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Researchers study genetics to prevent cereal diseases

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Fungal pathogens, such as rusts and mildews, are perhaps the greatest impediment to production of grain cereal plants worldwide. When environmental conditions are opportune for pathogen growth, between 30 and 50% of potential yield can be lost.

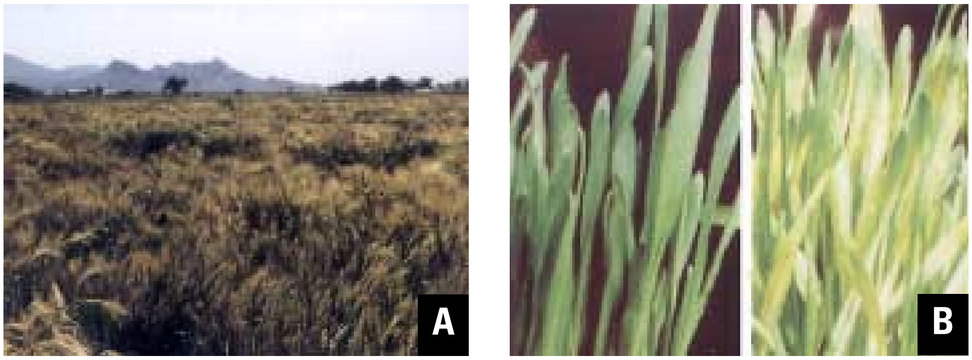
To offset crop losses from pathogens, plant breeders have turned to genetic varieties that help crops resist these diseases. In recent years, scientists have successfully cloned resistance genes from a variety of model plant species, such as Arabidopsis, rice, and tomato.

While the Arabidopsis genome – with 120 million letters of genetic code – is the smallest in plants, it has been difficult to isolate genes from crops that possess genomes that are even larger than that of humans.

For example, the barley and wheat genomes are 40 and 130 times larger, respectively, than that of Arabidopsis. Until recently, this size difference has hindered research into the mechanisms underlying resistance to devastating crop diseases.

SUCCESSFUL CLONING

With support from USDA's National Research Initiative (NRI), researchers at USDA's Agricultural Research Service at Iowa State University have cloned and characterized the *Mla* (powdery mildew) resistance gene from barley, the first successful cloning of a gene that confers active disease defense in small-grain cereals.



(A) BARLEY CROP NEAR MATURITY AT ARIZONA WINTER PROPAGATION. **(B)** UNINFECTED (LEFT) AND INFECTED BARLEY SEEDLINGS WITH POWDERY MILDEW.

> *It will then be possible not only to discover novel forms of resistance in nature, but also to create new forms in the laboratory.*

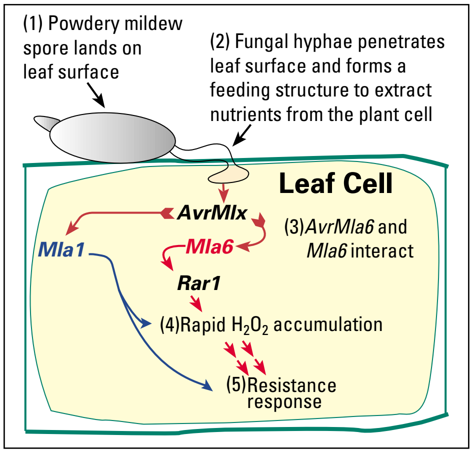
Their research has resulted in the molecular isolation of *Mla6* and *Mla1*, 2 of the 30 alternative forms of the *Mla* resistance gene from barley. The researchers used a functional test to demonstrate that *Mla6* also confers resistance to powdery mildew in wheat. This was the first demonstration of resistance gene transfer via genetic engineering among cereal crop species.

The information derived from the molecular isolation of *Mla6* and *Mla1* will provide the blueprint for scientists to isolate new and different resistance genes.

Isolating New Genes

Researchers can exploit the DNA sequence similarities among the recently isolated forms to "shortcut" the process of isolating new genes from cultivated or wild relatives of barley and wheat.

It will then be possible not only to discover novel forms of resistance in nature, but also to create new forms in the laboratory. These new genes can then be combined and engineered into elite breeding lines to combat pathogen infection and subsequent crop loss.



Model of *Mla*-mediated, resistance interactions. *Mla6* needs an additional host factor, designated *Rar1*. In contrast, *Mla1* does not require *Rar1* for function, indicating that there are at least two different *Ml* resistance pathways.

Future research is focused on clarifying the molecular events downstream of the initial recognition between host and pathogen. This will be accomplished by analyzing mutations in additional genes that are required for *Mla6*-mediated resistance.

Oftentimes, genes that control these downstream events are conserved among related species or wild relatives, even though they may function to confer resistance to different pathogens, such as bacteria, viruses, or nematodes.

Impact

NRI-sponsored research is providing a better understanding of the way disease resistance genes function in the interactions between pathogens and their host crop plants.

Introduction of novel resistances into cultivated species traditionally has relied on conventional plant breeding. The ability to isolate molecular clones of resistance genes now makes it possible to introduce them directly into the desired plant via genetic engineering.

The information derived from these investigations on resistance signaling will advance new methods of disease control for all cereal crops, which are among the world's most important food sources.

The research reported in this factsheet was sponsored by the Plant Genome Program of the Plants Division of the National Research Initiative Competitive Grants Program. To be placed on the mailing list for this publication or to receive additional information, please contact the NRI (202/401-5022 or NRICGP@reeusda.gov). The factsheet also is accessible via the NRI section of the Cooperative State Research, Education, and Extension Service website (http://www.reeusda.gov/nri).

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