A Genetic Map of Head Smut. (A00-waters121531-Oral)

Authors:

- J.L.Waters - *Brigham Young University*
- S.Meyer - *USDA Forest Service, Provo, UT*
- D.Nelson - *USDA Forest Service, Provo, UT*
- S.Clement - *USDA Forest Service, Provo, UT*
- D.Fairbanks - *Brigham Young University*
- T.Boguena - *Brigham Young University*
- A.Ramakrishnan - *Brigham Young University*

Abstract:

Cheatgrass, an exotic winter annual, displaces native vegetation, invades crops, and fuels rangeland fires across approximately 40 million hectares of the Intermountain West. Most attempts to control the weed have been unsuccessful, leading to a search for a biological control agent. Head smut is a natural species-specific, fungal pathogen. Despite apparent phenotypic uniformity in cheatgrass and head smut, susceptibility and virulence, respectively, are variable. Two apparently diverse strains of head smut, as judged by greenhouse virulence studies, were crossed as the parents for a segregating population. AFLP analysis was performed on this population to develop molecular markers for a framework genetic map. Apparently low levels of genetic diversity (approx. 13%), as revealed in a previous population polymorphism study, yielded low recombination rates and therefore fewer genetic markers. This was compensated for, however, by the addition of phenotypic and morphological markers obtained from the extensive greenhouse studies. Given this information, strains of head smut that may be more effective biological controls of specific genotypes of cheatgrass may be developed.

Corresponding Author Information:

Jennifer Waters
Brigham Young University
Brigham Young University, 201 WIDB
Provo, UT 84602

phone: (801)422-3958
fax: (801) 422-0008
e-mail: jlw92@email.byu.edu

Presentation Information:

Presentation Date: Monday, November 11, 2002

Presentation Time: 8:45 am

Keywords:
Genetic map, Head smut, Amplified fragment length polymorphism , Biocontrol