Structural organization and classification of cytochrome P450 genes in flax
(Linum usitatissimum L.)

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Abstract
Flax CYPome analysis resulted in the identification of 334 putative cytochrome P450 (CYP450) genes in the cultivated flax genome. Classification of flax CYP450 genes based on the sequence similarity with Arabidopsis orthologs and CYP450 nomenclature, revealed 10 clans representing 44 families and 98 subfamilies. CYP80, CYP83, CYP92, CYP702, CYP705, CYP708, CYP728, CYP729, CYP733 and CYP736 families are absent in the flax genome. The subfamily members exhibited conserved sequences, length of exons and phasing of introns. Similarity search of the genomic resources of wild flax species Linum bienne with CYP450 coding sequences of the cultivated flax, revealed the presence of 127 CYP450 gene orthologs, indicating amplification of novel CYP450 genes in the cultivated flax. Seven families CYP73, 74, 75, 76, 77, 84 and 709, coding for enzymes associated with phenylpropanoid/fatty acid metabolism, showed extensive gene amplification in the flax. About 59% of the flax CYP450 genes were present in the EST libraries.

References


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