

Genetic Variation in Ethiopian durum wheat

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INTRODUCTION

Triticum durum is an economically important crop in the world; it is the only tetraploid (2n=4x=28) species of commercially importance presently cultivated. Ethiopia has the second largest wheat growing area in Sub-Saharan Africa, with about 500,000 ha. Ethiopia is also an important area of diversity for this species (Fig. 1 & 2). The wide range of agro-ecological conditions coupled with diverse farmers' culture provided for this enormous diversity.

Microsatellite markers were applied to evaluate the genetic variability within randomly selected Ethiopian wheat accessions. The results are reported here.



Fig. 1. Different morphotypes of Ethiopian wheat



Fig. 2. Wheat samples collection in Ethiopia

MATERIALS AND METHODS

PLANT MATERIALS

A total of 200 genotypes belonging to 8 landrace populations were used in this study, supplied by the Gene Bank of the Ethiopian Institute of Biodiversity Conservation (IBC). The materials were collected in Shewa and Tigray (central highland and north ethiopia respectively).

DNA EXTRACTION

Total genomic DNA was extracted from young leaves of single plants, using the Macherey – Nagel Dneasy mini kit procedure, as described by Fulton *et al.*, (1995).

MICROSATELLITE MARKERS AND PCR AMPLIFICATION

Twenty-eight primer pairs representing 13 WMS, 9 WMC, 3 BARC, 2 CFA and 1 CFD were chosen for the analysis. Fragment analysis was performed in automated laser fluorescence sequencer with internal size standards.

RESULTS

The analyses indicated the presence of 230 microsatellite alleles, with size ranging from 125 to 296 base pairs. The total number of alleles per locus ranged from 4 (WMS205, WMS5, CFA2091, WMS159, WMS181 and WMS219) to 17 (CFD82) with an average number of 8 (Table 1). Both, Genome A (17 alleles per locus), and Genome B (15 alleles per locus) were highly polymorphic. The Genome A long arm was more variable (average of 9.3 alleles per locus) than the Genome B short arm (average of 6.7 alleles per locus).

AMOVA: Within population, variation (71%) was higher than among population (11%) and among regions (18%) (Fig. 3a). Over all, Shewa (18%) material was more variable than that from Tigray (8%) (Fig. 3b). Genome B short arm was more variable among regions (31%) and population (15%) than genome A (13%) and (9%), whereas, Genome A long arm was more variable among regions (20%) and population (12%) than that of genome B (6%) and (8%) respectively (Fig. 4).

RESULTS OF AMOVA

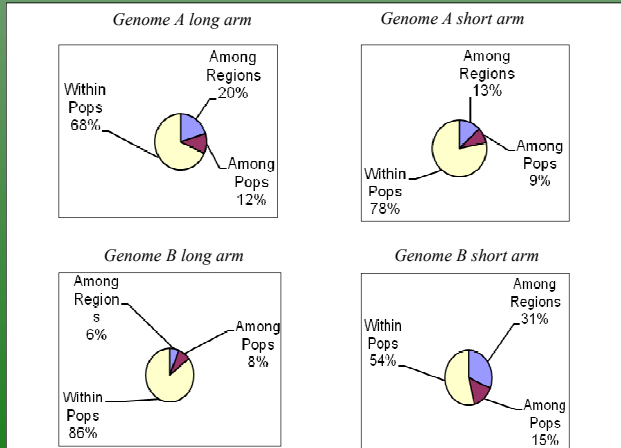
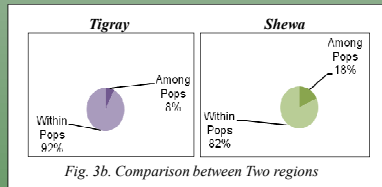
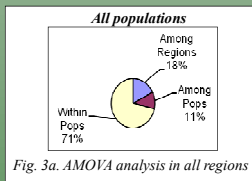


Fig. 4. Comparison between each chromosome arms based on AMOVA

PRINCIPAL COORDINATES ANALYSIS (PCA)

Comparison was made between chromosome arms; the highest variation was detected in Genome A short arm (47.61%) and long arm (35.73%), while genome B short and long arm were 29.16% and 22.96% respectively. Significant differences were detected among chromosome arms, the highest difference being between Genome A short arm (47.61%) and Genome B long arm (22.96%).

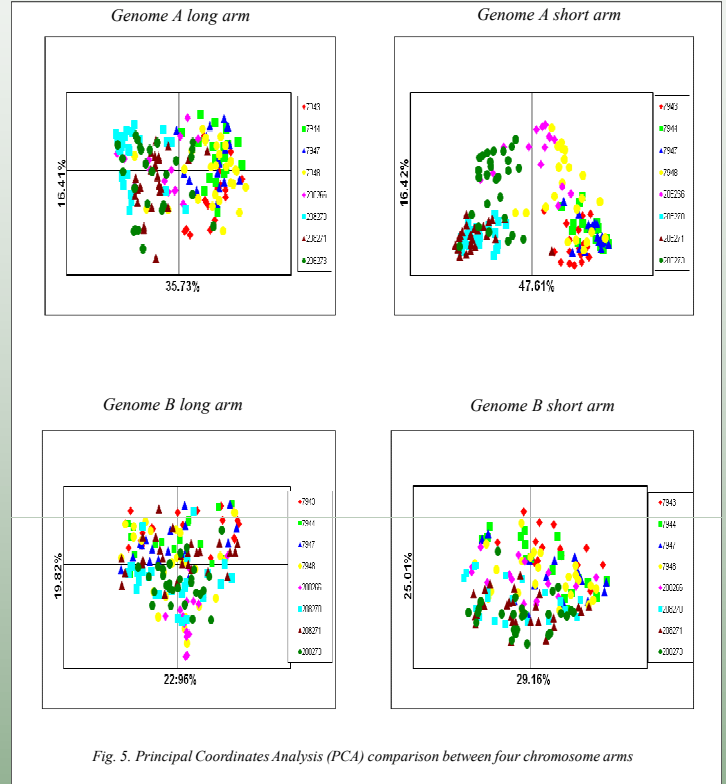


Fig. 5. Principal Coordinates Analysis (PCA) comparison between four chromosome arms

To measure the genetic differentiation among populations, we analyzed RST and FST based on Spatial Analysis of Molecular Variance (SAMOVA). The study categorized the populations into 3 groups. Group-2 comprises two populations, group-3 comprises three populations, group-4 comprises four populations (Fig. 6).

Group description	FST	RST	Group of Populations			
Group-2	12.67	17.62	(1,2,3,4,5)	(6,7,8)		
Group-3	13.11	19.40	(1)	(6,7,8)	(2,3,4,5)	
Group-4	13.71	19.81	(1,2)	(3,4,5)	(7,8)	6

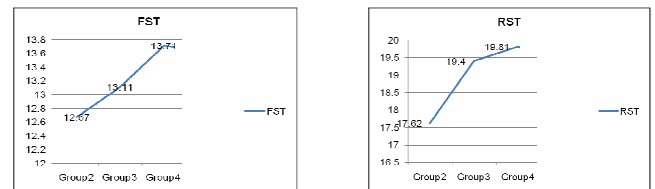


Fig. 6. Comparison between groups