

***Puccinia graminis* f.sp. *tritici* genome project**

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Puccinia graminis f. sp. *tritici* (Pgt) genome sequencing project is a collaborative endeavor with Christina Cuomo, Broad Institute, MIT and Harvard, Ralph Dean, CIFR, NCSU and Jacquie Schein, Genome Sciences Centre, BC Cancer Agency. NSF funds the Pgt genome project through the NSF/USDA Microbial Genome Sequencing program. A whole genome shotgun sequence of approximately 12X coverage was generated by paired-end sequencing of two plasmid libraries (4kb and 10kb) and a 42kb fosmid library. The current draft sequence assembly contains 392 supercontigs with an estimated genome size of 89 Mb and coverage of 7X. Additionally, a restriction fingerprint map was generated using *PstI/EcoRI* double digest of 22,000 fosmid clones. The assembled fingerprint map contains 1969 contigs with an estimated genome size of 94 Mb and 11X genome coverage. The current draft sequence assembly and fingerprint map are highly similar. Approximately 60,000 EST reads have been generated from three cDNA libraries generated from urediniospores, germinated urediniospores and teliospores. Preliminary analysis of the EST data indicates that only twenty percent of the unique gene set could be annotated (gene ontology categories) and thirteen percent was shared between the three-cDNA libraries.