

Chromosomal regions associated with nitrogen use efficiency and disease resistance in barley

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Introduction

Nitrogen use efficiency (NUE) is a complex trait which affects yield and is controlled by multiple genes. Due to cost and environmental effect of N fertilizer use, there is a constant need to improve NUE in crop plants. In Finland, no-tilling practice and neglecting crop rotation have enhanced the risks of seed- and stubble-borne diseases like net blotch, scald, and spot blotch. The aim of this study was to find chromosomal regions affecting NUE and disease resistance by using genome wide association mapping in barley.

Materials and Methods

Mostly European barley cultivars and landraces of Scandinavian origin were used for NUE and disease resistance studies. Barley germplasm was phenotyped (195 genotypes) in a two-year field trial (35 kg N/ ha and 70 kg N/ ha, 3 replicates) in Finland during 2011-2012. Disease resistance of seedlings was tested in greenhouse using appropriate scales: net blotch (Tekauz 1985), spot blotch (Fetch & Steffenson 1999), and scald (Jackson & Webster 1976). DNA was extracted by a small-scale CTAB method (Tinker et al. 1993) and genotyped with 1296 SNP markers (BOPA1, UCLA, USA, Close et al. 2009). Association mapping analyses were performed with the mixed linear model (Yu et al. 2006) approach with a kinship matrix (K) joined with the population structure (Q matrix for clusters) implemented by using TASSEL version 3.0 (Bradbury et al. 2007).

Results

Association studies showed several significant SNP markers associated with NUE in every chromosome of barley (Fig. 1). Especially, the SNP marker 11_20650 on chromosome 3H was significantly associated with NUE (Fig. 1 and 2). Association mapping of disease resistance revealed already known major genes/ QTLs e.g. on chromosomes 6H and 7H, for net type of net blotch (Fig. 3) and spot blotch, respectively, but also novel chromosomal regions on 2H, 3H, 5H, and 7H (Table 1).

Discussion

The SNP marker 11_20650 is located at the same chromosomal region on 3H as genes affecting semi-dwarfism (*sdw1/denso*). Selection for semi-dwarfism and higher yield may have positively affected NUE during barley breeding. SNP markers associated with NUE and disease resistance could be used in breeding to enhance introgression of and selection for the positive (higher efficiency, resistance) chromosomal regions in the breeding material.

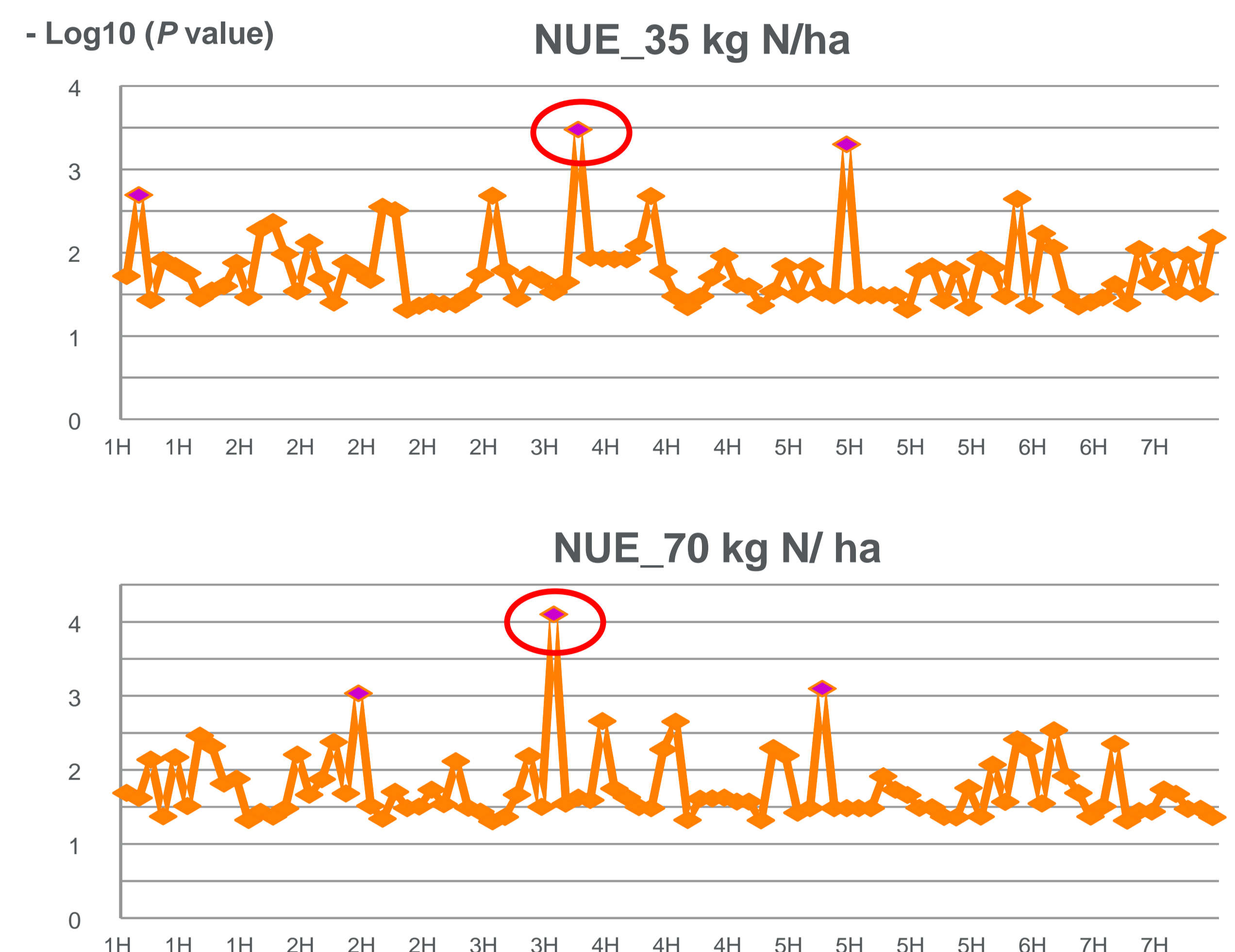


Figure 1. The most significant chromosomal regions associated with nitrogen use efficiency ($P < 0.05$).

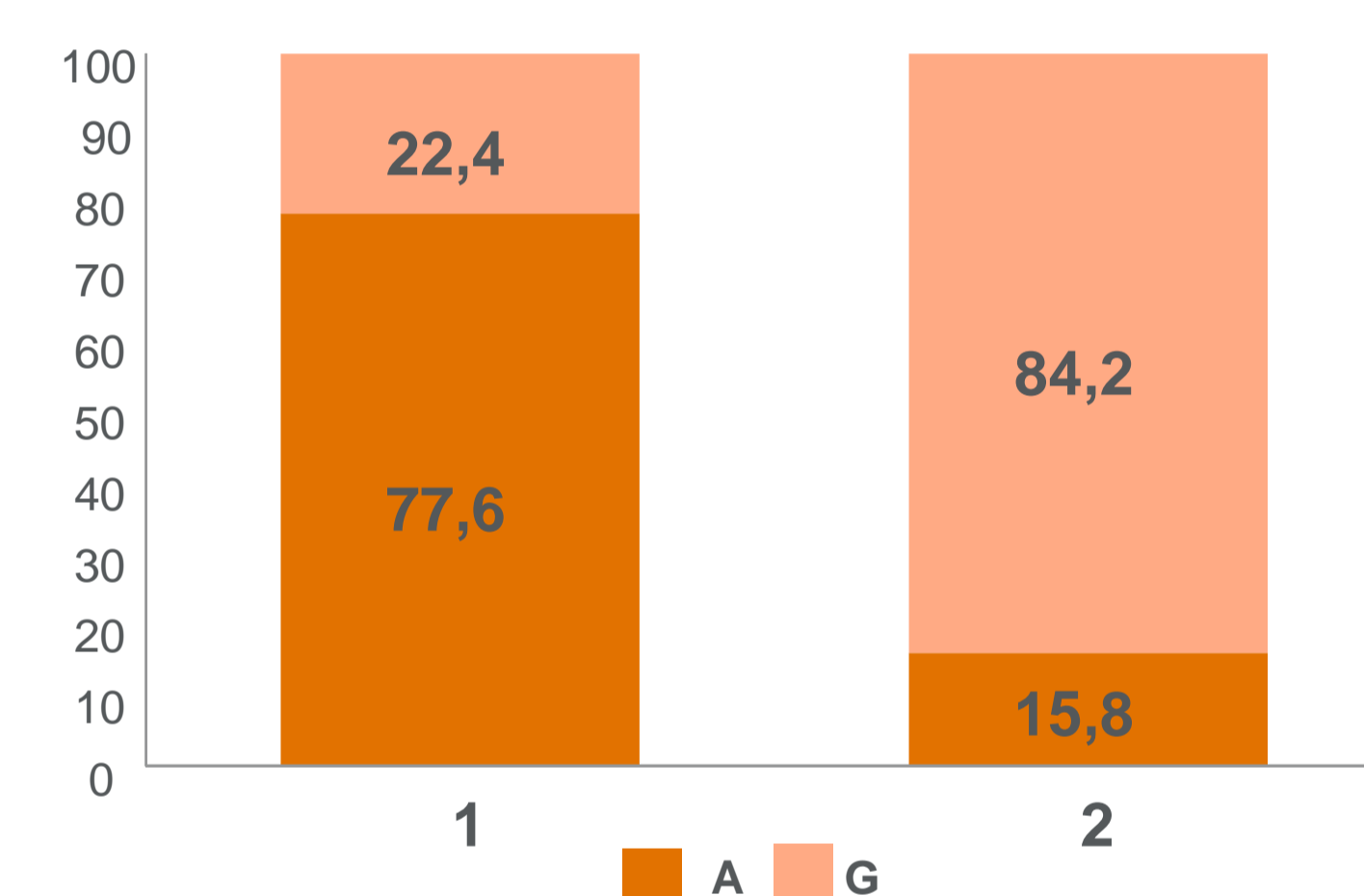


Figure 2. Allele frequencies of the SNP marker 11_20650 (A/G, %) associated with nitrogen use efficiency in old and modern cultivars (1= released before 1970 including landraces, 2= released 1970-2010), P value $5.37E-05$.

Net blotch:				Spot type			
SNP marker	Chr	cM	P value	SNP marker	Chr	cM	P value
11_10713	6H	55,94	8,38E-07	11_20650	2H	9,28	8,63E-04
11_10462	6H	44,77	1,52E-05	11_20298	5H	132,63	1,73E-03
11_20743	6H	44,77	9,63E-05	11_20239	5H	57,36	1,75E-03
Scald				Spot blotch			
11_10268	2H	70,54	1,31E-04	11_20162	7H	31,75	2,51E-04
11_10276	3H	74,78	9,78E-04	11_21267	3H	168,4	2,49E-03
11_20790	7H	55,63	1,39E-03	11_21265	2H	28,44	3,20E-03

Table 1. The most significant SNP markers associated with barley diseases and their chromosomal regions ($P < 0.05$).

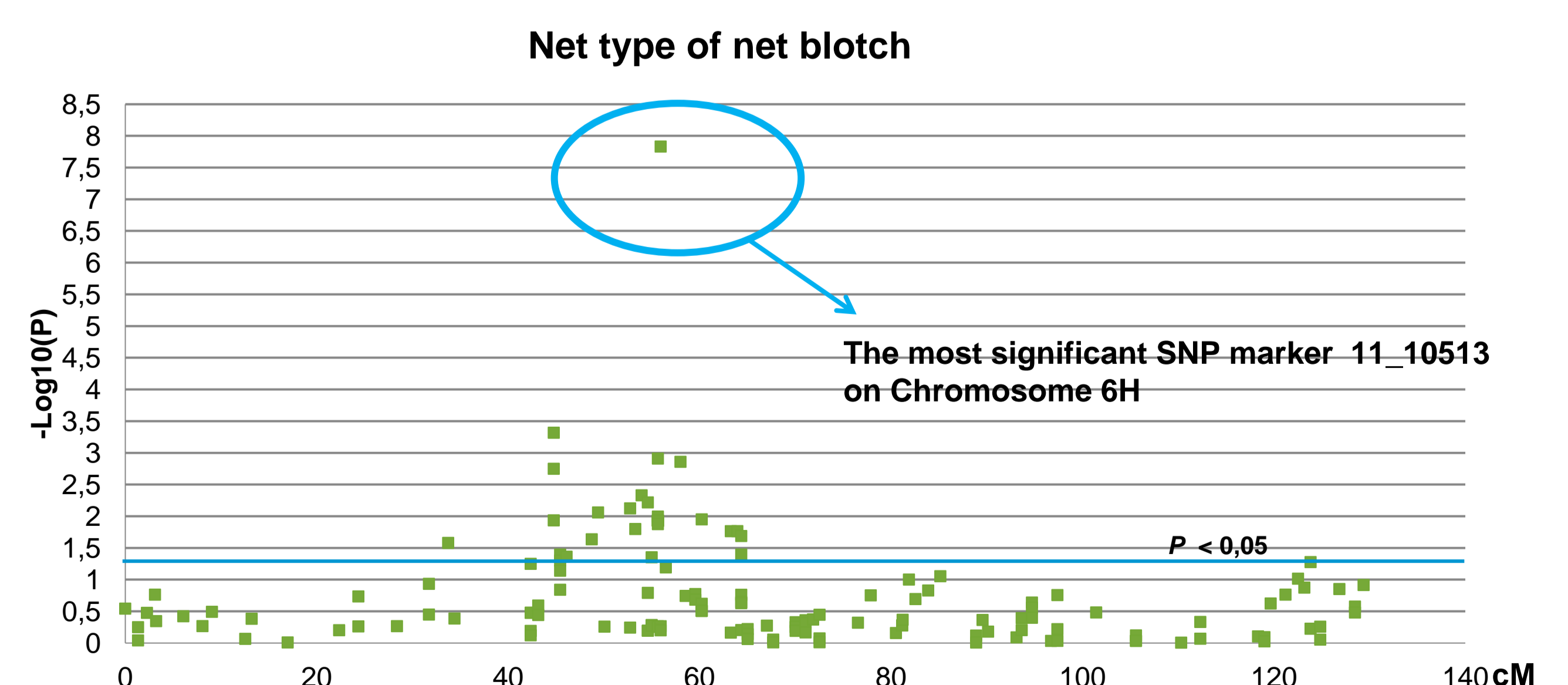


Figure 3. The location of the most significant SNP marker 11_10513 associated with net type of net blotch. A major resistance gene for net type of net blotch has earlier been located at the same region.