Mapping of net blotch resistance locus in barley line c-8755

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Introduction

Net blotch of barley (*Hordeum vulgare* L.), caused by the fungal phytopathogen *Pyrenophora teres* Drechs. f. *teres* Smedeg., constitutes one of the most serious constraints to barley production world-wide. Several barley lines with major gene resistance to net blotch have been identified. Recently a concise set of barley genotypes for differentiating virulences in *Pyrenophora teres* f. *teres* was formulated (Afanasenko et al. 2009). Here we present results from mapping the resistance genes in one of the barley genotypes included in the differential series, namely c-8755 (Ethiopian landrace).

Materials and Methods

The doubled haploid progeny (121 plants) between Harrington (susceptible) and c-8755 (resistant) was genotyped using Barley OPA SNP markers. Linkage groups were constructed using JoinMap® (Van Ooijen and Voorrips 2001) and QTL analyses were done with NQTL (version 26-Nov-2001, Tinker and Mather 1995). Barley plants were disease tested by infecting two week old seedlings at greenhouse and scoring the symptoms after ten days according to Tekauz scale (1985). The net type isolate V278 (previously Pt87, originated from Finnish cultivar Arve) was used for infection. Mean for four seedlings was used as the phenotypic value in QTL mapping. Statistical differences ($P < 0.05$) between genotypic classes were analysed by nonparametric one-way ANOVA (SAS® Enterprise Guide ® 4.3).

Results

The doubled haploid barley linkage map was composed of 604 SNP markers and extended altogether 1168 cM (Fig. 1). All of the seven chromosomes were formed and some of them were divided into two parts. The average infection responses (IR) of the resistant and susceptible parents were 3.25 and 7.50, respectively. With the net type isolate V278 a major resistance gene (LOD score 12.6) was located on chromosome 3HL (Fig. 1, 2A). The allele frequency of the closest marker (SNP 11-10821) in different IR classes is shown in Fig. 2B. The locus explained 38% of the phenotypic variation in the mean of IR scores among the progeny (Table 1). Nineteen markers were mapped in this QTL region.

Discussion

We found one major QTL affecting net blotch resistance on chromosome 3HL. Minor QTLs on 3H have been reported earlier but not many major ones (e.g. Cakir et al. 2003; Grewal et al. 2008; Manninen et al. 2006; Raman et al. 2003; Richter et al. 1998; Yun et al. 2005). According to cluster analyses of net-blotch reaction patterns in the differential series, Afanasenko et al. (2009) showed that the resistant genotype, c-8755, belongs to a different cluster than CI 9819 which has a major resistance gene on 6H (Manninen et al. 2006). This agrees with our results.

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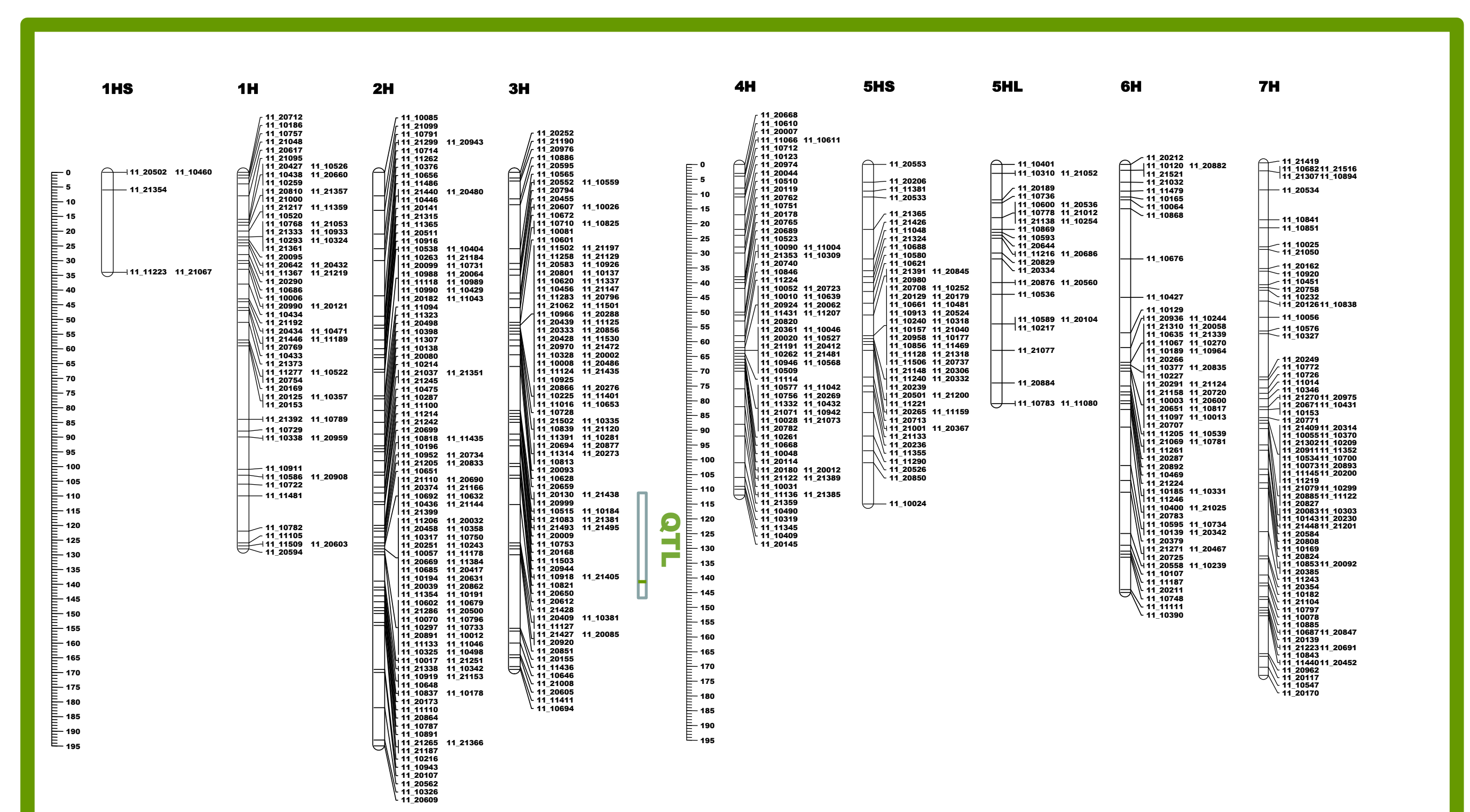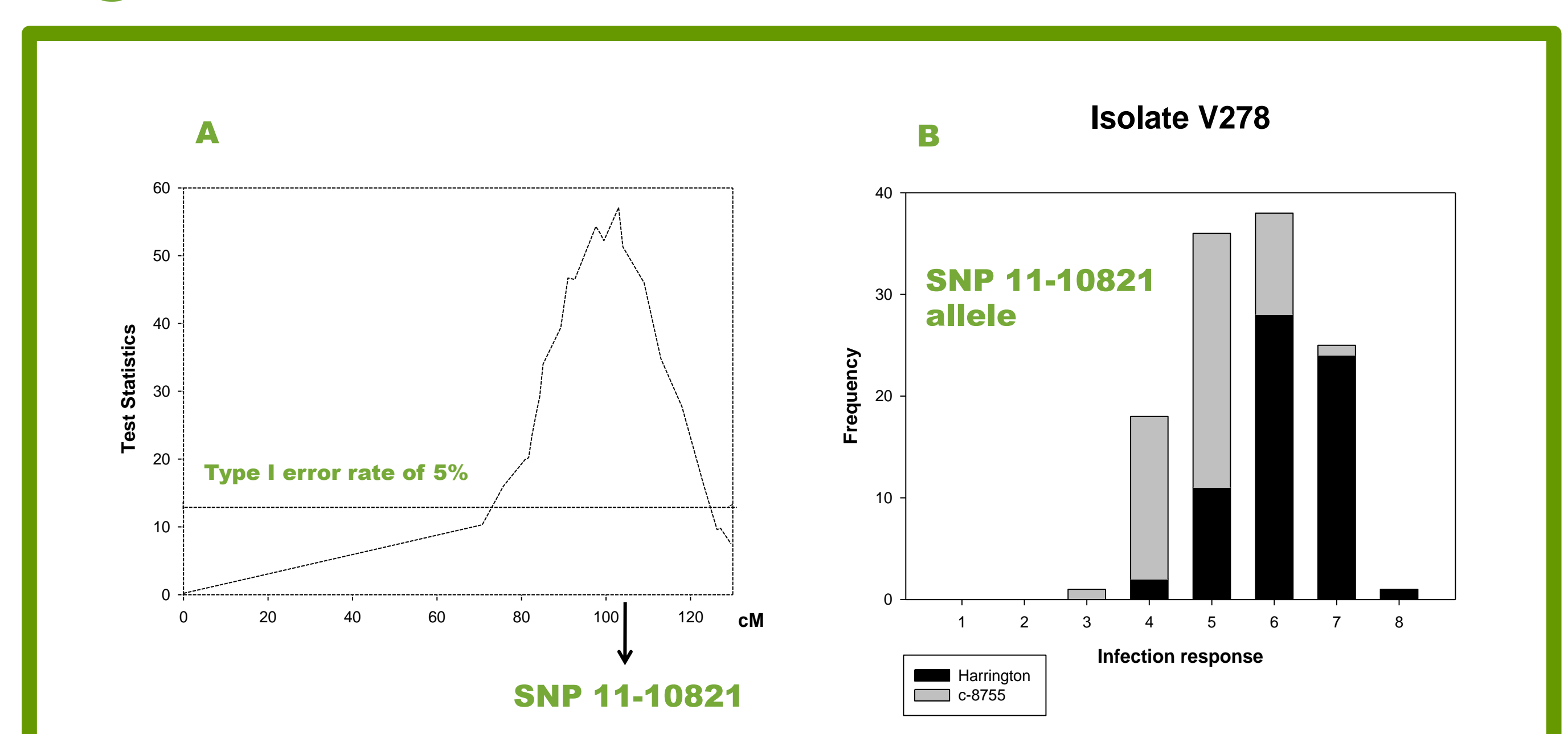
Fig. 1

Fig. 2

		Infection response			Effect of major QTL in the DH progeny			
Net type isolate	Origin	c-8755	Harrington	Parental difference	Location	Observed homozygous effect	% parental difference explained	R²
V278	Finland	3.25***	7.25***	4.0	3H	1.27	31.8	0.38

Table 1