

**0203-JA-087 Host specialization and genetic diversity in *Gibberella zeae* from corn, wheat & rice in Nepal.**

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PROJECT ABSTRACT

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The *Gibberella zeae* population in Nepal is highly diverse, with at least three of the seven worldwide lineages being endemic (O'Donnell et al. 2000). Further, a naturally occurring recombinant between lineages was also detected in Nepal -- The only known among lineage hybrid detected in a worldwide survey of *G. zeae* (O'Donnell et al. 2000). Thus, the *G. zeae* population in Nepal represents a distinct threat to the management of scab on wheat and barley because novel genotypes may migrate from this area and instigate new epidemics. We propose to evaluate this population for the level and pattern of diversity and determine the potential that novel genotypes may occur within the region. Samples from wheat, rice, maize, soil and weeds were collected from four farms in the Lamjung district of Nepal in 2000. *Gibberella zeae* isolates are currently being characterized for virulence on wheat and corn, mycotoxin production, and genetic structure. The proposed work for this aspect of the overall collaborative effort will utilize AFLP markers to determine the spatial and temporal pattern of diversity within *G. zeae* population in Nepal. We will specifically address whether the previously documented lineages remain distinct in Nepal, and assess whether the pathogen displays host specificity with the Nepal region. The combined results for the project will allow us to assess the potential for novel genotypes to be produced within Nepal and their potential epidemiological impact if they were to migrate to major wheat and barley growing areas of the world.