

The genetic characterisation of adult plant resistance to yellow rust in the winter wheat cultivar Claire

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BACKGROUND

Yellow rust (causal agent *Puccinia striiformis* f.sp.*tritici*) can reduce wheat yields by as much as 84% (Murray *et al.*, 1995). It is therefore of considerable economic importance to control this disease. Around 40 race-specific yellow rust resistance genes have been identified in wheat and deployed in wheat breeding programs (McIntosh *et al.*, 1995). Many race-specific yellow rust resistance genes have been defined by linked molecular markers. This type of resistance can however be broken down due to changes in virulence of the *P. striiformis* pathogen which overcomes the race-specific resistance genes (Table 1). The breeding strategy of relying on major genes as a source of yellow rust resistance is rapidly becoming superseded by the use of ‘durable’ resistance controlled by many loci.

Many sources of durable yellow rust resistance have been identified in wheat cultivars around the world and these have been the focus of genetic studies to identify the genes/QTLs conferring the resistance. In UK winter wheat breeding programs durable sources of yellow rust resistance from cultivars such as Cappelle Desprez and Carstens V are believed to be present within modern UK wheats. Carstens V has race-specific resistance to many European and North American yellow rust races (De Vallavielle-Pope and Line, 1990), but it is believed to contain a partial, durable adult plant resistance (APR) to yellow rust. Both Cappelle Desprez and Carstens V have been extensively used for yellow rust resistance breeding in Europe (Angus, 2001). One modern cultivar is the winter wheat Claire, which was commercially released by Nickerson Seeds UK Ltd in 1999. At the time of release it was given a NIAB rating of 9 (max. resistance) for resistance to yellow rust. In the UK it remains a good source of resistance, still with a NIAB rating of 9 on the Home Grown Cereals Authority (HGCA) 2008 Recommended List. Preliminary analysis shows yellow rust resistance in Claire to be polygenic. A doubled haploid (DH) population has been made between Claire and Lemhi. Lemhi is an American spring wheat which is susceptible to all UK *P. striiformis* isolates.

Table 1 Breakdown of race-specific resistance genes in the UK

Year of cultivar release	Cultivar	Year of resistance breakdown	Genes to which virulence developed
1993	Brigadier	1996	<i>Yr9, Yr17</i>
1987	Hornet	1988	<i>Yr2, Yr6, Yr9</i>
1983	Stetson	1983	<i>Yr1, Yr9</i>
1975	Clement	1975	<i>Yr2, Yr9</i>
1971	Talent	1972	<i>Yr7</i>
1968	Maris Ranger	1969	<i>Yr3a, Yr4a, Yr6</i>
1964	Rothwell Purdix	1966	<i>Yr1, (Yr2, Yr6)</i>
unknown	Heines VII	1955	<i>Yr2</i>

Claire x Lemhi Map

The construction of a genetic linkage map using SSR, NBS-AFLP, DArT, AFLP and EST-derived markers has allowed the estimation of the number, chromosomal position and degree of effect of yellow rust resistance QTLs within the DH population. The total linkage distance of the map is 1565cM, being composed of 54 linkage groups and covering all 21 wheat chromosomes. Six chromosomes; 1A, 1D, 3A, 5A, 5B and 6B are split between 2 linkage groups, one representing the short arm and one the long arm. Five chromosomes; 3D, 4B, 4D, 6D and 7D have one linkage group, which represents either the short or the long arm. Five chromosomes; 1B, 2D, 5D, 6A and 7B are represented by three linkage groups; four chromosomes; 2A, 2B, 4A and 7A by four linkage groups, while chromosome 3B is represented by five linkage groups. Three linkage groups could not be assigned a chromosomal location because of the absence of chromosomal-diagnostic SSR or DArT marker within these linkage groups. The average interval between each pair of mapped marker loci is 12.3cM, with an average of 10 markers per linkage group. The map consists of a total of 522 markers, 470 of which are DArT, 48 SSR and 4 of which are EST-derived STS markers.

Preliminary analysis of the Claire x Lemhi cross with phenotypic data collected over 2 years of field tests have identified a number of QTLs associated with APR to yellow rust. QTL loci have been identified on chromosomes 2BL, 2DL and 7B, the largest effect coming from 2DL. To improve the genetic map and facilitate the identification of 2 potential QTLs on 2D, wheat ESTs in the terminal deletion bin of 2DL have been targeted for SNP-marker development and added to the Claire x Lemhi genetic map. The linkage group 2Da, representing chromosome 2DL (Figure 1) had a

significant QTL peak located at the distal end of the long arm. This QTL explained 29.1% of the explained phenotypic variance and originated from the resistant parent, Claire.

Another linkage group, 2Db representing chromosome 2D has a significant QTL peak located on the long arm. This QTL explained 29.60% of the variance and also originated from the resistant parent Claire (Figure 2).

Figure 1. Yellow rust resistance QTL on linkage group on 2DL. Solid red line corresponds to the threshold LOD value.

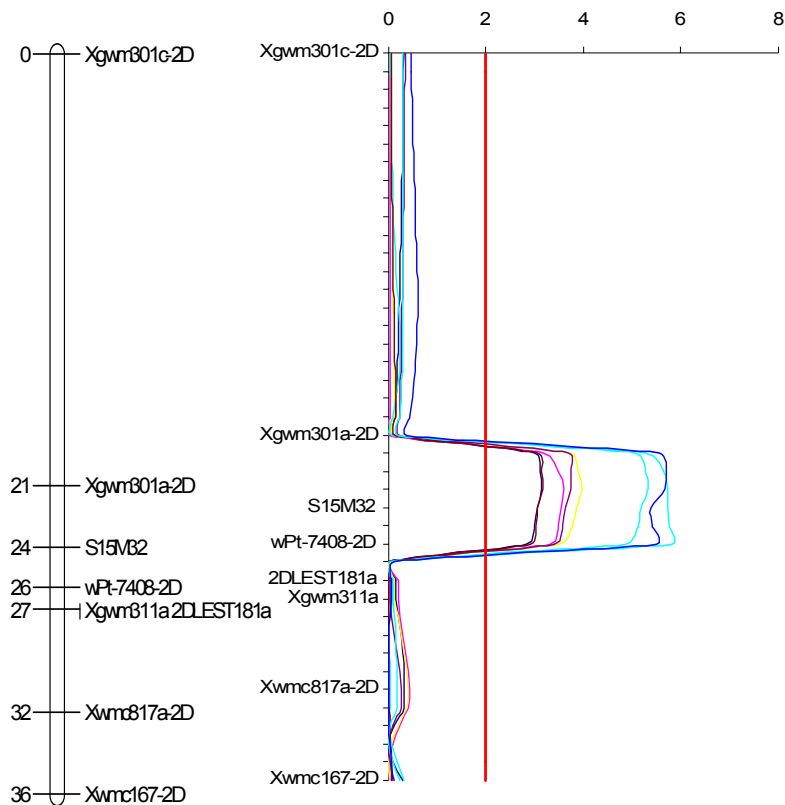
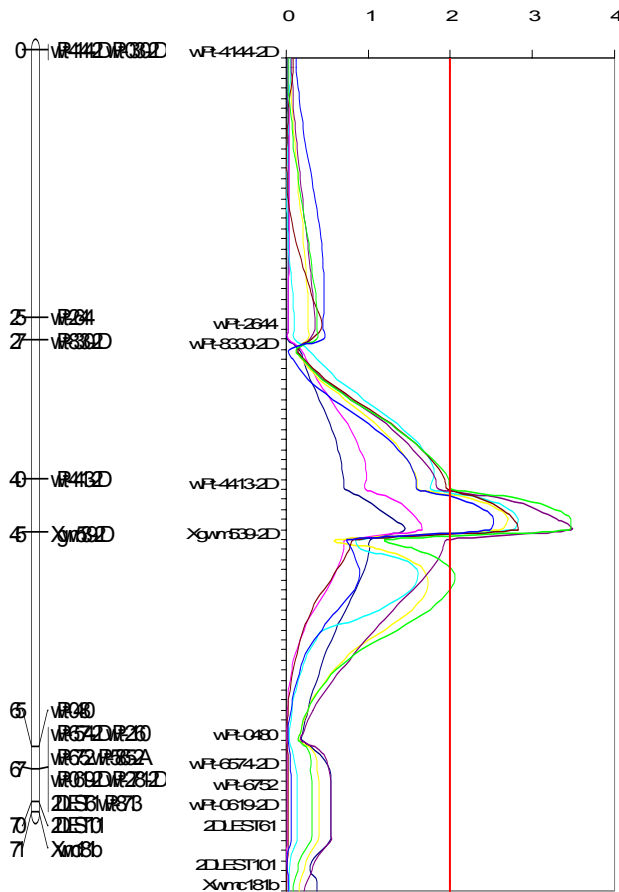


Figure 2. Yellow rust resistance QTL on linkage group on 2DL. Solid red line corresponds to the threshold LOD value.



The durable yellow rust resistance gene, *Yr16*, derived from Cappelle Desprez is reported to be 5.7cM away from *Xgwm539* (Tony Worland, personal communication). The QTL peak on 2Db also occurs at *Xgwm-539*. In addition, yellow rust resistance QTLs have been reported on 2DL within the region of *Xgwm-539* in the French cultivar Camp Remy (Mallard *et al.*, 2005). The second QTL on 2Da may be derived from an old German cultivar (Luke Jagger, personal communication).

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