that powdery mildew resistance in *Pisum sativum* is controlled by a single, and not two, recessive gene. The two-gene hypothesis of Heringa et al. (2) for this trait has been accepted as *fait accompli* without experimental verification. It is yet to be determined whether different strains of P. *fulvum* differ in their disease reaction. Nevertheless, discovery of resistance in this putative species leads to the conclusion that a common gene for powdery mildew resistance operates in the entire genus *Pisum*. Allelism of powdery mildew resistance genes in P. *sativum* ssp. *sativum* and primitive landraces has been confirmed experimentally (4).

The recessive gene for resistance in P. *fulvum* must be a different allele of the Er gene already known in P. *sativum* (1). The allele discovered in Wt 11256 is designated as er^{f} (f for *fulvum*).

- 1. Harland, S.C. 1948. Heredity, 2: 263-269.
- 2. Heringa, R.J., Van Norel, A. and Tazelaar, M.F. 1969. Euphytica 18: 163-169.
- 3. Sharma, B. 2003. Pisum Genetics, 35: 22-27.
- 4. Sharma, B. 2003. Pisum Genetics, 35: 30-31.