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В сборнике представлены материалы 4 Международной конференции по генетике, геномике, биоинформатике и биотехнологии растений (**PlantGen2017)**, проведенной в г. Алматы 29 мая -2 июня 2017 г. В публикациях изложены результаты оригинальных исследований в области изучения, сохранения и использования генетических ресурсов, генетики и селекции, биоинформатики и биотехнологии растений.

Сборник рассчитан на биологов, генетиков, биотехнологов, селекционеров, специалистов, занимающихся генетическими ресурсами растений, и студентов биологического и сельско-хозяйственного профиля.

Тезисы докладов представлены в авторской редакции.

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EVALUATION OF GENETIC VARIATION IN RARE TULIP SPECIES FROM KAZAKHSTAN

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According to Flora of Kazakhstan this country is home for 35 Tulip species, and, therefore, it is naturally one of the symbols of flora in Kazakhstan. Despite tremendous work in botanical description of local scientists, there was little effort in assessment of molecular phylogeny of representatives of this genus growing in Kazakhstan. The molecular phylogeny analysis is particularly important for taxonomy evaluation of endemic and rare Tulip species. In this study leaf material of thirteen Tulip species were collected in six different regions of the country during 2015-2016, six of those species were rare and four were endemic. DNA samples were extracted using Qiagene kits and preserved at -80^{0}C. The genetic analysis of Tulip samples was done based on using ITS (internal transcribed spacers) and *matK* DNA barcodes. It is interesting that unlike other flora representatives no PCR amplification was recorded for matK marker, suggesting that there is a deletion region in this location of chloroplast genome in all Tulip species studied in this work. However, PCR amplification was successful for ITS marker for all studied samples. The phylogenetic tree was constructed based on Neighbor Joining method in MEGA 6.0 package.

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