

Mapping of QTLs for tuber glycoalkaloid content in two reciprocal *Solanum* spp. populations

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Problem and Aim

Wild *Solanum* species are attractive for breeding purposes, but due to linkage drag, there is a potential risk of introducing high levels of glycoalkaloids in breeding lines. A method, which can select against high glycoalkaloid levels at an early stage will therefore be a help to speed up the breeding process. This may be possible by the identification of QTLs (quantitative trait loci) for tuber glycoalkaloid content, development of DNA markers closely linked to these and marker assisted selection.

The aim of this study was to identify QTLs for total glycoalkaloid (TGA) content in potato tubers from a cross between *S. tuberosum* and the wild species *S. sparsipilum*.

Materials and Methods

- Mapping population: Dihaploid BC₁, named HCDHDN. HCD originates from a cross between HAF (*S. tuberosum*₁) and HAG (*S. tuberosum*₂ x *S. sparsipilum*). HDN is its reciprocal cross
- Field trials: Two localities in Denmark, Gadbjerg and Vandel, 2004
- Analysis of TGA content: α -solanine and α -chaconine, high performance liquid chromatography (mg/kg fresh weight was transformed to mg/cm²)
- QTL mapping of TGA, the HAG parent: MapQTL® 4.0 (Van Ooijen et al. 2002)
- Graphic representation of the QTLs: MapChart (Voorrips 2002)

Results

The progenies of the HCDHDN population segregated into two distinct groups of high and low TGA content with means close to the values of each of the parents (Figure 1). This indicates that a part of the genetic variation is due to the presence of a major locus.

Four putative QTLs for high tuber TGA content were identified (Figure 2). Major QTLs were detected on chromosomes I and IX and minor QTLs were located to chromosome II and to an unassigned linkage group. The QTL on chromosome I had a high LOD score and variance explanation (Table 1) and this may be responsible for the bipartite distribution.

The trials are repeated in 2005 with a larger mapping population. This together with the mapping of the other parent (HAF) may increase the number of QTLs.

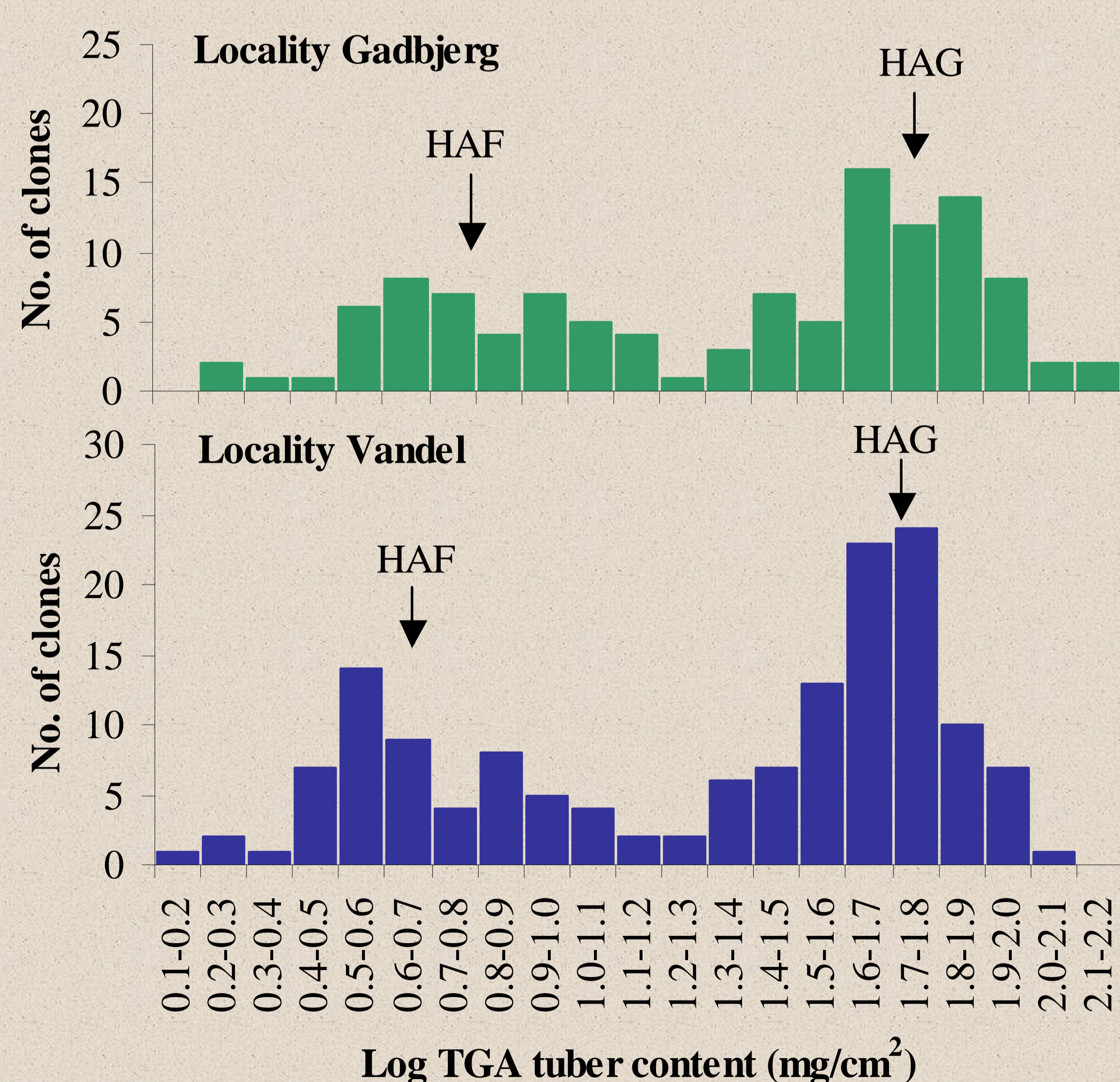


Figure 1. Frequency distributions of the logarithm of the tuber TGA content in the HCDHDN population. The TGA contents of the parents are indicated.

Acknowledgements

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Table 1. Location and effect of putative QTLs for tuber TGA content identified in the HAG parent.

Trial locality	Chromosome	Nearest marker	LOD [†] score	P < [‡]	Variance explanation (%)
Vandel	I	HC21	10.8	0.001 ^G	17.8
Gadbjerg			9.7	0.001 ^G	13.9
Vandel	II	EG35	4.5	0.001 ^{Ch}	4.6
Gadbjerg			2.6	0.004 ^{Ch}	3.7
Vandel	IX	Pt1	7.0	0.028 ^{Ch}	60.9
Gadbjerg			6.0	0.031 ^{Ch}	46.3
Vandel	Unassigned	EC40	5.5	0.001 ^{Ch}	5.4
Gadbjerg		EN8	2.4	0.006 ^{Ch}	8.9

[†] Logarithm of the odds ratio

[‡] ^G and ^{Ch} at the genome and chromosome wide LOD threshold, respectively

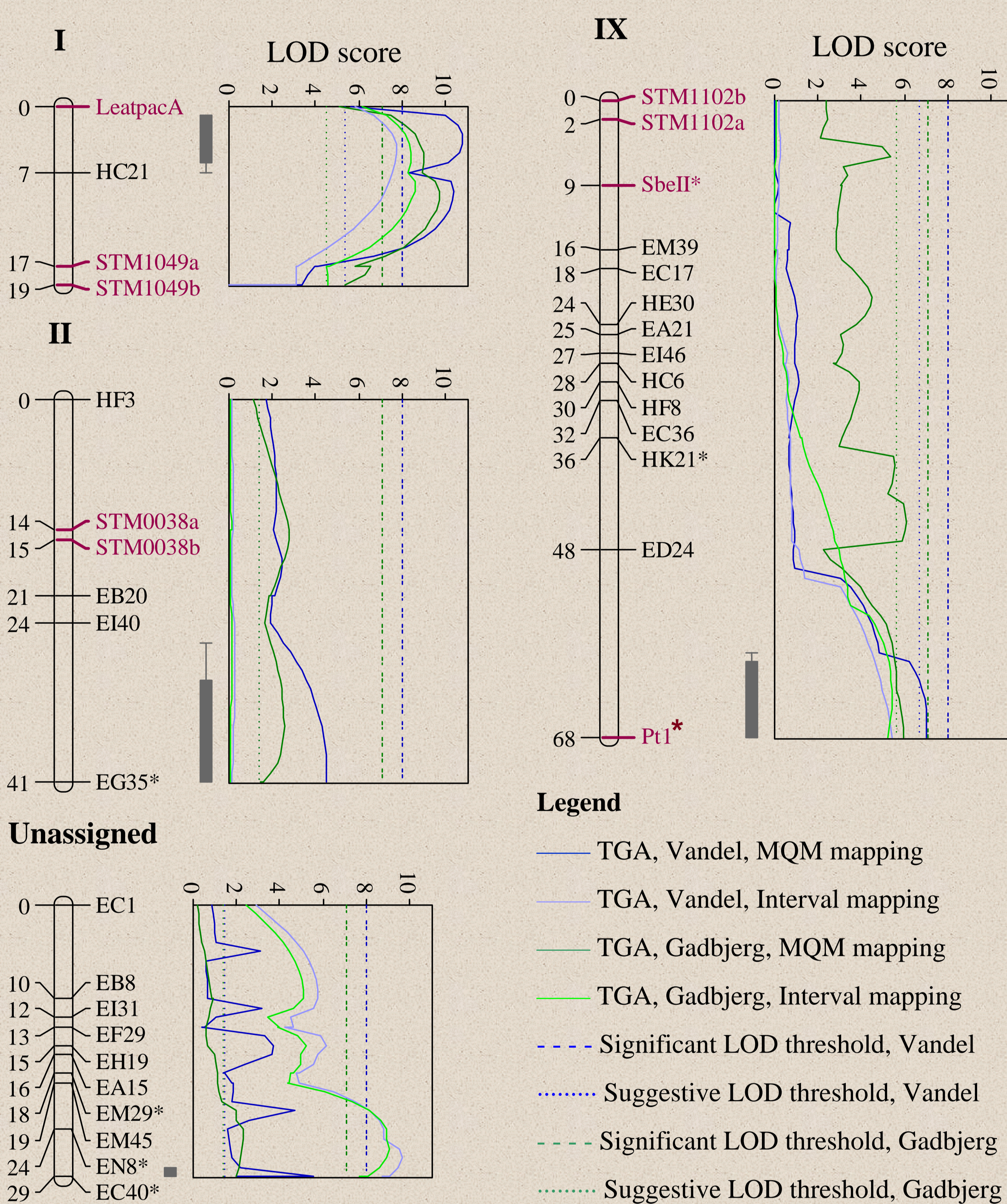


Figure 2. Likelihood maps of QTLs for tuber TGA content on chromosomes I, II, IX and one unassigned linkage group. Distances between markers are indicated in cM. The CAPS and SSR markers are indicated with **dark red** and the remaining are AFLP markers. **Grey** QTL bars represent support intervals with a LOD fall off of 1.

Conclusions

- At least four QTLs for TGA content are present in the HAG parent of the HCDHDN population
- The putative QTLs were located to chromosomes I, II, IX and an unassigned linkage group
- Major and minor QTLs seem to control tuber TGA content in the investigated population

References

- Van Ooijen JW, Boer MP, Jansen RC & Maliepaard C (2002) *MapQTL® 4.0, Software for the calculation of QTL positions on genetic maps*. Plant Research International, Wageningen, the Netherlands.
- Voorrips RE (2002) MapChart: Software for the graphical presentation of linkage maps and QTLs. *J Heredity* 93: 77-78.