Section 4 Moderator's Report

John F. Leslie

Department of Plant Pathology, Throckmorton Hall, Kansas State University, Manhattan, Kansas 66506-5502, USA

The chestnut blight fungus has long been an object of interest to many scientists, including myself, besides those who work with the organism. This disease is a classic example of the problems that may result from the introduction of a foreign pest. As a model system, it can be used to discern interactions between the fungus and a dsRNA that can infect the fungus and reduce virulence, and also to study vegetative compatibility—an important underlying mechanism employed by many fungi to distinguish self from non-self. Some researchers are interested in restoring the American chestnut as the dominant species in its native range, and others are interested in this tree as a horticultural crop either as a specimen or as an orchard tree. The common problem area for researchers with any of these interests is the pathogen, with studies of the American chestnut host significantly lagging behind the studies of the pathogen.

The papers presented in this section and elsewhere in this conference demonstrate that the most progress is being made in understanding the pathogen as a part of a model system. The success reported by Donald Nuss and his colleagues; however, indicates that this research community needs to be considering how the molecular successes will be applied to the control of the disease in either natural or horticultural settings. At present, much of the basic plant pathology and knowledge of the organism's life cycle under orchard or woodlot conditions is lacking. The genetic and molecular markers being developed to track this organism need to make the transition from the laboratory to the field, and be used there to answer fundamental questions such as:

1. How is the organism spread?
2. Are the VCG-induced subdivisions within the population serving roles other than to inhibit the spread of dsRNA?
3. What is the basis of the plant/pathogen interaction that leads to chestnut blight?
4. Are hypovirulent strains sufficiently competitive to be self-sustaining in a population?

Answers to some of these questions are being approached, but they will require closer coordination than is now evident for rapid progress to be made. A major problem in this respect is that the number of investigators actively working with the organism seems to be only at the threshold for critical mass. Consequently, the researchers in this area are quite dependent upon one another for the ideas and novel approaches that will be necessary to make the research in this area succeed.

Based on the research results presented at this meeting, some suggestions for future directions are:

1. Consciously make a shift from a descriptive and romantic approach to chestnut blight to an approach using clearly defined hypotheses that can be tested.
2. Clearly delineate goals and objectives as they relate to this disease in the context of a model system, in a horticultural setting, and in the restoration of the American chestnut to its native range.

3. Recruit additional expertise in biochemistry and plant physiology to study the plant/pathogen interaction.
4. Begin developing plans to implement the use of the molecular advances in the study of dsRNA in the implementation of a biological control program.
5. Continue development of genetic and molecular markers necessary for the infrastructure to make the pathogen a workable genetic entity. Some examples of these studies could include:
   a. Develop a nuclear genetic map using molecular markers such as RFLPs and RAPDs.
   b. Develop a karyotype using pulse-field electrophoresis.
   c. Continue identification and characterization of markers suitable for monitoring and characterizing field populations of the pathogen.
6. Continue to develop the unique features of this pathogen. Some examples of these studies could include:
   a. Genetic and physiological studies of vegetative compatibility; studies of both function and population aspects are warranted. Comparisons of this system with other fungi with similar properties would probably help to increase the overall understanding of this phenomenon within the fungi.
   b. Further the understanding of the basic mechanism of hypovirulence through studies of dsRNA within its pathogen host. In general, researchers in this group are positioned to make significant advances, primarily in the area of the model system, and hypothesis-based research should be encouraged during the coming years.

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