

Analysis of genes from the sex-determining region of *Populus x sibirica* revealed sex-associated differences in their expression

P-01.3-08

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The genus *Populus* is presented by dioecious species, which are characterized by significant diversity in the structure and location of the sex-determining region (SDR). We performed transcriptome sequencing of flowers, catkin axes, and leaves of male and female *Populus x sibirica* plants and genome sequencing of the same individuals on the Illumina platform for the first time. Analysis of polymorphisms of three genes from the SDR – encoding T-complex protein 1 subunit gamma (TCP), chloride channel protein CLC-c (CLC-c), and DNA-methyltransferase 1 (MET1) – was performed based on genome and transcriptome sequencing data. *P. x sibirica* is an intersectional hybrid likely between species from sections *Aigeiros* and *Tacamahaca*, so a significant number of heterozygous polymorphisms were identified. We revealed that both allelic variants of the *TCP1*, *CLC-c*, and *MET1* genes were expressed in females, while in males, both allelic variants were expressed for *TCP1* and *MET1*, but only one – for the *CLC-c* gene. Targeted sequencing of *TCP1*, *MET1*, and *CLC-c* gene regions obtained from DNA and cDNA of 10 male and 10 female plants of *P. x sibirica* confirmed the predominant expression of only one allelic variant of the *CLC-c* gene in leaves, flowers, and catkin axes of *P. x sibirica* males. Thus, identified sex-associated allele-specific expression of the *CLC-c* gene in vegetative tissues of *P. x sibirica* suggested that differences between male and female poplars could take place in not only generative organs but whole plants. The reported study was funded by RFBR according to the research project № 20-34-90159.