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RESEARCH ARTICLE

Mapping of candidate genes involved in fatty acid synthesis in *Brassica rapa*

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SUMMARY

Oilseed crops are valuable sources of oil content and fatty acid constituents. *Brassica rapa* is a well-known oilseed and vegetable crop grown throughout the world. *B. rapa* has higher genomic similarities with model plant *A. thaliana*. The genetic regulation of fatty acid biosynthesis is well studied in *A. thaliana* as well as in *B. napus*. However, only little information on genetic regulation of fatty acid biosynthesis has been known in *B. rapa*. The objective of this work was to identify and map the genes involved in fatty acid biosynthesis process in *B. rapa* DH population (Yellow Sarson, YS-143 x Pak Choi, PC-175). 172 lines of DH68 population was used for genotyping of markers. Comparative mapping was performed to predict positions of genes in *B. rapa* using two approaches; homology with chiifu sequence and genomic block synteny *A. thaliana* and *B. rapa*. Primers were designed for 18 candidate genes and their 16 paralogs genes in *B. rapa* using Chiifu sequence. Among 31 markers genotyped, 13 markers were mapped in DH68 population are in agreement with predicted positions in genomic blocks. Thus, the research will be useful to co-localise QTLs with candidate gene, identification of putative genes as well as cis and trans positions of genes in future.

Key Words : *B. rapa*, DH population, Candidate gene, Fatty acid biosynthesis, Comparative mapping.

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