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Poster Abstracts

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Development in groundnut core collection from Asian region

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Groundnut (*Arachis hypogaea* L.) is an important oilseed crop cultivated in 24 countries of Asia. The crop productivity of 1.50 t ha⁻¹ is low in Asia. The available large variability in the Germplasm accessions has not been adequately utilized in the crop improvement programs and most groundnut cultivars stand on a very narrow genetic base. This is due to lack of information on agronomic and other economic traits, which require extensive evaluation. The development of a core collection could facilitate easier access to groundnut genetic resources and enhance their use in crop improvement.

The ICRISAT genebank contains 4738 accessions from 21 Asian countries, consisting 267 *fastigiata*, 2414 *vulgaris*, and 2057 *hypogaea* types. The Germplasm accessions were stratified by country of origin within each of three botanical varieties. Data on 15 morphological descriptor traits: growth habit, branching pattern, stem (color, hair), leaf (color, shape, hair) flower, streak and peg (color), pod (beak, constriction, reticulation), seed (per pod, color) were used for clustering by Ward's method. From each cluster = 10 percent accessions were randomly selected to constitute a core subset consisting of 504 accessions, consisting 35 *fastigiata*, 251 *vulgaris*, and 218 *hypogaea* types. Newman-Keuls test for mean, Levene's test for variance, chi-square test and Wilcoxon rank-sum non-parametric test for distribution indicated that the available genetic variation has been preserved in the core subset. The Shannon-Weaver diversity index for different traits was also similar in the entire collection and core subset. High coincidence rate (80.7%) and variable rate (116.9%) confirmed that the core subset is representative of entire collection. This core collection provides an effective mechanism for the proper exploitation of groundnut Germplasm resources for the genetic improvement of this crop.