

# A cost of disease resistance: paradigm or peculiarity?

James K.M. Brown

Department of Disease and Stress Biology, John Innes Centre, Colney, Norwich NR4 7UH, UK

**Disease is one of the main driving forces of biological evolution. Parasites cause natural selection for disease resistance in populations of their hosts. Why then are all organisms susceptible to some parasites? One explanation is that resistance to disease is costly, reducing the fitness of the host in the absence of disease. A recent article shows that such costs might have helped to maintain polymorphism at a resistance locus. Other work, however, has questioned whether the costs of resistance are indeed necessary to account for polymorphism in host–parasite interactions.**

Plants are good models for studies of co-evolution because, unlike animals, their interactions with some important parasites are controlled by a fairly simple genetic system. In the gene-for-gene relationship [1], plants are resistant to some genotypes of a parasite species but not to others (Box 1). The asymmetry of this system has long fascinated evolutionary biologists because a resistance (*R*) allele should always have an advantage over a susceptibility allele by protecting the plants that have the *R* allele against pathogens that possess the matching avirulence (*Avr*) gene. How then is polymorphism for resistance and susceptibility maintained in plant populations? One possibility is that *R*-genes might impose metabolic costs on plants. A recent study by Joy Bergelson and colleagues [2] provides the first evidence for such a cost of a gene-for-gene resistance. This cost, balanced against the benefit of the *R*-gene in plant defence, is sufficiently high to have helped to maintain polymorphism at this *R*-locus for millions of years.

## Costly resistance

Polymorphism has persisted at the *RPM1* locus of *Arabidopsis thaliana* for at least 10 million years [3]. *RPM1* confers resistance to genotypes of the pathogenic bacterium *Pseudomonas syringae* pv *maculicola*, which express one of two *A*-genes, *AvrRpm1* or *AvrB*. Tian *et al.* [2] investigated whether a cost of resistance might have contributed to the longevity of this polymorphism. They produced four pairs of NEAR-ISOGENIC LINES (see Glossary) that were identical except at a transgenic ectopic *RPM1* locus, where they had integrated resistance alleles (*RPM1*<sup>+</sup>) or susceptibility alleles (*rpm1*; written as *RPM1*<sup>−</sup> in Ref. [2]). In the *RPM1*<sup>+</sup> lines, a 3.84-kb insert included *RPM1* itself, its promoter and its terminator and was flanked by *lox* sites. The expression and function of *RPM1* was phenotypically normal in these plants. Wild plants that are susceptible to *AvrRpm1* and *AvrB* isolates

of *P. syringae* pv *maculicola* lack the complete coding region of *RPM1* [4]. Thus, Tian *et al.* mimicked this allele via *cre*-mediated excision of the 3.84-kb insert at the *lox* sites to generate plants that possessed *rpm1*.

The effect of *RPM1* on the fitness of these plants was tested in a field trial in the absence of *P. syringae* pv *maculicola*. *RPM1*<sup>+</sup> plants were consistently smaller than *rpm1* plants, with smaller shoots, and had lower reproductive fitness, with fewer SILIQUES (seed pods) per plant and seeds per silique, resulting in 9% fewer seeds per plant in total (Figure 1). This high cost of resistance was consistent across the four pairs of transgenic lines, indicating that the cost of resistance was indeed associated with *RPM1* and was not an artefact of the position at which the transgene was inserted.

A resistance cost of 9% is surprisingly high. Indeed, it is probably not typical of gene-for-gene resistances. There are estimated to be 163 gene-for-gene *R*-genes in *A. thaliana* [5]. Thus, if *R*-alleles incurring a cost of 9% segregated at all these loci, the genetic load on the plant population would be unsustainable [2]. Gene-for-gene resistances are also used widely in plant breeding but any *R*-gene with such a high cost would be rapidly eliminated from breeders' germplasm.

There is circumstantial evidence from recent research on POWDERY MILDEW of barley that *R*-genes other than *RPM1* might incur costs. Transcripts of two *R*-genes, *Mla6* and *Mla13*, are induced between 16 and 20 h after inoculation, but only if the fungus has the corresponding *Avr* gene [6]. The fact that these *R*-genes are inducible

## Glossary

**Cultivar:** a variety of a crop plant, produced by plant breeding in modern agriculture or by natural selection among diverse genotypes in traditional farming systems.

**Downy mildew:** a plant disease that appears as a downy growth on leaves, flowers and fruit, caused by oomycetes in the order Peronosporaceae.

**Meristem:** a localized region of active cell division and differentiation in plants.

**Metapopulation:** a 'population of populations', in which an organism exists at several discrete sites. In each generation, the organism might become extinct at some sites and might be re-colonized from other sites.

**Near-isogenic lines:** a group of plant lines that are genetically identical except around one locus, produced by genetic engineering or by repeated backcrossing to a recurrent parent.

**Oomycete:** a group of organisms with an outward appearance similar to fungi, but actually part of the Stramenopile group of protists, which includes diatoms and brown algae among its better-known members.

**Powdery mildew:** a plant disease important mainly in humid, temperate environments, in which the fungal spores appear as a powder on leaves, stems and flowers, caused by ascomycetes in the order Erysiphales.

**Rust:** a common disease of many plants, in which pustules of spores break through the surface of leaves and stems, caused by basidiomycete fungi in the order Uredinales.

**Silique:** the elongated pod containing several seeds, typical of plants in the family Brassicaceae, including *Arabidopsis thaliana*.