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Plant Disease Resistance

There is always the possibility that a new plant disease will seriously threaten World food security. Morten Lillemo, a researcher at CIGENE in Ås, is looking for genes to combat diseases in bread wheat, using the newest SNP technologies

In the past, diseases have had devastating effects on food supply. Well-known examples are potato blight caused by *Phytophthora infestans* which led to the Irish Potato Famine in 1845–1852 and wheat rust caused by species of *Puccinia* which reduced wheat yields in North America during the 1950s by as much as 40%. As a matter of fact, dramatic outbreaks of wheat rust caused by new strains of *Puccinia* were reported as recently as 1998 in Uganda and in 2013 in Ethiopia where yield losses as high as 70% were seen [1]. In Norway, *Puccinia*-caused gold rust was an important wheat disease during summer 2015.

Disease research on wheat at CIGENE has been focused on important diseases in Norway such as powdery mildew [2], leaf blotch [3] and Fusarium head blight. As Morten Lillemo says, “For many years, our approach was to run genome screens, using about 550



DNA markers spread across bread wheat’s 17 Gbp genome [4] to locate quantitative trait loci (QTL) affecting disease resistance. This strategy corresponded to about one marker per every 30 Mbp of sequence, so it wasn’t very precise, even though we managed to identify some interesting QTLs.”

In 2014, an international team consisting of more than 40 scientists (including Morten Lillemo) published a report [5], describing about 90,000 single nucleotide polymorphisms (SNPs) in bread wheat and related species. The SNPs were identified based on large-scale RNA sequencing (approx. 140 gigabases) of 38 wheat varieties followed by analyses using an SNP discovery program. Approximately 47,000 SNPs were subsequently mapped to the draft wheat genome with over 41,000 SNPs assigned to single locations on the genome.

CIGENE screens wheat, using 90,000 SNP chips from either Illumina or Affymetrix, to conduct association mapping of Norwegian wheat for disease resistance markers. About 22,000 SNPs turn out to be useful for mapping, corresponding to about 1000 SNPs per chromosome. At this early stage of technology use at CIGENE, approximately 4000 samples are analyzed per year.

References

1. National Intelligence Council (USA) 2012.
2. Lu Q et al.: Theor Appl Genet 125 (2012) 297.
3. Lillemo M et al.: Theor Appl Genet 126 (2013) 711.
4. International Wheat Genome Sequencing Consortium: Science 343 (2014) 1251788.
5. Wang S et al.: Plant Biotechnol J 12 (2014) 787.

Lillemo pointed out that major QTLs for fungus diseases (so-called Resistance Genes) were identified several years ago in bread wheat and other plants. Biochemically, it was shown that they code for receptor kinases that respond to signals displayed by the pathogen, thereby activating a resistance response in the plant. Unfortunately, this type of

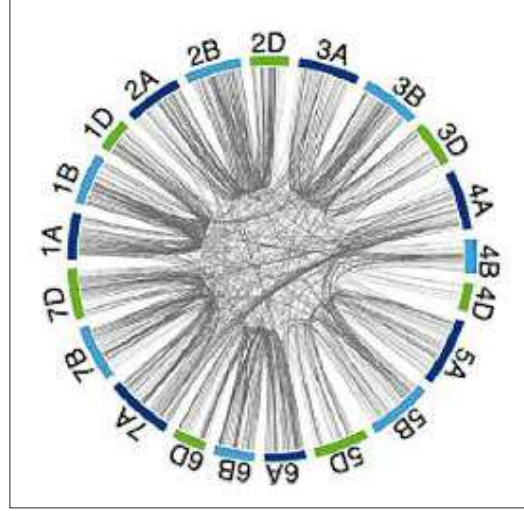


Figure 1. Distribution of SNPs identified in bread wheat that occur twice in the genome. Chromosomes for the A, B and D genomes are designated as 1A, 1B, 1D, 2A, 2B, 2D etc. This Figure is from an Open Access article [5] under the terms of the Creative Commons Attribution License.