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## Section 1 Moderator's Report

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The power of molecular biology and its technology to provide fresh understanding and new solutions to biological problems was dramatically highlighted by the reports in the session on the "Molecular Biology of Hypovirulence" at the 1992 International Chestnut Conference.

It has been known for sometime that *Cryphonectria parasitica* is the causative fungus of chestnut blight. Hypovirulent strains of *C. parasitica* often contain double-stranded RNA molecules (dsRNA) that were suspected to be prime factors in blocking the virulence of the fungus. Results at this session clearly demonstrated that this dsRNA is a RNA virus, and that this virus is the cause of hypovirulence. The genomic structure of the virus has been sequenced and subjected to comparative analyses with other known viral genomes. The data show that hypovirulent associated dsRNA (HAV RNA) shares common features with another plant virus group, the potyviruses, and both probably arose from a common ancestor.

Of most importance in this session was the presentation of a major advance in prospects for genetic engineering of HAV RNA to enable the transmissible hypovirulence of *C. parasitica* from one strain to another. Donald Nuss and his

coworkers at the Roche Institute of Molecular Biology have been able to prepare a clone of a full-length cDNA copy of the HAV RNA and have this DNA integrated into the nuclear DNA of *C. parasitica*. The integrated HAV eDNA then produces continuing quantities of the HAV dsRNA in the fungus. This extraordinary research accomplishment in molecular virology opens up new approaches for controlling chestnut blight and, perhaps, other fungal pathogens in both the plant and animal kingdoms.

Another immediate impact of this technology is that it provides a broad opportunity for genetic manipulation of HVA eDNA not available with the dsRNA genome itself. The ability to do molecular genetics offers a powerful approach for understanding both the mechanism of hypovirulence and the nature of the virulent genes of *C. parasitica*. In practical terms, the transformed *C. parasitica*, containing the HAV cDNA integrated into its own DNA may now transmit hypovirulence in an efficient and ubiquitous manner. This may be accomplished by increased production of spores containing HAV dsRNA, increased transmission of dsRNA during anastomosis and, most ex-

citing, by sexual crossings that would bypass vegetative incompatibility barriers that now seem to be the most important factor in suppressing the spread of hypovirulence in *C. parasitica*.

The success of a scientific conference can be measured by the fresh impetus and new research projects it generates. The molecular biologists working on chestnut blight have revealed new understandings and opened up new vistas for all workers concerned with this disease. Based on their work, it should be possible to identify the mechanism of

pathogenicity produced by *C. parasitica* and to extend a similar molecular genetic approach to other fungal pathogens.

It is apparent that revival of the American chestnut will require field tests of these new ideas and involve government and public approval that itself may take years. It is therefore of utmost priority that immediate steps be taken to initiate the first field tests of this new technology and realize the dream of restoring the American chestnut to its natural habitat.