

**U.S. Wheat and Barley Scab Initiative  
 FY02 Final Preliminary Performance Report (approx. May 02 – April 03)  
 July 15, 2003**

**Cover Page**

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<b>FY02 ARS Award Amount:</b>	<b>\$ 17,990</b>

**Project**

<b>Program Area</b>	<b>Project Title</b>	<b>USWBSI Recommended Amount</b>
EDM	Host specialization and genetic diversity in Gibberella zeae from corn, wheat & rice in Nepal.	\$18,440
	<b>Total Amount Recommended</b>	<b>\$18,440</b>

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 Principal Investigator

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 Date

**Project 1: Host specialization and genetic diversity in *Gibberella zeae* from corn, wheat & rice in Nepal.**

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

This project is part of a larger collaborative effort that is characterizing a population of *Gibberella zeae* from a 25-km<sup>2</sup> area in Nepal. Previous studies found that Nepal contains multiple lineages of *G. zeae* that have the potential to hybridize. Characterization of collections made from 1993 to 2000 indicate that *G. zeae* populations in Nepal contain three to five groups that differ in toxin production, virulence and host specialization. Therefore, Nepal represents an area where new genetic combinations of *G. zeae* could form. These new combinations pose a threat to our efforts to control wheat and barley scab.

The goal of the research funded by USWGSI is to characterize molecularly the Nepal collection to: 1) determine the amount and pattern of genetic variability of *G. zeae*, 2) assess the potential for hybridization among lineages, and 3) assess the risk of new combinations of *G. zeae* arising in Nepal and spreading throughout the world.

2. What were the most significant accomplishments?

We have completed molecular characterization of nearly 200 isolates using Amplified Fragment Length Polymorphisms (AFLPs). Our data indicate that the Nepal population is composed of three distinct lineages that correspond roughly to the sequence characterized (SCAR) groupings reported by Carter, Rezanoor, Desjardins and Nicholson in 2000. Based on our AFLP data, SCAR groups 1 and 2 are indeed distinct lineages, but groups 3 and 5 are part of a single interbreeding lineage (hereafter referred to as lineage 3/5). The three lineages differ in toxin production, virulence on wheat, and perhaps host specialization. Isolates from lineage 1 produce DON exclusively, isolates from lineage 2 only produce NIV, while lineage 3/5 isolates produce either DON or NIV (Table 1). Isolates from lineages 1 and 3/5 are, on average, more virulent on wheat than isolates from lineage 2. Our data indicate that Nepal contains the most genetically variable *G. zeae* populations in the world.

Table 1. Relationship between lineage and trichothecene chemotype for *Gibberella zeae* populations in Nepal.

Toxin	Lineage 1	Lineage 2	Lineage 3/5
DON	20	0	58
NIV	0	66	103

All lineages are delimited by differences in the frequency of informative AFLP bands, and not the presence or absence of bands. While this pattern is consistent with the hypothesis that lineages are hybridizing to some degree, our attempts to cross isolates from different lineages suggest that there are barriers to crossing. The pattern is also consistent with the hypothesis that the lineages have diverged recently, but are distinct.

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 the grant. Please reference each item using an accepted journal format. If you need more space, continue the list on the next page.

Desjardins, AE, RD Plattner and AM Jarosz. 2002 Biological diversity of *Gibberella zeae* from Nepal: genotypes, virulence, and toxins. *Phytopathology* 92: S19

Two manuscripts are being prepared for publication.