

Biometric Analysis of Transgenic Plants of Spring Rape with *cyp11a1* Animal Origin Gene and Bacterial *bar*

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Aim of the study: In our study, we used a mitochondrial gene of the ox (bull) adrenal cortex *cyp11A1* encoding P450scc cytochrome. The experiments in the transformation of tobacco plants by *cyp11A1* gene show its effect on the growth, development and physiological and biochemical characteristics of plants. Therefore, transgenic plants with *cyp11A1* gene of P450scc cytochrome developed based on economically valuable cultures, such as spring rape (*Brassica napus* L. var. *oleifera* D.C.), are of great interest. Earlier, we developed transgenic plants of spring rape, bearing c-DNA of *cyp11A1* gene of P450scc cytochrome and the *bar* gene in their genome. The aim of the present research was to study the effect of *cyp11A1* gene on the genome of transgenic spring rape plants by biometric analysis of a number of morphological characters and productivity elements.

Material and methods: The object of research constituted 525 plants of spring rape in T₁-T₃ generations of eight transgenic lines (*Brassica napus* L. var. *oleifera* D.C.) developed based on the Magnat variety of the Belarusian selection. Transgenic rapeseed lines were developed as a result of *Agrobacterium*-mediated transformation using pCB093 vector carrying two genes: c-DNA gene *cyp11A1* and a *bar* gene. To study the effect of the gene *cyp11A1* on the growth and development of transgenic rapeseed plants resistant to Basta herbicide in T₁-T₃ generations, we selected a number of characters: the plant height, the length and the number of lateral shoots of the main brush, as well as elements of the yield structure -- the mass of 1000 seeds and the number of pods on the main brush. Statistical processing of the experimental data was carried out using a variational analysis; to determine the significance of differences, a two-sample Student's t-test was used. A correlation analysis was used to assess the relationship between the studied phenotypic characters.

Results: In our study, the effect of c-DNA of the mitochondrial gene *cyp11A1* of P450scc cytochrome of a bull (ox) on the plant genome was shown for the first time -- a stable increase in the mass of 1000 seeds in T₁-T₃ generations, as well as the parameters of the main brush (length, the number of pods and lateral shoots). The variation coefficient analysis for three years (T₁-T₃ generations) revealed that the most constant and the least variable characteristics are the plant height and the mass of 1000 seeds. The correlation analysis for the dependence of the mass of 1000 seeds on the remaining productivity elements showed a close positive correlation: $0,3 < r > 0,86$ for T₁ generation, $0,4 < r > 0,52$ for T₂ generation, $0,4 < r > 0,7$ for T₃ generation. Bn9/93/21 line had the highest values of correlation coefficients in generations by most characters. In addition, that line had the highest values of both architectonics characters and the yield structure elements in different generations, which may be due to the effect of the transcriptional activity of heterologous genes *cyp11A1* of P450scc cytochrome and the *bar* gene on the rape genome.

Keywords: *Brassica napus* var. *oleifera* D.C., transgenic plants, biometric analysis, *cyp11A1* gene of P450scc cytochrome, *bar* gene, PCR and RT-PCR