

Identification of candidate genes for carotenoid esterification in common wheat using physical mapping and genomic tools

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Abstract text Carotenoids are important for cereal quality. They are essential for the production of tritordeum derived products, pasta from durum wheat and yellow alkaline noodles from common wheat. Carotenoid esterification allows a higher retention through the food chain and it constitutes a metabolic sink for carotenoid accumulation.

Chromosomes 7D and 7Hch carry genes for carotenoid esterification. In this work we identified candidate genes for lutein esterification in chromosome 7D. To do this we crossed a set of deletion lines for chromosome 7D in common wheat 'Chinese Spring' (CS) (each deletion line lacking a segment of chromosome 7D) and CS-Hordeum chilense substitution line CS(7D)7Hch (chromosome 7D substituted by chromosome 7Hch). After selfing of each F₁ hybrid we developed F₂ progenies of each cross segregating for chromosomes 7D⁻ and 7Hch.

Around 300 individuals of each progeny were genotyped and used for carotenoid analyses. Our previous studies have shown that the simultaneous presence of chromosomes 7D and 7Hch increases the amount of carotenoid esters. Our current results showed that the presence of a deleted chromosome 7D and 7Hch increased the amount of lutein esters in all progenies but one, which means that genes for lutein esterification are located in the missing region of chromosome 7D.

Using DArTSeq genotyping, the Wheat Reference Genome and the Wheat Expression Browser we identified ten candidate genes annotated as related to esterification processes in this region of chromosome 7D. Furthermore, two of these genes could be related to the *Lute* locus identified in a different background.

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