Poster 65. Identification and mapping of a new leaf rust resistance gene derived from Triticum turgidum var. dicoccum.

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Leaf rust, caused by the fungus *Puccinia triticina* (formerly *P. recondita* f. sp. *tritici*) is one of the most damaging foliar pathogens of wheat, causing significant yield losses annually in many wheat growing regions of the world. Sources of genetic resistance are valuable to increase the sustainability of cereal production, from both economic and environmental standpoints. If the genetics of leaf rust resistance has long been studied in hexaploid wheat (*Triticum aestivum* L.), a detailed analysis of the genetic bases in durum wheat has been undertaken only recently.

In order to investigate the genetic basis of leaf rust resistance, we developed a genetic linkage map on a RILs population (122 F_9 lines) derived from a cross between the susceptible durum wheat cultivar Latino and the resistant accession MG5323 of *T. turgidum* var. *dicoccum*. The infection type and the percentage of infected leaf area (DS) were evaluated on the RIL population by means of artificial inoculation with two *P. triticina* isolates (Villamarique de la Condesa and 12766). A total of 486 molecular markers well distributed on the whole genome were used to search polymorphisms between the two parents of the mapping population out of which 70% were polymorphic. A genetic linkage map for QTL analysis was developed using of 320 markers distributed within 16 linkage group and spanned greater than 1,400 cM. Using both simple interval mapping (SIM) and the Multiple QTL Model mapping functions (MQM), we identified three chromosomal regions specifically associated with leaf rust resistance. The largest and the most consistent leaf rust resistance locus was identified by a DS score (LOD 12, $R^2 = 38\%$) on the short arm of chromosome 1B flanked by SSR markers *Xgwm413* and *Xgwm448*. Two additional minor QTL were identified and were located on chromosome arms 5AS and 7BL. The major QTL is localized in a genomic region where no previously identified leaf rust resistance genes (*Lr* genes) have been positioned and suggests the identification of a new resistance gene to leaf rust in the durum wheat genetic background.

Poster 66. Utility of EMS mutants in rust resistance studies and map based cloning in wheat.

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Seeds of cultivars AC Domain and Kenyon were mutagenized with ethyl methanesulfonate (EMS), planted and grown to maturity (M_1 plants). M_2 seed of each cultivar were harvested and bulked separately. A total of ~12,000 M_2 seeds of AC Domain and Kenyon were planted in equal quantities in root trainers and inoculated 11–12 days later with a leaf rust pathotype avirulent on *Lr16*. Both AC Domain and Kenyon are known to carry *Lr16*. Two weeks later, seedlings were scored as resistant, intermediate or susceptible. The plants were selfed and grown to maturity for M_3 seed. Disease phenotyping resulted in the identification of 47 putative *Lr16* mutant plants; 29 AC Domain and 18 Kenyon. Next, genomic DNA was extracted from individual plants and screened with SSRs that were linked to *Lr16*. The SSR profiles of individual mutants were compared and correlated with their respective disease phenotypes, which was done to identify off-types and enable selection of true *Lr16* mutants with SSR profiles that were identical to either of their respective non-EMS-treated parental cultivars, AC Domain or Kenyon. As a result, a total of 27 true *Lr16* mutant plants, 17 AC Domain and 10 Kenyon, were identified. Furthermore, SSR markers from across the genome were screened on the select mutants. Although M_3 mutant seed stocks for cultivars AC Domain and Kenyon are a valuable resource for ongoing efforts in map-based cloning of important genes, they also would serve as a tilling platform for future functional genomic studies.