Composite Collection

Twenty-one SSR loci data on 852 accessions were analyzed. This composite collection showed rich allelic diversity (490 alleles, 23.3 alleles per locus, 246 common alleles and 244 rare alleles at 1%), group-specific unique alleles, and common alleles sharing between subspecies and geographical groups. Gene diversity ranged from 0.559 to 0.926, with an average of 0.819. Unique alleles are those detected in a group of accessions but absent in other groups. Group-specific unique alleles were 101 in wild Arachis, 50 in subsp. fastigiata, and only 11 in subsp. hypogaea. Accessions from America's revealed highest number of unique alleles (109) while Africa and Asia, respectively, had only six and nine unique alleles. The two subsp. hypogaea and fastigiata shared 70 alleles. The wild Arachis in contrast shared only 15 alleles with hypogaea and 32 alleles with fastigiata. A tree-diagram using DARwin 5.0 separated majority of the hypogaea from fastigiata accessions while wild Arachis accessions clustered with hypogaea.

Genetic Structure of Composite Collection

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