

NewPearl - Combining new phenotyping approaches and next generation sequencing to accelerate breeding in pearl millet, an orphan cereal from arid regions

OBJECTIFS

Providing tools and knowledge to accelerate the breeding of new pearl millet varieties with increased nutritional qualities as well as better adaptation to environmental stresses to increase food security in dry regions and in particular in sub Saharan Africa

ACTIONS

WP1: Root phenotyping

Task 1.1: Characterization of the root architecture of a collection of pearl millet inbred lines

Task 1.2: Screening for natural root exudation variation

Task 1.3: Correlation studies between root traits and agronomical characters

WP2: Seed quality phenotyping

Task 2.1: Phenotyping a collection of inbred lines for seed traits

Task 2.2: Identify and investigate the expression of relevant genes involved in phytic acid and C-glucosylflavones synthesis/accumulation in pearl millet seeds

Task 2.3: Alternative strategies for pearl millet biofortification: search for low phytic acid (lpa) and low C-glucosylflavones (lcf) mutants and impact of lpa traits on seed conservation and drought response

WP3: Genomic resources for pearl millet breeding

Task 3.1: Produce GBS data for selected inbred lines (>100) and for the RIL populations

Task 3.2: Genome wide association studies and QTL analysis

RESULTATS

• WP1: Root phenotyping

A collection of 192 pearl millet inbred lines was analyzed for root architecture traits (in particular primary root growth) and root exudation (which stimulates soil aggregation in root vicinity).

A field trial has been conducted to analyze the tolerance of these inbred lines to early drought stress. This experiment is currently replicated.

The cellular organisation of different root types was characterized.

• WP2: Seed quality phenotyping

A collection of 157 pearl millet inbred lines was analysed for phytic acid, goitrogens (C-glucosyl flavones) and essential minerals. Inbred lines with contrasting phenotype for the content of these compounds have been identified. Pearl millet orthologs of genes relevant for phytic acid and C-glucosylflavones synthesis/accumulation have been identified and their expression during seed development is under evaluation.

• WP3: Genomic resources for pearl millet breeding

All the inbred lines have been sequenced and the data are currently used to generate genotyping by sequencing information and to perform association studies.

Responsable :

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