Evolutionary Ecology, 1996, **10**, 323–325

COMMENT
Reply to Parker, *Evol. Ecol.* **10**, 319–22

Problems inferring the specificity of plant–pathogen genetics

Parker (1996, *Evol. Ecol.* **10**, 319–22) argued that data from agricultural genetics are sufficient to draw a strong conclusion about the nature of genetic specificity in plant – pathogen interactions. By contrast, I have argued that the current data are not sufficient (Frank, 1993, *Proc. R. Soc. Lond. B* **254**, 191; 1994, *Phil. Trans. R. Soc. Lond. B* **346**, 283; 1996a, *Evol. Ecol.* **10**, 307–17). There are biochemical, evolutionary, epidemiological and statistical reasons to doubt Parker's conclusion.

Biochemistry

Parker (1996, *Evol. Ecol.* **10**, 319–22) favours a strict form of the classical gene for gene interaction. In that model the host has two phenotypes, resistant (*R*) and susceptible (*S*). The pathogen has two phenotypes, avirulent (*A*) and virulent (*V*). A host resists attack only when the host – parasite pair has an *R-A* match. Recent biochemical models suggest that the avirulence allele (*A*) produces a gene product (elicitor) that can be recognized only by specific host receptors (*R*). This specific elicitor – receptor recognition induces a non-specific set of host defence mechanisms (Gabriel and Rolfe, 1990, *Annu. Rev. Phytopathol.* **28**, 365; Keen and Dawson, 1992, Genes involved in plant defense, 85. Springer-Verlag, New York). The virulence allele confers a universal host range, either because the host population lacks a matching receptor or because virulence corresponds to loss of the elicitor.

Parker's gene for gene interpretation requires that there be only a single pathogen elicitor at each locus with only one matching host receptor. However, it seems plausible that alternative elicitors can exist at the pathogen locus, each with matching specific receptors. Parker defends his point of view vigorously because his strict one-elicitor interpretation supports his claim that host – pathogen co-evolution cannot be the evolutionary cause of sexual reproduction (Parker, 1994, *Evol. Ecol.* **8**, 560). By contrast, multiple matching specificities can favour sex (Hamilton *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* **87**, 3566).

There is, at present, no direct biochemical evidence for multiple, matching specificities. However, there are cases in which a pathogen allele functions as the virulent (unmatched) alternative on one host species, whereas the same allele functions as the avirulent allele (matched elicitor) on another host (Gabriel and Rolfe, 1990, *Annu. Rev. Phytopathol.* **28**, 365). Thus different elicitor molecules can be recognized by different host resistance (receptor) genotypes, demonstrating that alternative matching specificities are possible.

A second line of biochemical evidence also suggests that multiple, matching specificities can occur. It has been shown that a single base-pair mutation in a pathogen elicitor can change the allele from avirulent (recognized by host) to virulent (unrecognized by host) (Joosten *et al.*, 1994, *Nature* **367**, 384). It is not surprising that minor changes in an elicitor can render it unrecognizable by a host receptor. It would be surprising if, in some cases, the host receptor could not mutate to a new conformation and recognize the mutant elicitor. If such host mutations are possible, then matching specificities occur.

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Evolution

The strict gene for gene model is asymmetrical. Pathogen virulence corresponds to a universal host range, whereas avirulence has a partial host range. Polymorphism of virulence and avirulence therefore requires that virulence has some cost associated with it (Vanderplank, 1984, Disease resistance in plants (2nd Edn), Academic Press, New York). Similarly, host susceptibility alleles can be attacked by all pathogen genotypes, whereas resistance alleles protect against some pathogens. Polymorphism therefore requires a cost of resistance.

In contrast, a series of matching specificities can be maintained by frequency-dependent selection without the need to invoke costs (Frank, 1993, *Proc. R. Soc. Lond. B.* **254**, 191). In an earlier paper, Parker (1990, *Evolution* **44**, 1872) argued that costs of resistance and virulence are not universal. If true, then strict gene for gene specificities are necessarily limited, in contradiction with Parker's (1994, *Evol. Ecol.* **8**, 560) recent interpretation of polymorphism data. My point here is that ambiguities remain. It is too soon to draw strong conclusions about specificity.

A second point about evolution concerns dynamics. A system with matching specificities is dynamically unstable (Frank, 1993, *Proc. R. Soc. Lond. B* **254**, 191). This instability leads to widespread fluctuations in allele frequencies and, very likely, common local extinctions of particular alleles. Thus, matching specificities will appear highly asymmetric at any point in time and space (Frank, 1993, *Proc. R. Soc. Lond. B* **254**, 191; 1994, *Phil. Trans. R. Soc. Lond. B* **346**, 283).

Parker (1996, *Evol. Ecol.* **10**, 319–22) suggested that if one sampled across spatial locations, the symmetry of matching specificities should be apparent. However, no one has yet analysed how widely one must sample to see the symmetry. I have shown that the time scale over which different specificities come and go within a single population is very long, perhaps hundreds or thousands of generations (Frank, 1993, *Proc. R. Soc. Lond. B* **254**, 191). Thus, extremely large spatial scales may be needed to smooth out local asymmetries.

Epidemiology

In an elicitor–receptor model, matching specificities correspond to alternative 'lock-and-key' fits between pathogen and host molecules. A loss of function mutation in the pathogen, leading to absence of the elicitor, will always have a universal host range. Presumably the elicitors are important for some pathogen function and loss has a fitness cost. Mutagens used in experimental screens for new virulence mutations uncover deletions, i.e. loss of function mutations (Flor, 1971, *Ann. Rev. Phytopathol.* **9**, 275). In experiments or when selection for virulence is very strong, deletion virulence is likely to appear quickly.

When host density is high, as in agricultural situations, epidemics may spread rapidly. Epidemic situations are particularly favourable to pathogen loss of function mutations because metabolic costs are easily outweighed by the transmission benefits of a wide host range. Thus, the strong selection in agricultural systems may be particularly favourable to gene for gene asymmetries. In any case, the strong epidemics are likely to reduce pathogen polymorphism. Most of Parker's (1994, *Evol. Ecol.* **8**, 560; 1996, *Evol. Ecol.* **10**, 319–22) examples of plant–pathogen diversity came from studies of agricultural systems.

Statistics

Detection of matching specificities depends on the frequencies of alleles in natural populations, on the sample sizes of plants and pathogens studied and on the methods of analysis. A major

portion of my earlier paper was devoted to showing that the strict gene for gene asymmetry would frequently be inferred from samples of natural populations that, in fact, had a wide diversity of matching specificities (Frank, 1996a, *Evol. Ecol.* **10**, 307–17). This result depends partly on sample size, as Parker (1996a, *Evol. Ecol.* **10**, 319–22) suggested, but depends much more strongly on the fact that allele frequencies fluctuate widely when there are matching specificities.

Summary

There are sufficient reasons to question whether plant–pathogen genetics invariably follow the strict form of the gene for gene model favoured by Parker (1994, *Evol Ecol.* **8**, 560; 1996, *Evol. Ecol.* **10**, 319–22). My point is simply that matching specificities cannot be ruled out by the presently available data and there are good biochemical reasons to suspect that they exist. Given the difficulties of inferring specificity solely from observed polymorphisms, it seems inevitable that a solution will be achieved by biochemical analysis coupled with studies of population diversity.

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