Soyagen: Improving Yield and Disease Resistance in Short-Season Soybeans

Several advancements were made in the area of soybean genomics. Two examples include the development of the first soybean haplotype map, which serves as a worldwide resource for plant breeders, and a precise PCR test for Phytophthora root rot and soybean cyst nematode diagnostics.

THREE IMPORTANT CHALLENGES exist when developing high-yielding soybean varieties suited to Canadian conditions:

1. varieties must mature and produce seed in record time,
2. they need to be resistant to pests and diseases and
3. impediments to further adoption of soybeans across western Canada must be identified and addressed.

Genomics, or exploration of the genetic code of soybeans, allows us to identify DNA markers that control aspects of plant growth like maturity and resistance to pests. Breeders can then use these markers to improve varieties rapidly and easily. A team of scientists from six research institutions across Canada was assembled to investigate soybean genomics, economics, and social impacts to maximize soybean industry growth.

This study involved five main activities:

1. development of cost-effective, high-throughput genotyping tools,
2. improved selection tools to achieve high yields of short-season soybeans,
3. improved diagnostics for the presence and type of Phytophthora root rot (PRR) and soybean cyst nematode (SCN),
4. improved selection tools for varietal resistance to PRR and Sclerotinia and
5. identification of needs to maximize the innovation potential of the soybean industry.

Technological advancements made in Activity 1 will assist breeders with choosing the most promising soybean lines to cross together, alleviating costs and challenges. For example, the first haplotype map for soybeans was constructed using whole-genome sequence data, now serving as a worldwide resource for applied genomics and breeding.

In Activity 2, two tools were developed to help breeders improve varieties and assess traits that cannot be distinguished visually:

1. DNA markers that provide immediate, relevant information on key genes controlling maturity and
2. a statistical model that accurately predicts how complex traits (e.g., yield) of a soybean line will perform in the field based on a plant's genetic makeup.

In Activity 3, the genetic makeup of various PRR pathotypes and SCN was characterized and enabled development of PCR tests to identify the presence of PRR and SCN. This precise diagnostic tool will help stakeholders reduce yield loss from these pathogens.
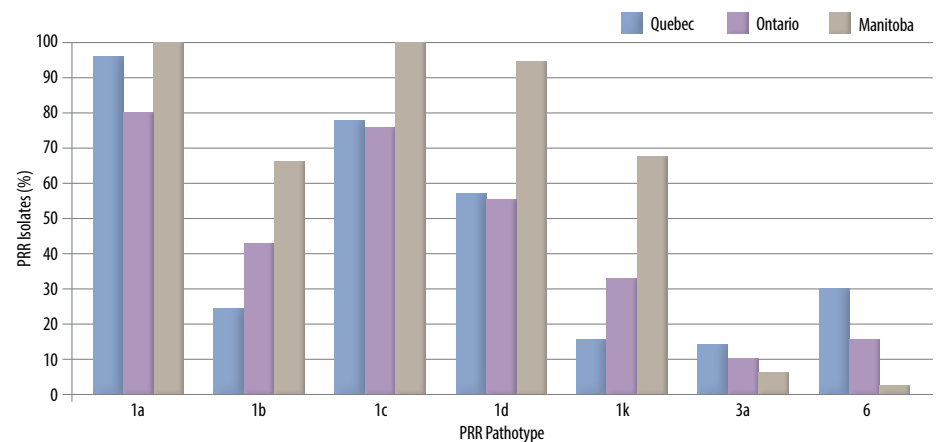
The PCR test from Activity 3 was used to evaluate the presence and distribution of PRR pathotypes in Activity 4 from samples collected across Canada (Figure 1). This characterization serves as a reference tool for breeders to track the evolution and status of PRR.

In Activity 5, farmers, extension specialists and agronomists identified soybean production knowledge gaps and barriers to adoption. Containerized transportation systems, processor demands on quality and grower investments in plant breeding were also assessed. Results have shown, for example, that the availability of higher-yielding, short-season soybean varieties could increase adoption across western Canada and that protein and oil contribute equally to the value of the soybean crop.

Economic benefits of this research have the potential to reach $278 million annually, based on soybean yield potential increases, improved resistance against diseases and other pests, and reduction in pesticide use. ◗

Figure 1. Percentage of Phytophthora root rot (PRR) isolates carrying a given pathotype from 295 isolates sampled from QC, ON and MB fields (2018–2019).