

# **Repetitive DNA comparison of *Aegilops tauschii* from a different geographical origin**

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The majority of large plant genomes are formed of repetitive DNA, mostly by transposable elements and tandem repeats (satellite DNA). In order to identify and explore these parts of genomes are usually used some special tools such as RepeatExplorer. In this study, we analyzed the differences in the structure of repetitive DNA for two genomes of *Aegilops tauschii* from different geographical origins.

We explore a sample consisting of 623000 reads from two species and run RepeatExplorer2 clustering with the additional option —Perform comparative analysis and Tarean. Then we use the output to characterize repetitive genome fractions and provide phylogeny, using DANTE, muscle, and Geneious.

In order to understand if there exists any statistically significant difference between the proportion of all the types of repetitive elements for the two species, we used Mann-Whitney U-test with a significance level of 0.05. As a result we haven't recognized any special repetitive elements that can help differentiate one organism from another (p-value=0.49). We explain it by the small size of the sample.