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Development of Barley Tilling Mutants Tolerant to Aluminium Stress

Aluminium is the third most abundant element in the Earth's crust. In acidic soils it solubilizes to Al3+ ions, that are phytotoxic and cause root growth inhibition. Around 50% of arable lands are acidic. Barley is one of the crops most sensitive to Al it is a good model for studying Aluminium response. The common mechanism of Aluminium tolerance is related to excretion of organic acids. Here we investigate another pathway of Aluminium tolerance through changes in genes related to cell cycle progression and DNA repair to generate Al-tolerant mutants in barley. We used HorTILLUS plat form and TILLING strategy to identify mutants in HvATR (cell cycle checkpoint regulator), HvALT2 (halting cell divisions) and HvSOG1 (Transcription factor (TF) involved in DNA damage response (DDR)). Mutants were screened in hydroponic system in Hoagland solution containing 20μM, 30μM and 40μM of bioavailable Al. After one week, root systems were scanned and analysed in detail. DNA damage caused by Aluminium was investigated on the cytological and molecular levels. We have identified 44 mutations in the three selected target genes. Mutants carrying missense or splice junction mutations were screened for Aluminium response. We found several forms with increased Aluminium tolerance. Their root system was less affected by Al3+ ions than the system of the wild types after treatment with different doses of Aluminium. The cell cycle and mitotic index in root meristems were analysed in mutants and wild type after Aluminium treatment. Aluminium is a very important factor limiting crop production on acidic soils. Developing Aluminium tolerant forms is of great importance for plant breeding. Our barley TILLING mutants carrying changes in genes related to cell cycle progression and DNA repair may help to elucidate the alternative pathways of Aluminium response and are a valuable material for breeding barley more tolerant to Al toxicity.

Country or International Organization

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