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# *BRACHYPODIUM DISTACHYON* AS A SUITABLE PATHOSYSTEM MODEL

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Cereals rusts (Puccinia spp.), caused by highly specialised *Basidiomycetes* in the order *Uredinales*, are among the most destructive plant diseases, responsible for recurrent episodes of catastrophic yield loss and economic hardship among grain-based agricultural societies for at least the past 300 years. Within this broad class of diseases, stem rust (causal organism *P. graminis* Pers. f. sp. tritici), stripe or yellow rust (causal organism *P. striiformis* f. sp. tritici), and leaf rust (causal organism *P. triticina*) of wheat (*Triticum aestivum*) are the most prominent in their historical relevance to agricultural productivity. While it is possible to mitigate losses to these pathogens through the timely application of fungicides, it is not always efficient. Plus it should never be forgotten, that the food security is one of the major global issues. Today, global average wheat yields are about 2.5 t ha but an estimated 4.0 t ha will be needed to sustain the world in 2020 (Sears, 2006).

Most of the resistance genes discovered and deployed in defense against the wheat rusts are the so called major genes (also known as race-specific resistance genes), single loci conferring effective levels of resistance against specific physiologic races of the pathogen, generally throughout the life cycle of the host. It should be, however, noted that a race-specific resistance gene, though effective against some races of the pathogen, is by definition vulnerable to at least one other race (extant or potential) of the same pathogen, as are *combinations* of such genes.

Indeed, the long-term unreliability of the defense afforded by major genes is inherent, particularly given pathogen populations whose rates of genetic change far outpace that of modern cultivated wheat. To illustrate this fact, consider that of the approximately 70 identified major resistance genes to stripe rust, only 3 (*Yr5*, *Yr15*, and *Yr24/26*, each neither widely nor long-deployed) remain effective against all detected races of the pathogen in the United States (Chen, 2007).

The most promising long- term control strategy is to breed and deploy cultivars carrying durable adult plant resistance based on minor, slow-rusting genes with additive effects. Combining four to five slow-rusting resistance genes result in a high level of resistance, comparable to immunity. Traditional genetic and molecular mapping studies have demonstrated high genetic diversity for such minor genes in wheat germplasm and often resistance to brown and yellow rusts is under pleiotropic genetic control. Cloning of gene Lr34 has shown that this pleiotropic slow-rusting resistance gene is different from race-specific resistance genes. It should be noted that having minor gene-based resistance in several backgrounds eases future selection for these resistance genes through intercrossing of these adapted parents (Singh, 2008).

Research to understand the genetics of host resistance to pathogen in cereal gra- [illegible]