



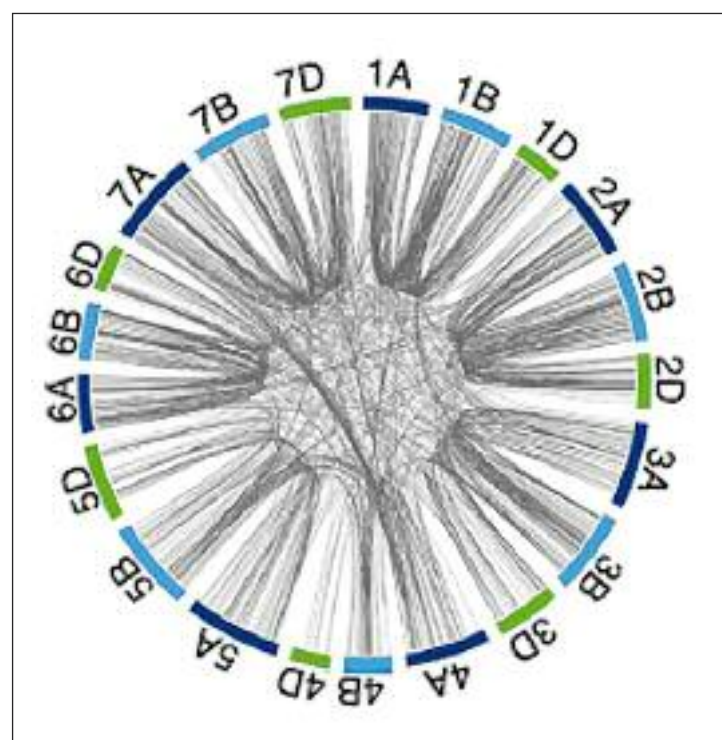
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# Plant Disease Resistance

*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



**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.



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.

Finding single location SNPs in bread wheat was a challenge, given the fact that bread wheat is a hexaploid species generated, starting about 800,000 years ago, when hybridization of two related species produced a tetraploid species which was the precursor of durum wheat used for pasta today. A subsequent

species hybridization, occurring about 400,000 years ago, produced hexaploid bread wheat. Individual subgenomes in hexaploid bread wheat (AABBDD) are designated as A, B and D with each subgenome containing about 5.5 Gbp divided among 7 chromosomes. Reflecting ancestral similarities between the subgenomes, Fig. 1 shows the distribution of the 2508 individual SNPs that were found to occur twice in 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.

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

resistance has to be considered as unstable since a single mutation in the fungus that alters the "signal", making it unrecognizable by the receptor kinase, can nullify the Resistance Gene's effect. As Morten Lillemo says, "We are focused on trying to identify several "partial" resistance genes for a given disease because this is a more sustainable strategy for disease resistance."

Asked to comment on the prospects of this type of research, Morten Lillemo said that CIGENE is a participant in an international effort to develop this technology as a practical tool for plant breeding. "So, breeders want markers while we are also interested in identifying biochemical mechanisms in plant disease resistance."

## References

1. National Intelligence Council (USA) 2012. ([www.dni.gov/nic/globaltrends](http://www.dni.gov/nic/globaltrends))
2. Lu Q et al.: Theor Appl Genet 125 (2012) 297.
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