

Flood Tolerance In Maize: Genetic Assessments

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Flooding is one of the most important stresses that may occur in plants. Plant under this stress starts diverse biochemical pathways to guarantee survival and reproduction. Soon after decreasing oxygen availability in the soil, the regular respiration mechanism collapses, glycolysis increases and the plant starts to produce ATP via fermentation. At the same time enzymes like alcohol and lactate deshydrogenase, osmosensors and hemoglobin increase their expression. Acclimatization to this new environment involves the formation of aerenchyma and adventitious roots. Although intense research has been conducted, little is known about mechanisms involved at molecular level in response to flooding stress in plants. In southern Brazil maize may be an excellent alternative to the continuous rice cultivation in lowland areas that represent over six million hectares. However, flooding tolerance is a major issue for maize cultivars in this area. There are evidences that complex environmental interactions are present in the manifestation of flood tolerance. Amount of ammonium and sodium has strong effect on plants submitted to flooding. In addition high temperature has been shown to affect flooding tolerance. As a consequence, assessment of flooding tolerance should consider these different factors. Genetics in maize has indicated dominance and heterosis on the inheritance of flood tolerance. Also complementary gene action indicated the influence of many loci on this trait. QTL analysis performed in southern Brazil maize germplasm detected three markers associated to flood tolerance. These markers were located near loci that codify for glutamine synthetase, zein, and triosephosphate isomerase.