

PI: Gina Brown-Guedira

PI's E-mail: gbg@ksu.edu

Project ID:

FY04 ARS Agreement #: NA

Research Area: VDUN

Duration of Award: 1 Year

Project Title: Developing FHB Resistant Soft Wheat Varieties by Accelerated Backcrossing.

PROJECT 1 ABSTRACT

(1 Page Limit)

Backcrossing (BC) is a useful method of introgressing genes to further improve a useful genotype. A drawback in many backcrossing (BC) schemes is that a recurrent parent (RP) is selected for BCing when it is close to release or post-release. This weakness may be addressed by using molecular markers to select for RP genetic background as well as the target trait at the BC1F1 and BC2F1 stages. This can save one or two cycles of BCing (perhaps 1 year) while increasing the likelihood that FHB resistant derived lines will have the desirable characteristics of the recurrent parent. We are proposing to use this approach in a set of four crosses targeted to each of the soft winter wheat sub-regions (Cornbelt, Mid-Atlantic, Deep South and North). We propose using moderately resistant soft wheat lines as RPs in an accelerated BCing scheme to introgress two or more exotic QTLs and to rapidly develop a set of high-yielding FHB-resistant varieties. A set of RPs and donor parents (DPs) is being selected by breeding programs in each of the four sub-regions. The lines derived from BCing will be available for testing and cultivar release to programs within these sub-regions. They will also serve as excellent parents for subsequent crossing as each will have two tagged QTLs plus their own native resistance. In each soft wheat growing region breeders will coordinately select RP and DP combinations so that BC derived lines with complementary QTLs are generated (Asian QTL on 3BS plus other complementary QTL). These select lines will then be intercrossed to form new breeding populations that are fixed for 3BS and allow for further pyramiding of QTLs in a MAS recurrent selection scheme. We will also validate the effect of the QTLs used in the BCing by creating near isogenic lines (NILs) for QTL combinations in different genetic backgrounds at the last stages of the BCing.