

Resistance Gene Management: Concepts and Practice

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Abstract

There is now a very long history of genetics/breeding for disease resistance in annual crops. These efforts have resulted in conceptual advances and frustrations, as well as practical successes and failures. This talk will review this history and its relevance to the genetics of resistance in forest species. All plant breeders and pathologists are familiar with boom-and-bust cycles of single major resistance genes. Though there may be occasional situations where a single-gene approach to resistance is reasonable, most interest is in finding alternatives to this approach. This is especially true of long-lived species, for which durability of resistance becomes essential.

Combinations or “pyramids” of major genes can greatly increase durability of resistance and have provided some major success stories in annual crops. The mechanisms by which pyramids contribute durability, however, still are not entirely clear, and this is of importance to potential for success of this approach. Accumulating multiple resistances in a single genotype is complicated by epistatic effects of major genes, though both phenotypic and marker approaches can reduce this difficulty to some degree. Deploying major genes in mixed populations has been highly successful in some cases, including for some woody perennials. There is considerable variation in the epidemiological effectiveness of mixtures, however, and much is yet to be learned about the mechanisms behind this variability. Concern about selection for “superraces” in host mixtures has likely been greatly overstated, and the mechanisms by which selection for multiple virulences occur are much more complex than a simplistic evaluation of “virulence costs.”

Once firmly established in a breeding program, the value of quantitative resistance (QR) is difficult to argue against. Though erosion due to pathogen adaptation may be possible, QR has a solid history of durability. Some have avoided QR because of its perceived complexity of inheritance. Research has shown, however, that QR is much less complex than initially thought. In recent years, many QTL studies have been conducted, and this information may be useful in both augmenting field selection for QR and in avoiding “Vertifolia effects” in the presence of effective major genes. A significant challenge, however, will be in identifying QTL that express in multiple genetic backgrounds of the host.

Theoretical considerations aside, the best approach to breeding for resistance also will depend strongly on availability of resistance sources and on other traits being addressed in the breeding program. Flexibility and forethought must also be used in preparing for changes in silvicultural practices, introduction of new pathogen populations, and climate change that may influence disease. Combining different approaches to resistance should increase both the epidemiological effectiveness and durability of resistance.

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