

## 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

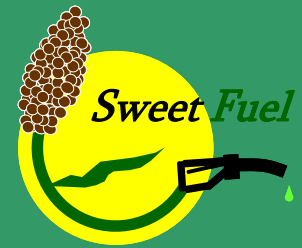
Specific primers designed (SCAR markers) need to be screened on F2 sorghum populations for early identification of appropriate genotypes for sweet sorghum pre-breeding programs focusing on bioethanol production.

#### 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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