Poster 10. BIBAC library and physical map construction of the Puccinia triticina pathotype PRTUS3.

Arlene Pacheco, Hongbin Zhang, and Dirk B. Hays. Department of Soil and Crop Science, Texas A&M University, College Station, TX 77843, USA.

Leaf rust is the most common and one of the most important cereal diseases of the world. Current leaf rust control has consisted of breeding for resistant cultivars by identifying Lr genes in the host. These cultivars quickly become susceptible to infection due to the tremendous extant genetic diversity of the pathogen that allows it to overcome resistant cultivars in 2–4 years. Development of alternate methods of control are limited, because little is known about the *Puccinia* genome and plant-pathogen interaction. Construction of a genome-wide physical map is important in order to fully understand the infection mechanism of the pathogen and its interaction with the host. In an effort to discover more about the genetic potential of leaf rust in terms of AVR and VIR gene regulation and create novel plant resistance breeding strategies in the future, we have proposed to study the pathogen's genome by constructing a BIBAC library and a physical map of the pathogen. The BIBAC library is being constructed from pathotype PRTUS 3, which has AVR-1 disrupted using T-DNA mutagenesis via particle bombardment. The characterization of the AVR-1 in the BIBAC library will serve as a point of reference for cloning heterologous AVR and VIR genes, and defining their regulation and mode of inheritance and recombination.

Poster 11. Defining the pleiotropic nature of heat-tolerance QTL controlling end-use quality and yield stability during reproductive-stage heat stress in wheat (Triticum aestivum).

Francis Beecher, Esten Mason, Suchimita Mondal, Amir Ibrahim, and Dirk B. Hays. Department of Soil and Crop Science, Texas A&M University, College Station, TX 77843, USA.

High temperature during reproductive development is a major factor limiting wheat production and end-use quality in the southern Great Plains and in many other environments worldwide. We have initiated a project to integrate genotypic (QTL), multiple phenotypic, and transcript level data to identify genes controlling reproductive-stage heat tolerance in wheat. Heat tolerance is defined here as the maintenance of yield and end-use quality during reproductive-stage heat stress. Efforts have initially focused on building recombinant inbred lines (RILs), collecting RIL morphological and yield response data from field and controlled environment studies, and mapping QTL linked to reproductive-stage heat tolerance. Our mapping has, to date, focused particularly on yield maintenance QTL. Given the importance and known sensitivity to heat stress, QTL associated with end-use quality maintenance were mapped in correlation with yield maintenance QTL to determine the collective pleiotropic effects of heat-tolerance QTL. Mapping of end-use quality QTL was done by SDS sedimentation of grain from each RIL harvested in both growth chamber- and field-imposed heat stress experiments. The hard white spring wheat Halberd was used as the source of heat tolerance. Two populations were used; one consisted of 64 F_6 'Halberd/Cutter' and the other a population of 120 'Halberd/Karl 92' F_6 RILs. Each population was grown under both heat stress and control conditions in the field and greenhouse. Heat stress in the greenhouse was applied by a 3-day treatment of 38°C applied 10 days after pollination. Quality results were analyzed for their relation to mapped yield-maintenance, heat-tolerance QTL. The resulting map will allow us to determine whether grain quality traits and yield-maintenance QTL segregate together or independently from heat-tolerance QTL. An improved understanding of the correlation between end-use quality and yield-stability QTL (heat tolerance) during reproductive-stage heat stress will aid in breeding plants possessing both attributes using marker-assisted selection and in basic research aimed at defining the molecular basis of heat tolerance.