

# Genetic Analysis of Nonhost Resistance to Wheat Stem Rust in *Brachypodium distachyon*

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Wheat is the cereal crop with the third largest production in the world, after rice and maize (FAO, 2013). Climate change and disease are the main threats to wheat production (Oerke and Dehne, 2002; Wheat CRP Annual Report, 2013). Wheat stem rust, caused by the obligate fungal parasite *Puccinia graminis* f.sp. *tritici*, is one of the most severe diseases of wheat and can cause 50% yield losses in a short period of time (Roelfs et al., 1992). It was a huge problem in the beginning of the 20<sup>th</sup> century, but has been under control for more than 30 years thanks to the eradication of the alternate host (barberry), which eliminated the chances of sexual reproduction and genetic recombination of the pathogen, and the development of wheat resistant varieties (Milus et al., 2010).

However, a new highly virulent race of this pathogen, called Ug99, emerged in Africa and overcame the resistance gene *Sr31*, which is present in most of the wheat varieties in the world (Pretorius et al., 2000). Originally found in Uganda, the pathogen is evolving into new races, breaking resistance of other important genes, such as *Sr24* and *Sr36* (Jin et al., 2008; Jin et al., 2009), and is spreading through Africa and towards Middle East and Asia, which are areas where wheat production is very important. This situation demonstrates that current race-specific genes are not effective enough in fighting against Ug99 races. Therefore, there is a need for more durable and broad-spectrum resistance genes.

There are two types of resistance: (1) host resistance, where the entire species is susceptible to an adapted pathogen, except for varieties that have specific resistance genes (Heath, 2000; Mysore and Ryu, 2004), like wheat and the fungus wheat stem rust; and (2) nonhost resistance, where the entire species is resistant to a non-adapted pathogen (Mysore and Ryu, 2004), like *Arabidopsis* and the fungus that causes powdery mildew in barley. The latter explains why most of the plants cannot be infected by most of the pathogens, because a non-adapted pathogen did not evolve to overcome all the physical, chemical and molecular barriers imposed by the nonhost plant. Thus, finding resistance genes related to nonhost resistance may contribute to providing more durable and broad-spectrum resistance.

*Brachypodium distachyon* is a model plant for temperate grasses (wheat, barley, etc.) and a nonhost for the wheat stem rust pathogen. However some *Brachypodium* accessions allow pathogen development to some extent. This is very useful, because it is possible to map nonhost resistant genes involved in this “susceptibility” by crossing it to a resistant accession.

For this study, two *Brachypodium* mapping populations are available. The first one explores the natural variation of *Brachypodium* germplasm, and it is composed by 154 Recombinant Inbred Lines (RILs) derived from a cross of Bd21 (resistant parent) and Bd2-3 (“susceptible” parent). The second population has 126 RILs from a cross with the same resistant parent (Bd21) and the “susceptible” mutant  $\gamma$ AL6.2 (originated from gamma irradiation of a Bd21 plant). Thus, the objectives of this study are: (1) to perform genetic analysis of major *Brachypodium* nonhost resistance genes by infecting the plant wheat stem rust pathogen in both populations; (2) to map these genes using Bulk Segregant Analysis and bioinformatics approach; (3) to fine map / validate genes using DNA markers.

## REFERENCES:

- FAO (Food and Agriculture Organization of the United Nations). 2013. **FAO Statistical Year Book – World Food and Agriculture**. Available at:  
<http://www.fao.org/docrep/018/i3107e/i3107e.PDF>
- Heath MC. 2000. **Nonhost resistance and nonspecific plant defenses**. *Current Opinion in Plant Biology*, 3:315-319.
- Jin Y, Szabo LJ, Pretorius ZA, Singh RP, Ward R, Fetch T. 2008. **Detection of Virulence to Resistance Gene Sr24 Within Race TTKS of *Puccinia graminis* f.sp. *tritici***. *Plant Disease*, 92:923-926.
- Jin Y, Szabo LJ, Rouse MN, Fetch T, Pretorius ZA, Wanyera R, Njau P. 2008. **Detection of Virulence to Resistance Gene Sr36 Within TTKS Race Lineage of *Puccinia graminis* f.sp. *tritici***. *Plant Disease*, 93:367-370.
- Milus G, DeWolf E, Dill- Macky R, Steffenson B, Wegulo S, Bergstrom G, Sorrells M, McMullen M, Paul P, Hunger R, Mundt C, Isard S, Stein J, Murray T, Baker H, Bulluck R, Divan C, Engle J, Hebbbar P, Bowden B, Carson M, Chen X, Jin Y, Marshall D, Smith K, Szabo L. 2010. **Recovery Plan for Stem Rust of Wheat**. *National Plant Disease Recovery System (NPDRS)*. Available at:  
<http://www.ars.usda.gov/sp2UserFiles/Place/00000000/opmp/Wheat%20Stem%20Rust%20Ug99%20101016.pdf>
- Mysore KS, Ryu C. 2004. **Nonhost resistance: how much do we know?** *Trends in Plant Science*, 9(2):97-104.
- Oerke EC, Dehne HW. 2002. **Safeguarding production—losses in major crops and the role of crop protection**. *Crop Protection*, 23:275-285.
- Pretorius ZA, Singh RP, Wagoire WW, Payne TS. 2000. **Detection of Virulence to Wheat Stem Rust Resistance Gene Sr31 in *Puccinia graminis* f.sp. *tritici* in Uganda**. *American Phytopathological Society*, 84(2):203.2-203.2.
- Roelfs AP, Singh RP, Saari EE. 1992. **Rust diseases of wheat: Concepts and methods of disease management**. *CIMMYT*, 81 p. Mexico, D.F (Mexico).
- Wheat CRP Annual Report 2013: the vital grain of civilization and food security. 2014. **CGIAR Research Program on Wheat**: 24 p. Mexico, DF (Mexico). CGIAR. CIMMYT. Series: CRP Wheat Annual Report Available at:  
<http://repository.cimmyt.org/xmlui/handle/10883/4016>