

SUMMARY

The main objective of the thesis work was the detailed characterization of pearl millet (*Pennisetum glaucum* (L.) R. Br.) genotypes contrasting for terminal drought tolerance. For that work, we used a set of near isogenic lines (NIL-QTLs; carrying terminal drought tolerance quantitative trait locus (QTL) from a drought tolerant donor parent on the genetic background of a sensitive parent) and a recombinant inbred lines population (RIL; developed from a cross between the tolerant and sensitive genotype). In these contrasting genotypes we investigated following physiological traits. Transpiration rate (Tr), transpiration efficiency (TE), transpiration response to increased vapor pressure deficit, threshold in volumetric soil moisture where transpiration begins to decline (FTSW threshold), stomatal density (SD), sensitivity of plants' growth to VPD below and above 2kPa. Regarding biochemical traits, we followed content of chlorophyll (Chl), carotenoids (Car), abscisic acid (ABA), proline (Pro), we conducted isozyme analysis of antioxidative enzymes [superoxid dismutase (SOD), ascorbic peroxidase (APX), catalase (CAT)].

The main leading thread for understanding the drought tolerance mechanisms of pearl millet came from the analysis of traits related to the control of water losses under fully irrigated conditions. We could clearly distinguish drought tolerant genotypes from the sensitive ones based on: i) lower Tr in well-watered conditions measured on full plant basis and on detached leaves ii) higher leaf ABA content in well-watered conditions iii) sensitivity of transpiration to high VPD condition under well-watered conditions. Furthermore, the leaf expansion of tolerant genotypes was sensitive to VPD conditions in which plant development took place and these conditions determined the dynamics of water utilisation during plants development. Based on the biochemical parameters we could rarely distinguish between tolerant and sensitive genotype. Though we documented differences in the activity of APX5 isoenzyme and proline accumulation dynamics under water limiting conditions between tolerant/sensitive genotypes, this variation was probably not directly linked to the yield variation of these genotypes under terminal drought conditions.

It is concluded that the major terminal drought tolerance mechanism of investigated tolerant pearl millet genotypes is linked to their lower Tr. Low Tr of these genotypes probably contribute to saving the water in the soil profile and so leaving a critical amount of water available for grain filling stage (in fact drought avoidance mechanism). It is further discussed that Tr could be influenced by the level of leaf ABA and the hydraulic properties of plant tissues. However, these "water saving" drought tolerance mechanisms seems to be specific to the environmental conditions in which plants' development took place. The importance of these water saving mechanisms is also being validated in RIL population. The biochemical parameters tested under drought conditions appeared to have no major significance for terminal drought tolerance.