Towards identification of quantitative loci for sclerotinia resistance in *Brassica napus* germplasm and the underlying defence genes

L. Buchwaldt, F. Fu, S. Gyawali, D.D. Hegedus and I.A.P. Parkin, Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, Canada, SN7 0X2

Contact: lone.buchwaldt@agr.gc.ca, phone : +1 306-956-2826

Control of the fungal pathogen *Sclerotinia sclerotiorum* in *Brassica* crops using cultural practices and fungicides have limited effect and economic benefit. We therefore embarked on research to identify *B. napus* lines with high level of quantitative resistance along with molecular markers to aid transfer of resistance into canola-quality varieties. A world collection of 400 accessions held at Plant Gene Resources of Canada was phenotyped with *S. sclerotiorum* isolate #321. Plants at full flower were inoculated by attaching mycelium grown on nutrient media to the main stem with Parafilm. Measurements of lesion length from 7 to 21 days were used to calculate AUDPC (area under the disease progress curve). Accessions with low AUDPC originated from South Korea, Japan, Pakistan, China and a few European countries. A subset of 158 of the most resistant or susceptible accessions was genotyped with 84 SSR (AAFC) and 6000 SNP markers (Illumina).

At this point, association analysis of the SSR data using Tassel software (adjusted for low allele frequency, population structure and kinship) have shown that many quantitative resistance loci (QRL) and susceptibility loci (QSL) were shared by accessions from South Korea, Japan and some lines from China, while different loci were present in European lines. More accurate mapping was carried out in bi-parental, doubled haploid populations derived from a Chinese variety ZY821 and two Pakistani accessions, PAK54 and PAK93. Individual SNP/SSR linkage maps were generated with Joinmap, and QTL Cartographer was used for QRL/QSL analysis. Assuming homologue regions harbour similar defence genes (Parkin et al. 1995), seven significant QRL were mapped in ZY821 on linkage groups A1a/C3, A1b/A3, A6a/A7b, A7a/C6, A5, A6b and C9 (Buchwaldt et al. 2011). Four QRL were mapped in PAK54 on A3 and C6 (similar to QRL in ZY821), A4 and A10. Four QRL were also mapped in PAK93 on A5 and C6 (similar to ZY821 or PAK54), C2 and C7. However, QSL were different in each DH population.

Identification of candidate defense genes underlying QRL is underway. A gene-specific marker developed for O-methyl transferase (OMT) was mapped to the QRL on A7a/C6, and was upregulated in ZY821 in response to sclerotinia infection (Zhao et al. 2006). The OMT methylates precursors of indol glucosinolates. Several lectin-encoding genes were also upregulated and tentatively mapped to QRL on A1b/A3 and A7a/C6 using alignment with the *B. rapa* genome sequence (http://brassicadb.org). These lectins could be involved in pathogen recognition. The long term objective is to determine the least number of QRL needed for transfer of adequate sclerotinia resistance to canola-quality varieties from a few selected *B. napus* accessions.