



Directed Evolution of Disease
Suppressive Bacteria: The Role of Root
Lesions on Take-all Diseased Wheat.

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Abstract

Take-all disease (caused by *Gaeumannomyces graminis var tritici*, Ggt) can be suppressed by soil microorganisms after continuous monoculture of wheat (take-all decline, TAD). Fluorescent pseudomonads have been implicated in this suppression. Two strategies for controlling take-all are the *in situ* development of disease suppressive soil, and/or the application of a biocontrol agent. However, TAD takes up to 10 years to develop after initially high levels of disease, and the performance of bacterial biocontrol agents has been inconsistent. It is not known what environmental factors select for disease antagonists. In this work the role of diseased root lesions in directing the evolution of a native pseudomonad community, and a model disease antagonist, *Pseudomonas corrugata* strain 2140 (Pc2140) for increased disease suppression was investigated.

This work shows that root lesions are a distinct niche, supporting increased populations of total aerobic bacteria (TAB), pseudomonads and Pc2140 (compared to non-lesioned sections of diseased roots and healthy roots). Lesions selected for fluorescent pseudomonads and pseudomonads which increase take-all severity. In contrast, lesions selected for non-pseudomonads which decrease take-all, and healthy roots selected for non-fluorescent pseudomonads which decrease take-all. It was concluded that non-fluorescent pseudomonads and non-pseudomonads were important in reducing take-all, but not fluorescent pseudomonads.

Pc2140 produced multiple variant phenotypes *in vitro* and on wheat roots which were altered in (1) their ability to inhibit pathogens *in vitro* and control take-all, and (2) GC-FAME and BIOLOG profiles to the extent that some variants were identified as different species. Different sets of phenotypes were produced *in vitro* and on roots. After 108 weeks culture of Pc2140 on root lesions and healthy wheat roots, variant colony types were generally slightly decreased in ability to reduce take-all, and reisolates with the wild type colony morphology were generally slightly increased in ability to reduce take-all compared to the ancestral Pc2140. This is the first report on the diversification of a pseudomonad biocontrol agent on roots, and has implications for the taxonomic identification and grouping of isolates based on phenotypic characteristics.

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