Wheat leaf rust EST sampling from all life cycle stages

Guus Bakkeren[1], Guanggan Hu[1], Junhuan Xu[1], Rob Linning[1], Yehoshua Anikster[2], Tamar Eilam[2], Brent McCallum[3], Travis Banks[3], John Fellers[4], Li Huang[4], Sarah Munro[5], Michael Mayo[5], Brian Wynhoven[5], Johar Ali[5], Richard Moore[5], Yaron Butterfield[5], Jerry Liu[5], Robert Kirkpatrick[5], Jeff Stott[5], George Yang[5], Duane Smailus[5], Steven Jones[5], Marco Marra[5], Jacqueline Schein[5]
[1]Agriculture & Agri-Food Canada, Pacific Agri-Food Research Centre, Summerland, BC, V0H 1Z0, Canada; [2] Tel Aviv University, Israel; [3] Agriculture & Agri-Food Canada, Cereal Research Centre, Winnipeg, MB, R3T 2M9; [4] USDA-Manhattan, KS; [5] Michael Smith Genome Sciences Centre, Vancouver, BC, V5Z 4S6, Canada. bakkereng@agr.gc.ca
BakkerenG@AGR.GC.CA

We are in the process of increasing genomic resources for the obligate wheat pathogen, the leaf rust fungus *P. triticina*. Approximately 17,000 EST reads covering a teliospore stage from senescent wheat and pycnio- and aeciospore stages from an alternate host infection on *Thalictrum speciosissimum* (meadow rue), were added to our previously established, 30,000 reads-large EST database (holding ESTs from urediniospore, appressorium and other wheat infection stages). An additional 8,000 reads were generated from an isolated haustoria-specific cDNA library constructed by the Fellers' lab. The new spore stages contributed approximately 65%, 80% and 45% new unigenes to the existing database, respectively. From initial analyses it appears that aeciospores might express gene complements more similar to the urediniospore stages from wheat we sampled previously; this might illustrate the possible resemblance of function of these spores, i.e., infecting wheat. The pycniospores stage, which represents the sexual stage, displayed the largest pool of new genes. Other trends, comparisons and tools will be presented.