Identifying Responsible Salt Tolerant Genes in Chenopodium Quinoa through Genomic Sequencing Analysis

AlSinan, Abduallah (School: Dhahran Ahliyya School)

The world today faces an increasing shortage of food production due to the exponential growth in the human population, hence the deficiencies in resources, especially water. According to the United Nation's World Water Development Report in 2019, agriculture consumes 69% of drinkable water and this demand is expected to reach 93% by 2050. The current solutions to this problem include updated genetic engineering and the use of novel agro-chemicals for crop management. However, these create drawbacks towards the environment and public health. This project aims to approach food and water shortage by understanding the mechanisms of how salt-tolerant crops, such as Chenopodium quinoa, survive in harsh environments. These mechanisms could help address the need for increased food production and allow the use of saline water sources. To investigate salinity tolerance in Chenopodium quinoa, 1000 genomic DNA were extracted. Samples were prepared for next-generation DNA sequencing on HighSeq 6000 illumina short read sequencing platform. The sequences were analyzed through BOOST bioinformatics algorithm program to identify possible salt tolerance genes. The NCBI gene bank was used to cross-reference potential matches. Na+/H+ antiporter genes, similar to NHX genes, were identified to be important for salinity tolerance. The genes were then investigated through cross-referencing and identified salt tolerance genes, like NHX1-8. The genes were recognized for the first time in Chenopodium quinoa. These results are a promising step to curtail the $27.3 billion in agricultural damage from salinity and can help in increasing crop yield production to feed the growing population.

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