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Wheat arabinoxylans: Exploiting genetic variation in amount and composition to develop enhanced varieties

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Introduction

Arabinoxylans (AX) are major components of cell walls in wheat endosperm. The water-extractable part, WE-AX, is largely involved in the response of wheat grain to different processes (bread-making, starch extraction etc), and in animal feeding. Furthermore, WE-AX are soluble dietary fibre with potential health-promoting effects in human nutrition (Fincher and Stone, 1986). AX exhibit large natural variation in their amount and structure, which are reflected in their arabinose to xylose ratio (Martinant *et al.*, 1999). Despite their high value for human health, few studies have been carried out on the genetics of WE-AX content and structure in bread wheat.

Results and discussion

Genetic and environment variation for AX amount and composition was explored in a core collection representing the world diversity of bread wheat and was found to be mostly of genetic origin (high heritability, between environment correlations >0.9). Populations of recombinant inbred lines (RILs) have been developed from crosses between lines with highly contrasted contents of WE-AX. However, the progeny distribution is far from being bimodal in shape (Fig. 1), as expected if a single major gene were segregating. Indeed, our preliminary QTL analyses failed to find major QTL. Instead we found several medium sized QTLs (h²~18%) on chromosomes 1B and 7A (Fig. 2), as previously reported in the literature (Martinant *et al.*1998; Groos *et al.*, 2004).



Fig. 1. Asymmetric continuous distribution of flour extract viscosity in a 300 RILs progeny

viscosite potentielle

Variation in AX structure can be assessed by an enzymatic fingerprinting approach (Ordaz-Ortiz *et al.*, 2005). This approach allowed us to classify French cultivars into a few discrete clusters (Fig. 3). The fingerprinting of our core collection is now in progress. QTL analysis based on canonical

components from this fingerprinting is likely to provide QTLs and markers for manipulating AX structure in wheat breeding programmes.



Fig. 2. QTL for AX viscosity found in a RIL population.



Fig. 3. Canonical analysis of enzymatic fingerprinting of AX structure for a set of French wheat cultivars

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