Analysis of population structure and genetic diversity of Egyptian and exotic rice (Oryza sativa L.) genotypes

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Abstract:

Understanding the population structure and genetic diversity is a very important goal to improve the economic value of crops. In rice, loss of genetic diversity in the last few centuries is observed. To address this challenge, a set of 22 lines from three different regions: India (two), and Philippines (six), and Egypt (fourteen) were used to assess the genetic diversity and the features of population structure. These genotypes were analyzed using 106 SSR markers which showed a clear polymorphism among the lines. The genetic diversity was estimated based on the number of different alleles, polymorphism information content (PIC), and gene diversity. A total of 106 SSR alleles was identified from the 23 SSR and used to study the population structure and cluster analysis. All SSR loci showed a wide range of the number of different alleles extended from two (one loci) to seven alleles (three loci). Five and eight Loci showed high PIC and gene diversity (≥0.70). The results of population structure are in agreement with cluster analysis results. Both analyses revealed two different subpopulations (G1 and G2) with different genetic properties in a number of private alleles, a number of different alleles (Na), a number of effective alleles (Ne), expected heterozygosity (He) and Shannon's Information Index (I). Our findings indicate that five SSR loci (RM 111, RM 307, RM 22, RM 19, and RM 271) could be used in breeding programs to enhance marker-assisted selection through QTL mapping and association studies. Moreover, the genotypes in G2 showed a remarkable genetic diversity among them. These genotypes can be also used to produce rice cultivar with high agronomic features and resistance to abiotic stresses

Published In:

Comptes Rendus Biologies, Accepted, In Press