ant Disease sistance ROHTUA **THORI SHOR**AND SEA HONTENSKAP, SÅ SKARSPATTENSVAND ON WOMEN STATENSVAND ON

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

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

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

2D 4B 4D 09 Q5 89 **A**9

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 Figure 1. Distribution of SNPs identified in bread wheat that the Creative Commons Attribution License.

wheat (AABBDD) are designated as tribution of the 2508 individual SNPs species hybridization, occurring about 400,000 years ago, produced hexaploid bread wheat. Individual subgenomes in hexaploid bread 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 disthat were found to occur twice in the

every 30 Mbp of sequence, so it

managed to identify some inter-

esting QTLs."

disease resistance. This strategy cor-

ONA markers spread across bread

wheat's 17 Gbp genome [4] to locate quantitative trait loci (QTL) affecting responded to about one marker per wasn't very precise, even though we

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

activating a resistance response in the plant. Unfortunately, this type of displayed by the pathogen, thereby 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

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

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

> wheat and related species. The SNPs were identified based on large-scale gigabases) of 38 wheat varieties followed by analyses using an SNP

RNA sequencing (approx.

polymorphisms (SNPs) in bread

genome.

Lillemo)

Morten

(including

nucleotide

about 90,000 single

consisting of more than 40 scientists published a report [5], describing

In 2014, an international team

References

. National Intelligence Council (USA) 2012.

with over 41,000 SNPs assigned to

single locations on the genome.

mapped to the draft wheat genome

discovery program. Approximately 47,000 SNPs were subsequently 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

- 2. Lu Q et al.: Theor Appl Genet 125 (www.dni.gov/nic/globaltrends) (2012) 297.
 - International Wheat Genome 3. Lillemo M et al.: Theor Appl Genet 126 (2013) 711.
- Sequencing Consortium: Science 5. Wang S et al.: Plant Biotechnol 1 343 (2014) 1251788.

produced a tetraploid species which was the precursor of durum wheat used for pasta today. A subsequent



