

# Genome Power for Rye



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## Background

In Finland, rye ranks sixth in area under cultivation; 2015 was the first time Finland was self-sufficient for rye in 15 years, due to an unusually good yield. Winter rye breeding has had difficult tasks to prevent pre-harvest sprouting in ears to get a good quality yield and decrease lodging. Effective plant breeding is based on knowing the genes as well as their function, variation, and distribution in natural and breeding populations. Sequencing of the genome thereby provides a basis for accelerating breeding.

## Rye genetic studies in Finland

A decade ago, we constructed the first genetic linkage map of rye using doubled haploid genomes of the male gametes (Figure 1.); it contained 281 markers (Figure 2.). We found DNA markers linked to a major QTL (quantitative trait loci) affecting alpha-amylase activity (Figure 3.), which can be used for marker-assisted selection for pre-harvesting sprouting resistance in rye breeding. In addition, markers for the short-straw growth habit were found.

## International Rye Genome Sequencing Consortium

An International Rye Genome Consortium, led by Nils Stein (IPK, Gatersleben, D) with 18 partner institutions, including Luke, in nine countries has been established to produce a sequence of the whole rye genome (7.9 Gbp). Sequencing will be carried out by NRGene using advanced methods. We expect to have sequencing completed by the end of the summer 2017, with publication in 2018. The sequencing of the rye genome enables searches for genes affecting human health (Figure 4.), which, through breeding, can improve rye and expand markets for rye products.



Figure 1. Hand-crossed rye doubled haploids by Teija Tenhola-Roininen

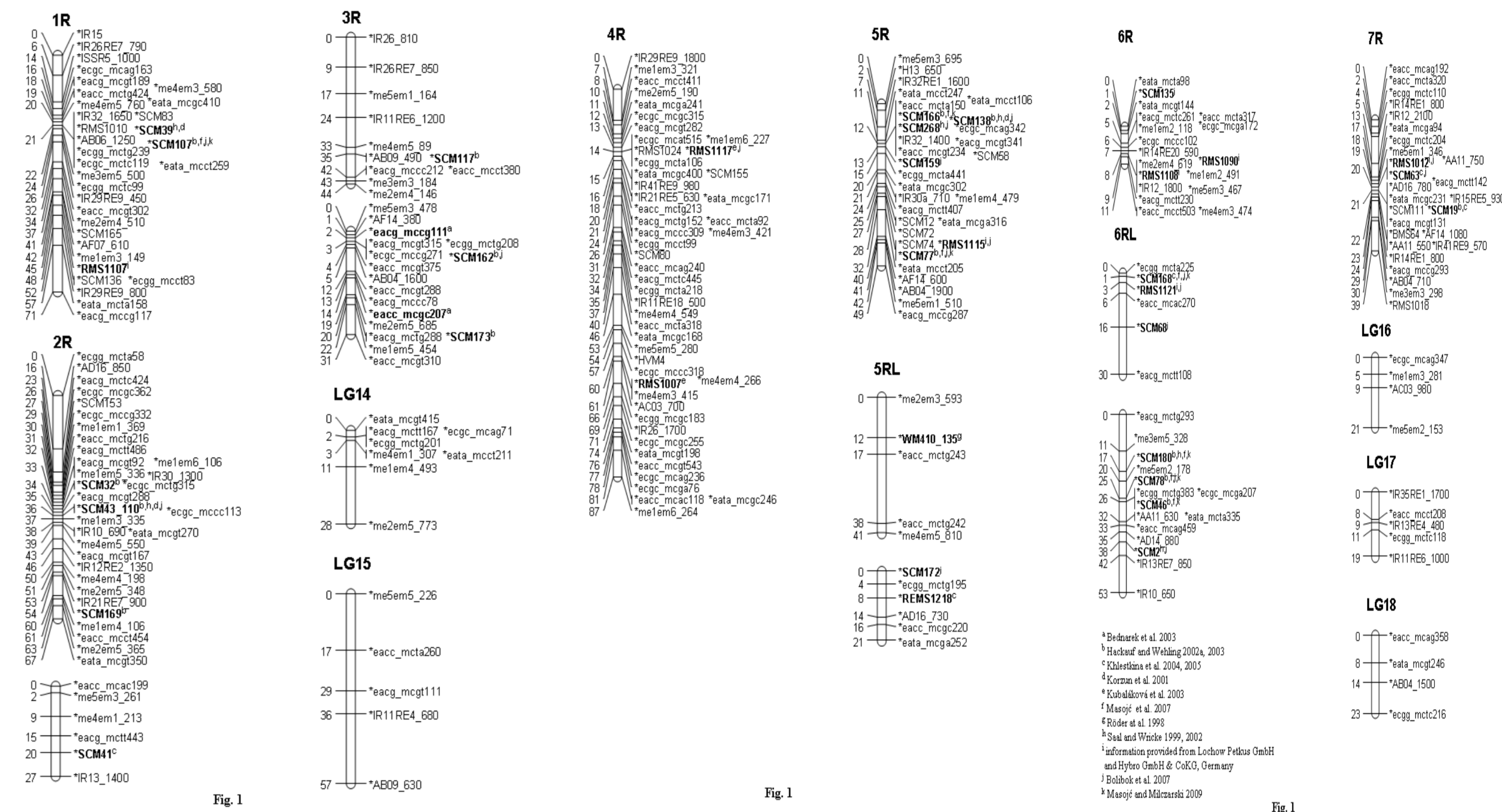


Figure 2. A genetic map of rye using doubled haploids

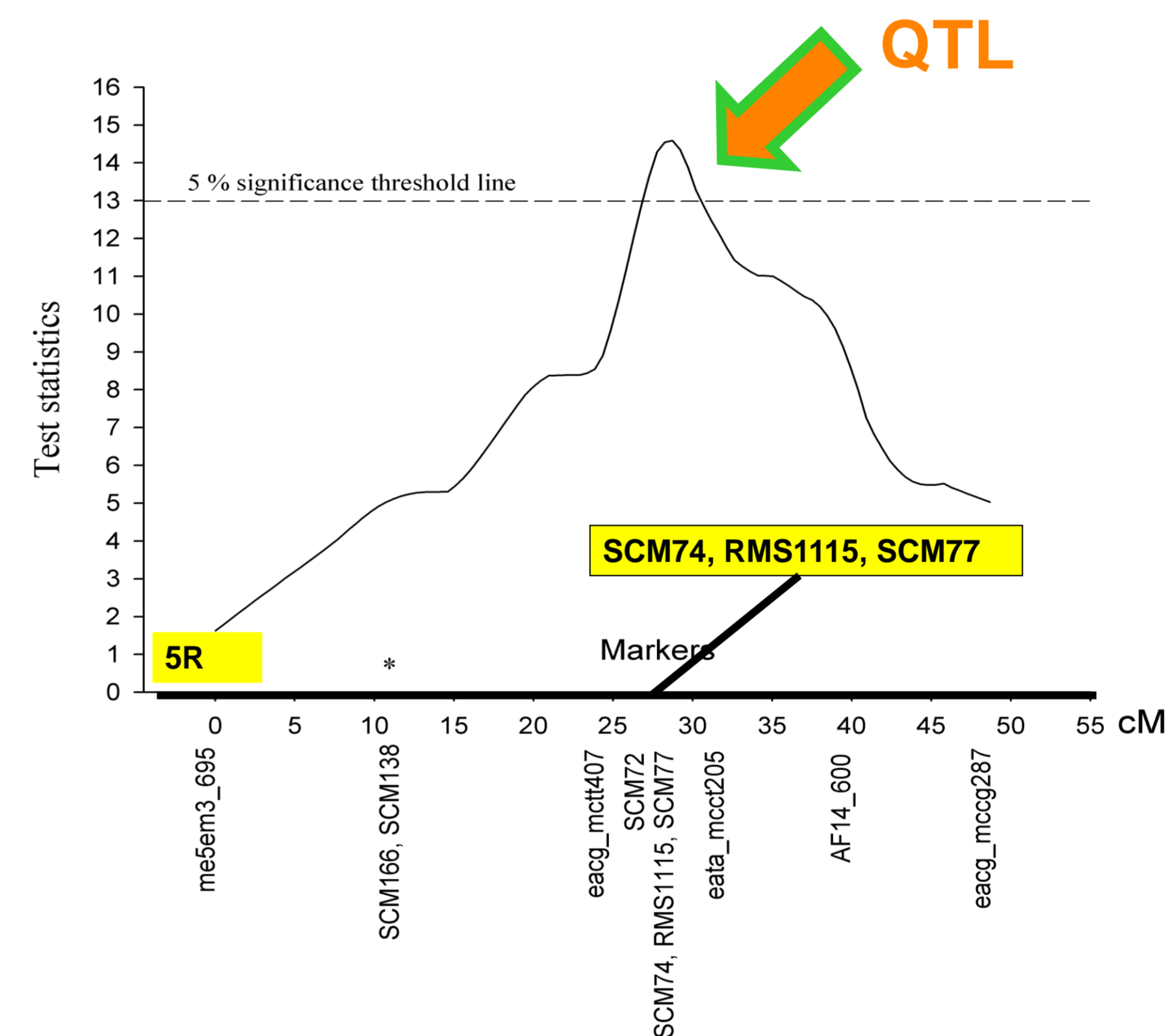


Figure 3. One major QTL affecting alpha-amylase activity was found on chromosome 5R. Centromere is indicated with an asterisk.

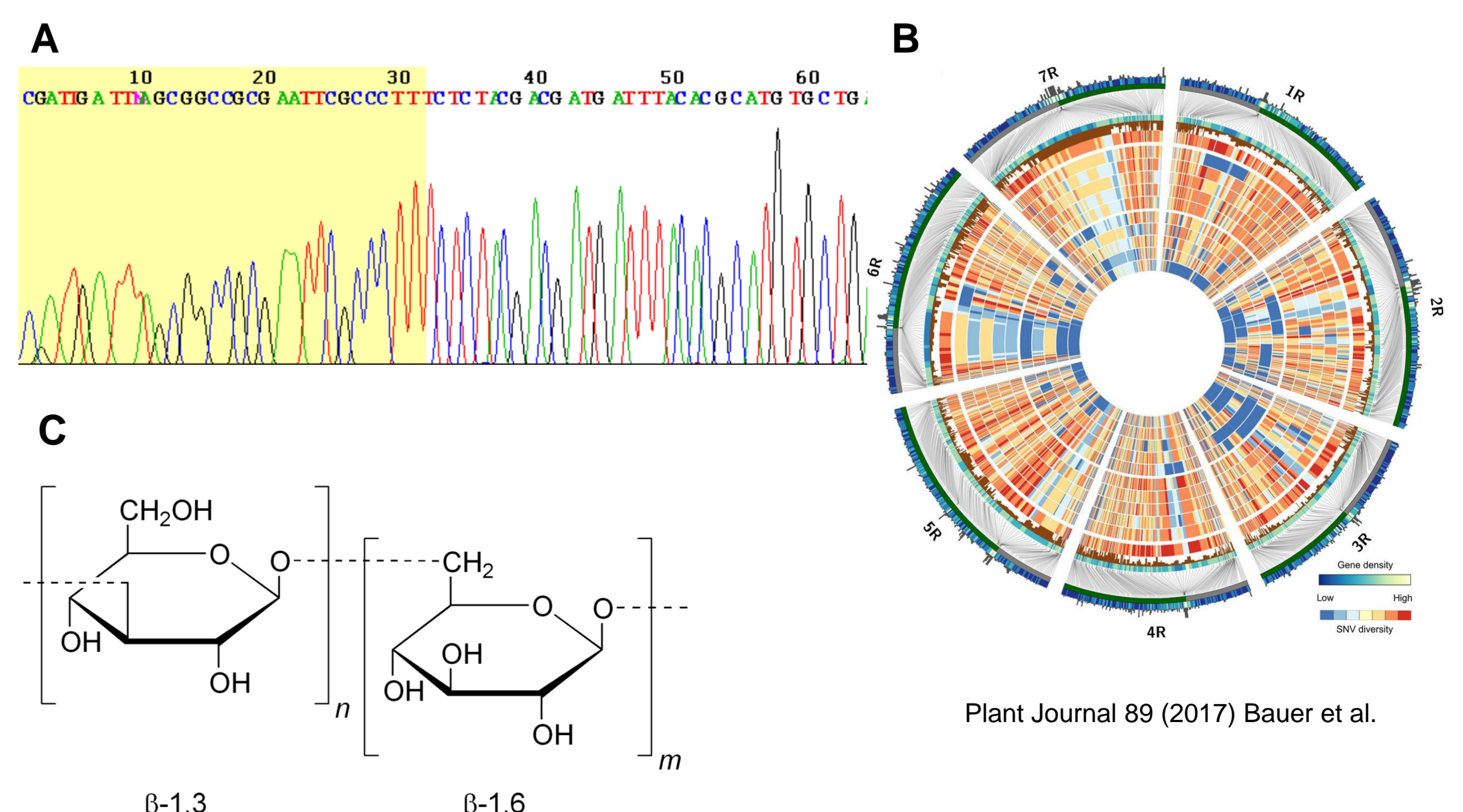


Figure 4. How to use the rye genome for searching 'health-affecting' genes? **A.** By producing a sequence of the whole rye genome. **B.** Finding the genes of the whole genome. The partly sequenced rye genome by Bauer et al. 2017. **C.** Exploring traits affecting human health. *E. g.* Finding genes affecting beta-glucan content in rye and improving their effects by genetic modification (e.g. CRISPR-Cas9 method).