USDA-ARS / USWBSI
FY04 Final Performance Report
July 15, 2005

Cover Page

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Year: FY2004 (approx. May 04 – April 05)
FY04 ARS Agreement ID: 59-0790-4-101
FY04 ARS Agreement Title: Uniform Nursery for SRWW and Breeding Scab Resistant
Varieties for Ohio.
FY04 ARS Award Amount: $ 69,980

USWBSI Individual Project(s)

<table>
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<tr>
<th>USWBSI Research Area*</th>
<th>Project Title</th>
<th>ARS Adjusted Award Amount</th>
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<tr>
<td>VDUN</td>
<td>Uniform Nursery for SRWW and Development of Scab Resistant Varieties.</td>
<td>$ 63,639</td>
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<tr>
<td>BIO</td>
<td>Development of MAS in Soft Red Winter Wheat.</td>
<td>$ 6,341</td>
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Total ARS Award Amount $ 69,980

Principal Investigator          Date

* BIO – Biotechnology
CBC – Chemical & Biological Control
EDM – Epidemiology & Disease Management
FSTU – Food Safety, Toxicology, & Utilization
GIE – Germplasm Introduction & Enhancement
VDUN – Variety Development & Uniform Nurseries

(Form – FPR04)
Project 1: Uniform Nursery for SRWW and Development of Scab Resistant Varieties.

1. What major problem or issue is being resolved and how are you resolving it?

Host resistance is crucial for control of Fusarium Head Blight (FHB). FHB resistance must be combined with high yield, quality, agronomic value, and resistance to many other disease to have a positive impact on growers. Despite many technological advancements in breeding and genomics, field screening is the only sure way to achieve this objective. Many new genotypes must be screened each year to find the needed combination of FHB resistance and all the other traits. In addition, multi-location testing is needed due to variation of the environment.

2. What were the most significant accomplishments?

We screened 1184 lines for FHB resistance in the 2003-04 season. Of the lines in their first year of testing, 66% had FHB resistance that was equal or superior to that of the moderately resistant check Freedom. Over 76% of our more advanced lines had FHB resistance that was equal or superior to that of the moderately resistant check Freedom. This resistance is almost exclusively derived from adapted soft red winter wheat (SRWWs). Many crosses among SRWW produced progeny with low FHB. This is important as it indicates that selection within the SRWW pool can produce resistance and that there are likely to resistance genes from many SRWW sources. This is very important as it shows that MAS for a single QTL, such as 3BS from Chinese sources, may be useful in SRWW. The current QTLs will not produce adequate resistance on their own so they must be placed in genetic backgrounds that already produce a below average FHB score, such as the SRWW lines we have identified.

We are continuing to develop germplasm via marker-assisted backcrossing to assess the value of exotic (and some domestic) QTL on resistance in SRWW. We have now generated BC2F1 progeny with QTLs from Frontana, Wuhan, and Sumai 3, in resistant, moderately resistant, and susceptible SRWW lines.

The 2003-04 NUWWSN was very effective at assessing the FHB resistance of SRWW. Fifty entries from 13 programs and 6 checks were assessed. Eight new SRWW lines with excellent FHB resistance were identified, five of these had no exotic germplasm in their pedigree. Results were distributed to all SRWW breeders, several hard wheat breeders, and were posted on the USWBSI web site.

1. What major problem or issue is being resolved and how are you resolving it?

SRWW does not appear to have major genes for FHB resistance even though there is considerable FHB resistance in the SRWW gene pool. Identifying new genes from exotic sources is important as we need to complement the native genes we do have. One source may be Frontana, a spring wheat from Brazil that is reported to have type I and II resistance. While that claim is unproven, there are several conflicting reports of major genes for FHB resistance in Frontana. Our objective was to assess which of these genes may be useful. In addition, we could breed for FHB resistance more efficiently in SRWW if we knew where the SRWW genes were and their effects. Thus we will continue to assess QTLs from the SRWW line Freedom.

2. What were the most significant accomplishments?

We mapped resistance in a double haploid population of Augusta/FHB148 (a DH from Harus/Frontana). We assessed the value of key chromosome segments (2AS, 3AC, 3BS, 6BS, 4BC) that have been reported to be associated with FHB resistance in Frontana or other sources. Only the 4BC region showed any significant, though modest effect in our study. Interestingly, FHB148 appears to have Harus genes in this region, not the Frontana genes. We had hoped to assess 3AC but FHB148 again had Harus alleles in this region. As we did not detect any important QTLs from FHB148, we decided not to create NILs to assess FHB148 QTLs.

We genotype a RIL population derived from Freedom/OH546 with markers from 2AS to confirm the previously reported 2AS QTL. Several 2AS markers were significant, with the best (Xgwm1053) accounting for 10% of the variation and an additive effect of 4% on FHB index.

We planted F4:5 families from the crosses Ernie/Hopewell, Hopewell/OH599, Pioneer 25R18/OH685, Hopewell/OH685, and Roane/OH685. Significant segregation was noted in each cross including lines that were numerically superior to the most resistant parent.
Include below a list of the publications, presentations, peer-reviewed articles, and non-peer reviewed articles written about your work that resulted from all of the projects included in your grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

