The *Brt* (branched roots) and *Lrt* (long roots) genes control the development of roots in peas (*Pisum sativum* L.)

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Until very recently only three mutants in pea (*Pisum sativum* L.) were known of with altered root systems [1-3]. Following exposure of seeds of cultivar 'Rondo' to 0.15% ethyl methanesulfonate, three mutant phenotypes, ? 8?, ? 17?, and ? 18?, were identified as having altered roots. ? 8? and ? 17? have strongly branching roots, whereas ? 18? is noted for a very long root (Fig. 1). Here, we provide a summary of the genetic analysis that was performed on these mutants and the results of experiments performed to determine levels of endogenous auxin and gibberellin in the roots of the mutants and the original cultivar.

Each of the mutants was crossed to the original cultivar, and the phenotypically similar ? 8? and ? 17? were crossed for an allelism test (Table 1).

The results of the genetic analysis suggest that these are monogenic recessive mutants. Furthermore, crossing ? 8? x ? 17? revealed allelism. The mutant gene controlling the extensively branched root phenotype seen in ? 8? and ? 17? was denoted by *brt* (branched roots). The mutant gene producing the long root phenotype in ? 18? was designated by *lrt* (long roots).

The mutant lines were examined for altered nodulation response using *Rhizobium leguminosarum* (strain 250?). ? 8? and ? 17? were found to form few or no nodules. ? 18? displayed a relatively normal nodulation phenotype, nodulating well at low or moderate nitrate levels and developing few nodules in the presence of high nitrates.

Fig. 1. Roots: 1 - Rondo, 2 – ? 18? (the lrt gene), 3 - ? 17? (the brt gene).

Auxin and gibberellin levels were determined at the onset of flowering, both with and without *Rhizobium leguminosarum*, under greenhouse conditions. The plants were grown in pots. The substrate used was bloating clay and a standard mineral solution. The light regime was 16/8 hrs (day/night); temperature 20-21^{o}C at day and 12-13^{o}C at night. Auxin and gibberellin levels were determined using techniques described elsewhere [3].

Table 1. Segregation in F_2 hybrid progenies.

Hybrid	F_2 segregation (original : mutant) observed	F_2 segregation (original : mutant) expected	c^2 (3 : 1)	P
? 8? ? Rondo	27:9	27.00:9.00	0	1
? 17? ? Rondo	147:48	146.25:48.75	0.015	0.95-0.90
? 18? ? Rondo	89:30	89.25:29.75	0.025	0.90-0.80

Auxin levels were reduced in both mutants compared to those found in Rondo (Fig. 2). This reduction occurred either with or without the presence of *Rhizobium leguminosarum*. The presence of the bacterium reduced root auxin concentration in all genotypes tested. The long-rooted ? 18? was found to have a high level of gibberellin relative to the Rondo control and Kita (Fig. 2). This significant increase in the level of gibberellin was observed both with and without *Rhizobium leguminosarum*.

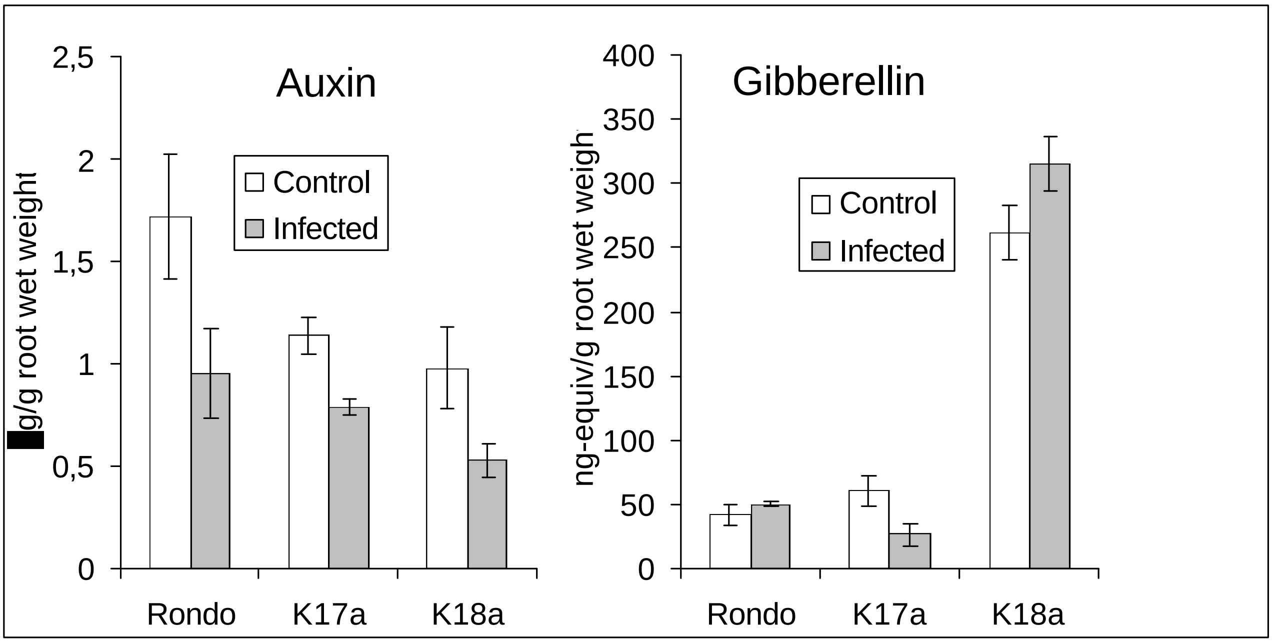

Fig. 2. Auxin and gibberellin levels in the roots of the symbiotic mutants and the original cultivar, Rondo, at flowering.

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