

ANALYSIS OF TRANSPOSONS IN TRANSGENIC PEA, *PISUM SATIVUM* L.

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Presented work is element of research conducted in the Department of Genetics, Faculty of Biology, Warmia and Mazury University relating to analysis of transposons in transgenic pea *Pisum sativum* L.

The aim of the work was the finding of the answer on the question, if transgenic pea line with introduced *PGIP* gene from raspberry (*Rubus idaeus* L.) and the line with introduced *Vst1* gene from grape-vine (*Vitis vinifera* L.), as line with the two transgenes together show differences in relation to biometrical traits and molecular profiles in relation to the parental Baroness cultivar.

Transgenic pea used in my investigations come from University in Hannover in the Germany. For the analysis 4 lines were chosen the Baroness cultivar and three transgenic lines *PGIP*, *Vst1* and *PGIPxVst1*. Mentioned above lines were analysed biometrically with the use of following features stems number, the heighest stem height, seeds weight, pods number and seeds diameter.

The following DNA markers *PGIP*, *Vst*, transpozon *Tpo1* coming from family CACTA and retrotranspozons *Lolcopia1*, *Lolcopia2*, OGRE, BARE were used in molecular investigations.

Transgenic lines, in the comparison to the Baroness cultivar, had lover values of seeds mass and plant height. The smallest seeds mass had line *PGIP* and it showed statystically significant differences in comparision to Baroness cultivar and transgenic line *PGIPxVst1*. The *PGIP* line characterize with the shortest plant high and it difference to the control Baroness cultivar was statystically significant. Only *Vst1* line did not differ from remaining lines. For remaining morpfological features such as the number of pods and the number of the stems statystically significant differences was not observed.

Molecular analysis of 4 pea lines with the use of 5 transposon elements *Tpo1*, *Lolcopia1*, *Lolcopia2* OGRE, BARE enabled to identify 264 the products of the aplification.

The detailed comparative investigations of the genotypes of transgenic lines in relation to the control Baroness cultivar, with the use of transposon elements showed the presence of specific bands.

Total analysis of molecular profiles obtained with the use of IRAP markers showed, that the largest changes in pea genome (39,02%) was observed in the *PGIP* line. In case of *VstI* and *PGIPxVstI* lines changes concerned 29,26% of the genome. The genome analysis with the use of SSAP primers showed, that the largest change (47,36%) characterize the *VstI* line the smallest (12,10%) concerned the *PGIPxVstI* line.

The genetic similarity values between transgenic lines and Baroness cultivar were ranged from 0,72 to 0,98. The highest genetic similarity (0,89-0,97) were estimated between Baroness cultivar and *PGIPxVstI* and also between *PGIP* and *VstI* (0,95-0,98). The lowest similarity ranged from 0,67 to 0,98 was obtained for two transgenic lines *PGIP* and *PGIPxVstI*.