

Report on SSR diversity analysis of the BnaDFFS founder lines

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Background

Materials and methods

Plant material

Single plants from the founder accessions of the BnaDFFS were germinated and grown in the glasshouse. Seedling leaf was harvested.

SSR assays

Small scale plant DNA extractions were performed using the Qiagen DNeasy 96 Plant DNA extraction kit from fresh leaf tissue.

Approximately 10ng of purified genomic DNA was amplified using the Amersham GenomiPhi™ whole genome amplification kit in 20 µl reactions and subsequently diluted to 100µl.

SSR PCR reactions were set up with approximately 10ng template genomic DNA, Products were resolved on an Applied Biosystems 3130xl Genetic Analyzer.

The trace files were analysed using GeneMarker version 1.6 (SoftGenetics LLC; www.softgenetics.com) and further collated in Microsoft Excel.

Results

- [Download Excel workbook of results](#)

The BnaDFFS founder lines were screened with sixteen polymorphic SSR markers. The data is tabulated in two forms in the Excel workbook. The normalised data worksheet includes null scores where the assay was performed but no product detected. The marker_allele worksheet excludes the null values and provides a presence (1) or absence (0) look-up reference. This latter dataset was used to perform principal coordinates analysis on the data, shown in figure 1. This figure shows that the different crop types have distinct sets of alleles.

Figure 1. (next page) Scatter plot of the first two principal coordinates from a principle coordinates analysis. The points are colour-coded to represent crop type groupings.

