DIVERSITY OF THE RUST PATHOGEN AND COMMON BEAN GUIDES GENE DEPLOYMENT FOR DEVELOPMENT OF BEAN CULTIVARS WITH DURABLE RUST RESISTANCE

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The high virulence diversity of *Uromyces appendiculatus*, the rust pathogen of the common bean (*Phaseolus vulgaris*), greatly complicates the development of cultivars with durable disease resistance. The virulence diversity of this pathogen varies in time and space, thus bean varieties that are resistant in one year or location may be susceptible in another. Understanding the virulence and genetic diversity and the evolution of the rust pathogen, as well as the diversity of its common bean host is essential to the development of bean cultivars with durable resistance.

**Diversity of the Common Bean**

Two major groups of beans, known as the Middle American and Andean gene pools, are recognized in cultivated common bean. Many distinguishing characteristics such as morphology (5), allozymes (6), seed proteins (3), DNA polymorphisms (1), and chloroplast data (2) separate these two very distinct groups of beans. These gene pools reflect multiple and independent domestications events within distinct wild populations in Middle America (Central America and Mexico) and the Andes region of South America.

**Diversity of the Bean Rust Pathogen**

The rust pathogen is autoecious, biotrophic and macrocyclic (8). It readily produces uredionospores and teliospores but the basidiospores, pycniospores and aeciospores are found infrequently. The five spore stages of *U. appendiculatus* are evidence of the genetic recombination capacity of this fungus and its plausible ability to produce new virulent strains (4). Recent virulence diversity studies of the rust pathogen using Andean and Middle American bean differential cultivars, and genetic diversity studies using molecular markers show that *U. appendiculatus* has two distinct groups of isolates mirroring the diversity of its common bean host (5). One group identified as Andean, is made of isolates that have narrow and specific host range; they are compatible only with or mostly with Andean cultivars. These isolates occur in Mozambique and Ecuador where Andean beans predominate. Another group, called Middle American is comprised of isolates having a broad and nonspecific host range; they are compatible with Andean and Middle American beans (5). These isolates are often found in Central America, Mexico and other countries where Middle American beans predominate. A phylogenetic analysis of sequence data of approximately 2.2 KB of the elongation factor 1-alpha gene (EF-1a) used to explore genetic diversity of the same isolates, resolved two distinct groups of isolates that corresponded to the Andean and Middle American virulence groups (5). The notable correspondence of the two groups of isolates of the rust pathogen with those of its bean host suggests coevolution between these organisms.

**Development of bean cultivars with durable rust resistance**

The diversity and coevolution studies described above have shown that rust resistance genes from beans of Andean origin tend to be susceptible to Andean races of rust pathogen; however, these genes are often very effective against many important Middle American races. Conversely, the rust resistance genes from Middle American beans often have broad resistance and but are
susceptible to many Middle American races and particularly resistant to most Andean races. For example, Ur-11 a rust resistance gene of Middle American origin is resistant to all known races of the rust pathogen except race 108 which is of Middle American origin. On the other hand, the Andean Ur-4 rust resistance gene is susceptible to most Andean races of the rust pathogen, but Ur-4 is resistant to race 108 and to many other Middle American races. The Ur-3 and Ur-5 rust resistance genes of Middle American origin are susceptible to several Middle American races of the rust fungus but they provide resistance to most Andean races. Therefore, a practical consequence of the bean-rust diversity and coevolution studies is the realization that combining rust resistance genes (gene pyramiding) from Andean and Middle American gene pools could result in bean cultivars with effective and durable rust resistance throughout the world. In collaboration with scientists from Michigan and North Dakota state universities and the University of Nebraska, we have developed six great northern (known as BelMiNeb-RMR-8, -9, -10, -11, -12, and -13) and five pinto (known as BelDakMi-RMR-19, -20, -21, -22, and -23) bean germplasm lines that are unique in the world for the genes they combine. They contain two Middle American (Ur-3 and Ur-11) and two Andean (Ur-4 and Ur-6) genes for resistance to all known races of Uromyces appendiculatus and two genes (f and bc-3) for resistance to all known strains of the also variable bean common mosaic and bean common mosaic necrosis potyviruses. So far, these beans have been evaluated as resistant under greenhouse conditions to all 90 strains of the rust pathogen maintained at Beltsville, MD and under field conditions the US, South Africa and Honduras. In summary, understanding the diversity of the rust pathogen and of its common bean host has provided a rational basis for gene pyramiding of Andean and Middle American disease resistance genes and the possibility of having durable resistance in bean cultivars to highly variable pathogens.

References