SWEET MAIZE INBREDS GENETIC DIVERSITY AND POPULATION STRUCTURE REVEALED BY SNP MARKERS

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The significance of sweet maize production is not negligible and improving breeding strategies are of great importance. With the aid of new molecular genetics tools, significant advances can be achieved. One of them, Single Nucleotide Polymorphisms (SNPs) now predominate applications in modern genetic analysis. The advantages of SNPs are high genomic abundance, locus-specificity and potential for high throughput analysis, hence they are suitable for genetic structure and diversity analysis of breeding material.

- A set of 50 sweet maize inbreds included in Maize Research Institute „Zemun Polje“ breeding programs was examined with 25k maize array. After filtering, 14134 SNP markers were used for further analyses.
- The analysis of genetic diversity parameters (gene diversity, heterozygosity, PIC) and Roger's distance were calculated using PowerMarker software V3.25.
- Based on calculated distance dendrogram (Neighbour Joining method) was constructed in MEGA 7. Association among genotypes was revealed using PCoA analysis (software DARWIN 6.021).
- Infering population structure was done using model-based approach implemented in STRUCTURE 2.3.4 software (burn-in 10000, Markov Chain Monte Carlo (MCMC) iterations 50000, K=1-10 with 5 simulations for each K.
- The *best* number of K was chosen according to ΔK method using CLUMPAK software.

- Gene diversity was in a range from 0.040 to 0.500, average 0.325.
- The average heterozygosity was 0.019.
- The average PIC value was 0.265 , ranging from 0.04 to 0.375.
- Roger's distance was in a range from 0.01 to 0.61 (average 0.36).
- Results of clustering, STRUCTURE software-based analysis and PCoA are shown in Figures 1, 2 and 3 respectively.
- As presented by cluster analysis fifty sweet maize inbreds were grouped in three main clusters (I, II and III).

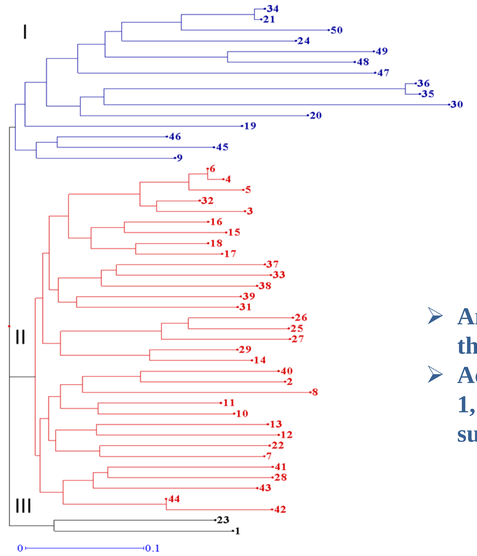

Figure 1 cluster analysis of 50 sweet maize inbreds

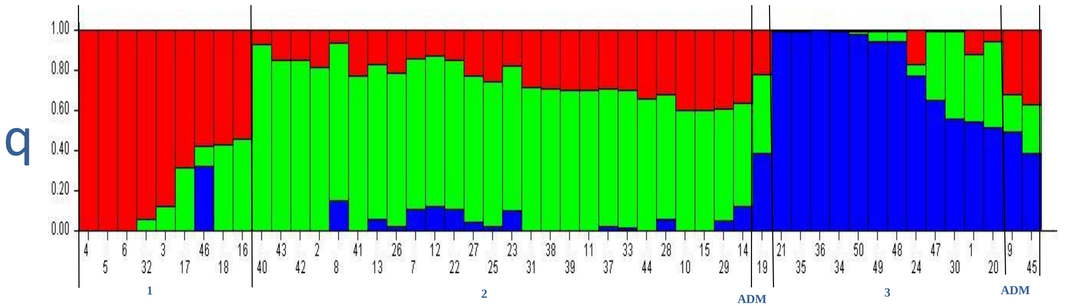

Figure 2 Population structure analysis of 50 sweet maize inbreds: Results are shown for K = 3 - corresponds to the number of subpopulations that sufficiently defines genetic variation. Subpopulations are named as 1, 2 and 3. Each inbred is represented by a vertical line, partitioned into colored segments that represent the estimated membership fractions (*q*) in each subpopulation. Individuals of admixed (ADM) ancestry (highest *q* < 0.5) are indicated

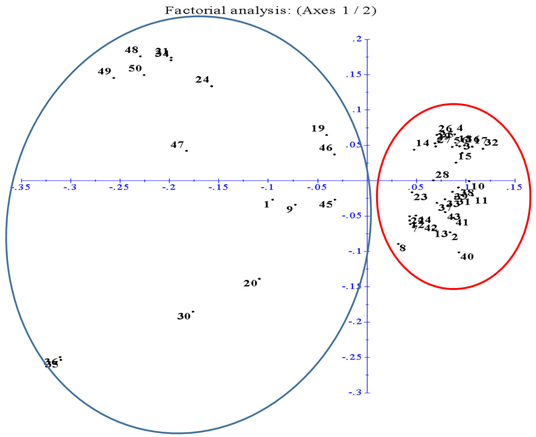

Figure 3 PCoA analysis of 50 sweet maize inbreds

- An admixture-based clustering model with correlated allele frequencies was used to infer the genetic structure of analysed sweet maize inbreds (STRUCTURE software).
- According to the ΔK inference approach, a model with three subpopulations (marked as 1, 2 and 3) best fitted the data in which 94% of the genotypes were assigned to a specific subpopulation (membership coefficient q >0.5) and 6% inbreds showed admixed ancestry.

- Most genotypes from subpopulations 1 and 2 are grouped together in cluster analysis (cluster II), while cluster I is predominately comprised of inbreds which are grouped in subpopulations 3 and ADM groups.
- PCoA showed similar results. On the positive side of the PC1 axis genotypes grouped mainly in cluster II and subpopulations 1 and 2 were positioned, while inbreds assigned to cluster I and subpopulations 3 and ADM were predominantly on the negative side.

❖ **All three analyses exhibited a similar classification of inbreds in agreement with their pedigree data.**

❖ **These are preliminary results. More detailed and profound analyses will be done**.