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Experimental evolution in an agricultural pathogen *Ralstonia solanacearum*

Pathogens are usually thought to evolve exclusively in a tightly linked relationship with their hosts. Environmentally transmitted pathogens, however, are repeatedly exposed to selection pressures that are not directly connected to their hosts. These outside-host selection pressures may include abiotic factors but also interactions with parasites, predators, and competing species. A good example of this phenomenon is the diverse plant root-associated microbiome protecting the hosts from invading soil-borne pathogens. It is estimated that 10-20% of global food production is currently lost to plant diseases and *Ralstonia*-inflicted damage to potato alone exceeds \$950 million per year. Still, very little is known about how rapid evolutionary processes shape these pathogen invasions depending on the resident community diversity and the identity of the invading pathogen strain. I tackle this question by means of experimental evolution: Different *Ralstonia* strains are let to evolve across a diversity gradient of plant-protective *Pseudomonas* strains in all possible strain combinations in order to disentangle strain identity and diversity effects.