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ABSTRACTS

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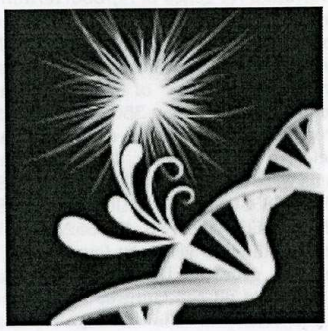

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5.12.

Stilbene synthase gene expression in callus cultures of *Vitis amurensis* with different levels of resveratrol production

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Resveratrol is known to have antioxidant, anti-inflammatory, and antiviral activity. It is also a strong antitumoral agent effective against many types of cancer (Aggarwal et al., 2004). Stilbenes, including resveratrol, are synthesized via the phenylpropanoid pathway. Stilbene synthase (STS, EC 2.3.1.95) condenses three molecules of malonyl-CoA and one molecule of cumaryl-CoA to form resveratrol. *STS* exists as a multigene family. In *Vitis vinifera*, closely related to *V. amurensis*, 25 *STS* genes per haploid genome were predicted. The large number of *STS* genes has aroused considerable interest. We suggested *STS* genes of *V. amurensis* encoding protein products with different activity in resveratrol biosynthesis. We analyzed *STS* gene expression in callus cultures of *V. amurensis* with different levels of resveratrol production: 0.30–3.15% dry wt. in *rolB* transgenic cell cultures (Kiselev et al., 2007); 0.10–0.15% dry wt. in *rolC* transgenic cell cultures (not published); 0.05–0.10% dry wt. in nontransgenic cell cultures treated with 50–300 μM of salicylic acid (not published); and 0.02–0.03% dry wt. in nontransgenic cell cultures used as control (Kiselev et al., 2009). It is known integration of individual *rol* genes of *Agrobacterium rhizogenes* into the plant genome may enhance biosynthesis of certain groups of secondary metabolites. The total expression of *STS* genes was approximately on the same level in the *V. amurensis* cultures. Then, we analyzed the quantity of clones of individual *STS* genes. We sequenced more than 350 clones of different *STS* genes obtained from cDNA probes of the explored *V. amurensis* cell cultures. We detected 10 *STS* genes. The sequenced fragments of seven *STS* gens were deposited in GeneBank: *VaSTS1* (EU659862), *VaSTS2* (EU659863), *VaSTS3* (EU659864), *VaSTS4* (EU659865), *VaSTS5* (EU659866), *VaSTS6* (EU659867), *VaSTS7* (EU659868). We divided the *STS* genes on four groups:

a) *STS* gene which was being constantly expressed on a high level in all cell cultures. The expression of the gene slightly increased in cells with high resveratrol content (*VaSTS1*).
b) *STS* genes which expression was significantly increased in the cell cultures with high resveratrol content (*VaSTS2*, *VaSTS3*, *VaSTS4*, *VaSTS5*, *VaSTS7*).
c) *STS* genes which expression was strongly activated by SA (*VaSTS6*) or by *rolC* gene (*VaSTS9*, *VaSTS10*). However, these genes were weakly expressed in the *rolB* transgenic cell culture (highest resveratrol content).
d) *STS* gene (*VaSTS8*) which transcripts were extremely rare in cDNA probes obtained from the cultures with high resveratrol content.

We propose that an increase in the expression of the second group of *STS* genes is required to a high level of resveratrol production in a *V. amurensis* cell culture. Further study is needed to confirm this hypothesis.

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5.13.

Chromosomal analysis of *Secale cereale* × *Dasypyrum villosum* amphiploid and its parents by use of cytogenetic methods

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The wild species from *Triticeae* tribe has played an important role in the processes of increasing the genetic variation of rye (*Secale cereale* L.). The genus *Dasypyrum* comprises many agronomically important traits including disease resistance, drought and freezing tolerance, high protein content and quality, and therefore might be used as a valuable source for crops improvement. Our research was carried out on *Secale cerale* × *Dasypyrum villosum* tetraploid (2n=4x=28; RV-genome) which resulted from the intergeneric crosses between *S. cereale* (2n=2x=14; R-genome) and *D. villosum* (L.) P. Candargy (2n=2x=14; V-genome), and then obtained from colchicine treatment. In the present study, we attempted to investigate the genome structure of this amphiploid and its parents, and the analysis was conducted on somatic metaphase chromosomes using fluorescence and genomic in situ hybridization (FISH/GISH). The FISH provided valuable chromosomal landmarks to detect chromosome variations, and was able to identify rDNA-bearing chromosomes.

This approach revealed chromosomal rearrangements and allowed identification the chromosomes implied in chromosome rearrangements. For more detailed amphiploid genome analysis, a silver staining method (Ag-NOR) was applied, but no nucleolar dominance was occurred. The interspecific and intergeneric hybrids between rye cultivars and wild diploid species *D. villosum* are important for introgression breeding programs, and can be used, for example, to transfer of abiotic and biotic stress resistance traits from *Dasypyrum* species into *Secale species*.