

Sample Short Research Paper for 'Plant Genetic Resources' (Bologna Special Issue)

Genetic diversity in eggplant (*Solanum melongena*)

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Apart from the "Abstract" and the "Materials and Methods", you may chose whatever and how ever many headings you wish. The maximum word count for the ms is made up of: Abstract: 200, the remainder (excluding title, authors, institutions, key words, list of citations and legends to figures and/or tables) 1200.

Abstract (maximum word limit: 200)

This is a sample text only and so makes no sense at all. Please ensure that your Abstract does not exceed 200 words. That is vital, otherwise it will be returned to you for correction. Genetic diversity in *Solanum melongena* for morpho-agronomic and fruit traits revealed existence of considerable diversity ripening of watermelon fruit. Such collections show seed multiplication. Plant height, fruit length and fruit acidity contributed mostly towards total divergence. Cluster analysis conducted separately for each species, in the relation to the genetic status of accession (sub-species, botanical or variety group, cultivar and population), grouped the accessions into several distinct and significant clusters. No relationship was found between genetic diversity and genetic status of sample. In addition, some fruit discrete descriptors were used as a classification variable to ascertain whether some of them correspond to certain morpho-agronomic properties. The genotypes included in the diverse clusters could be used as parents for hybridisation in order to obtain a high heterotic response and better segregants in eggplant.

Key words: *Solanum spp.*, germplasm, phenotypic diversity, multivariate analyses.

Introduction

This is a sample text only and so makes no sense at all. That is vital, otherwise it will be returned to you for correction. Please note also how references are cited within the text. Genetic diversity in *Solanum melongena* for morpho-agronomic and fruit traits revealed existence of considerable diversity (Sol *et al.*, 2003; Long *et al.*, 2005). Collections show seed multiplication (<http://www.icugi.org>; Jones *et al.*, 2006). Diversity has been observed between the different species. Relationships among them were analysed by Principal Component Analysis in order to summarize the data and reduce the number of variables for clustering. Plant height, fruit length and fruit acidity contributed mostly towards total divergence (Green and Smith, 2003; Loron, 2005). Cluster analysis conducted separately for each species, in relation to the genetic status of accession (sub-species, botanical or variety group, cultivar and population), grouped the accessions into several distinct and significant clusters. No relationship was found between genetic diversity and genetic status of sample. In addition, some fruit discrete descriptors were used as a classification variable to ascertain whether some of them correspond to certain morpho-agronomic properties. The genotypes included in the diverse clusters could be used as F1 parents for hybridisation in order to obtain a high heterotic response and thus better segregants in eggplant.

Materials and Methods (maximum word limit: 300)

For the validation of the PCR assays, DNA was extracted from a number of *Rht* isogenic lines in the varietal backgrounds ‘Maris Huntsman’, ‘Mercia’ and ‘Bezostaya’, together with ‘Ai-bian 1’ and ‘Ai-bian 1a’, and the two dwarf *T. aethiopicum* accessions ‘TRI 15657’ and ‘TRI 15760’ (Table 1). This material covered all the known GA insensitive *Rht-1* alleles. The 82 genebank accessions comprised 77 hexaploid and five tetraploid wheats (Boris *et al.* 1987), originating from Europe, the Near East, Asia, South America and Australia (Table 2). During the multiplication of ‘Ai-bian 1’, numerous tall off-types are detected. As these could have originated from cross pollination with tall

wheats, we considered only the selfed progeny (by bagging) of four seeds harvested from a single off-type (designated 'Ab37o') which was twice as tall as 'Ai-bian 1'. These progenies are denoted Ab37o-S1, Ab37o-S2, Ab37o-S3, Ab37o-S4, Ab37o-S5. DNA was isolated from 3-5 seedlings using the NucleoSpin Multi-96 Plant kit (Macherey-Nagel, Düren, Germany). Primer sequences were as given by Ellis et al. (2002), and the primer combination BF-WR1 was used to detect *Rht-B1a*, BF-MR1 for *Rht-B1b*, DF2-WR2 for *Rht-D1a* and DF-MR2 for *Rht-D1b*. The PCR protocol was adjusted slightly, in that 50ng of template DNA was used per reaction, and a HotStarTag DNA polymerase activation step of 15min at 94°C was included at the start of PCR. PCR products were separated by 2% agarose gel electrophoresis, in the presence of ethidium bromide.

Results and Discussion

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Legends to Tables and Figures

Table 1. Off-type (o) and normal dwarf (n) progenies of the cross ‘Ai-bian 1’ (*Rht-D1c*) x ‘Stamm 1.147568/80’ (*Rht-D1b*).

¹ Alleles other than *Rht-B1a*, *Rht-B1b*, *Rht-D1a* or *Rht-D1b* are indicated in **bold**.

² Unexpected alleles are indicated in **bold**.

Figure 1. PCR analysis of wheat accessions from the IPK genebank collection. First row from left to right: amplification of *Rht-B1* (primer pair BF-MR1 for *Rht-B1b* and BF-WR1 for *Rht-B1a*). Second row: amplification of *Rht-D1* (DF-MR2 for *Rht-D1b* and DF2-WR2 for *Rht-D1a*). The size standard is Gibco BRL 1kb ladder.