EXPLOITABLE FOREGROUND

Development of SCAR markers for identifying sweet sorghum genotypes with high sugar content in sweet sorghum elite materials of FAUANL

Explanation and Purpose

SCAR (Sequence Characterized Amplified Region) is a possible technique to identify markers associated with sugar concentration. In sorghum, previous work done using this technique, has been focused to identify a RAPD (randomly amplified polymorphic DNA) marker closely linked to a gene for resistance to anthracnose *Colletotrichum graminicola* (Ces.) and resistance to blight *Exserohilum turcicum* leaf.

Within SWEETFUEL 54 RAPD markers were identified that had the property of being present in the high genotypes sugar: AN601 x FAUANL-39, FAUANL-35A x FAUANL-39 and FAUANL-33A x FAUANL-5 while they were absent in the lowest genotypes sugar: FAUANL-37A, FAUANL-33A and FAUANL-35A. The sequencing process was not successful for all fragments. However, for fragments aligned with genomic sequences of *Sorghum bicolor* sp. six SCAR primers were identified.

Exploitation Strategy

SCAR markers obtained provide a further biotechnological technique that could be used to define strategies for marker assisted selection in sorghum germplasm for sweetness to improve bioethanol production.

Further Research

Specific primers designed (SCAR markers) need to be screened on F2 sorghum populations for early identification of appropriate genotypes for sweet sorghum pre-breeding programs focusing on bioethanol production.

Impact of Exploitation

Development of SCAR markers will allow an early selection of individual plants as potential candidates to improve the breeding focused on high content of sugar.

SWEETFUEL

Sweet Sorghum: an alternative energy crop

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