

Abiotic and biotic stresses play an important role in plant adaptation. Plants have evolved many molecular mechanisms to adapt their growth and development to different environmental pressures to cope with them. To understand the evolutionary success of plants and the adaptive systems evolved, comprehensive studies at different levels of the plant organisation are essential.

The unique combination of biological and phylogenetic traits of *Brachypodium distachyon* (Brachypodium) allows its use as a model species for cereals and cultivated grasses of the temperate climate zone. An additional advantage of Brachypodium is its widespread occurrence in the Mediterranean basin and the Middle East, with Turkey considered the centre of its biodiversity. The climatic diversity to which the Brachypodium genotypes are exposed suggests developing a population-specific genetic model shaped by selection pressures.

This study aimed to determine the Brachypodium variation at the genomic and DNA methylome level and changes in metabolomic processes and phenomic diversity in relation to variable environmental conditions where the seeds were collected. Moreover, it also aimed to identify changes in cellular processes under salinity stress. For this purpose, comprehensive multiomic, molecular and cytological analyses were carried out.

The performed studies have shown the presence of variability at the genome and DNA methylome levels within the population, which was linked to climatic variations in the natural occurrence of Brachypodium. Moreover, this variability is reflected in the metabolomic profiles of the plants. The analysis of metabolic pathways under control and induced drought stress conditions allows us to conclude the occurrence of differences determining the increased tolerance to stress between the studied genotypes.

Cytohistochemical analyses and findings regarding the expression of genes responsible for cell cycle regulation (CYC and CDK) and cell wall structure (AGP, FLA) revealed that salt stress substantially affects Brachypodium development and growth. These studies showed that salinity induces epigenetic modifications of histones, disrupts the cell cycle and significantly affects the expression of key genes responsible for proper cell cycle progression.

The results obtained in this study provide valuable knowledge that can be used in analogous analyses of adaptation mechanisms in crop plants closely related to *Brachypodium*.