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## ASSOCIATION MAPPING OF ASCORBIC ACID CONTENTS, ANTIOXIDANT ACTIVITY AND SEED WEIGHT IN PEANUT (ARACHIS HYPOGAEA L.) MUTANTS.

Cultivated peanut (Arachis hypogaea L.) is valued for its edible oil and for direct consumption. It is rich source of nutrients and antioxidants. These traits are polygenic in nature and association mapping is an ideal approach for efficiently exploring the genetic basis for these traits. In present study, 98 peanut genotypes including diverse mutants were used to identify molecular markers associated with ascorbic acid, seed weight and antioxidant activity. For this, 58 polymorphic markers consisting of SSRs and transposable element (TE) markers were employed. The ascorbic acid content and the antioxidant activity [measured as 2, 2- Diphenyl-1picryl hydrazyl (DPPH) reduction assay and ferric reducing antioxidant power (FRAP) assay] were measured spectrophotometrically in all the genotypes in two replicates for two seasons. Seed weight was determined as hundred kernel weight. The 58 markers amplified a total of 115 loci. The average polymorphic information content (PIC) of the markers was 0.48, ranging from 0.12 to 0.91. Subsequently, these markers were scored in tetraploid fashion to access population structure. The most significant LnP (D) was observed at K =3 in these genotypes. Using mixed linear model by simultaneously accounting for structure and kinship matrix, significant association (p < 8.3 x 10-3) of four markers (TE 129, TE 426, TE 457, TE 121) with ascorbic acid, two (TE 129 and GM 2032) with DPPH reducing activity, three (TE 129, TE 459 and GM 2032) with FRAP and one (GM 1742) with seed weight was identified. All these markers explained 7.5 -18.0 % of phenotypic variation (PVE) for each trait. The marker TE 129 was simultaneously associated with ascorbic acid and DPPH and GM 2032 with FRAP and DPPH content. The favourable alleles of these markers can be potentially utilized for marker assisted selection in peanut breeding programs.

## **Country or International Organization**

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**Track Classification:** Enhancing agricultural biodiversity through new mutation induction techniques