

Research Article

Role of *AhMITEI* in the mutation and sub-specific differentiation of groundnut (*Arachis hypogaea* L.)

■ VARSHA KUMARI, VINOD TASIWAL, M.V.C. GOWDA AND M.K. MEENA

SUMMARY

AhMITE1 is an active miniature inverted repeat transposable element (MITE) in peanut (*Arachis hypogaea* L). Twenty-one mutants belonging to different botanical types of groundnut was checked for (FST1-linked) site using *AhMITE1*-specifc PCR, which used a forward primer annealing to the 50-flanking sequence and a reverse primer binding to *AhMITE1*. The parent Dharwad early runner (DER) was found to be free of *AhMITE1* insertion at the FST1-linked site. Another EMS mutagenesis effort with VL 1, a Valencia mutant from DER, (28-2 and 110), showed insertion of *AhMITE1* into the FST1-linked site. Origin of NLM, a Virginia bunch type mutant from TMV 2, ainvolved excision of *AhMITE1* from the predetermined site. 28-2(s) and 110(s) obtained spontaneously from 28-2 and 110, respectively, were also associated with excision of the transposable element. Excision and insertion of *AhMITE1* at this particular site among the mutants their presence in all the Spanish types and absence in all Virginia and Valencia types; led to gross morphological changes resembling alternate subspecies.

Key Words : Groundnut, AhMITEI, Mutants, Subspecies

How to cite this article : Kumari, Varsha, Tasiwal, Vinod, Gowda, M.V.C. and Meena, M.K. (2012). Role of *AhMITEI* in the mutation and sub-specific differentiation of groundnut (*Arachis hypogaea* L.). *Internat. J. Plant* Sci., **7** (2) : 371-175.

Article chronicle : Received : 21.12.2012; Revised : 25.05.2012; Accepted : 16.06.2012

Found is believed to have originated in the Bolivian region of south America where the greatest diversity is found (Gregory and Gregory, 1976). There are about 70 species, most of them diploid (2n=2x=20). The cultivated groundnut is an allotetraploid having A and B genomes, which have been contributed by two diploid species. Groundnut [Arachis hypogaea (L.)] is classified into two subspecies, viz., ssp. hypogaea (Krap. and Rig.) and ssp. fastigiata (Wald.)

- MEMBERS OF THE RESEARCH FORUM -

Author to be contacted :

VARSHA KUMARI, Department of Genetics and Plant Breeding, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA Email: poonm4354@rediffmail.com

Address of the Co-authors:

M.V.C.GOWDA, Department of Genetics and Plant Breeding, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA

VINOD TASIWAL, Department of Plant Pathology, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA

M.K. MEENA, Department of Crop Physiology, University of Agricultural Sciences, DHARWAD (KARNATAKA) INDIA

based on variation in morphology. Further, the ssp. hypogaea is bifurcated into var. hypogaea (Virginia bunch/runner) and var. hirsuta (Peruvian runner), and likewise ssp. fastigiata into var. fastigiata (Valencia), Peruviana, aequatoriana and var. vulgaris (Spanish bunch) (Stalker and Simpson, 1995). Only four botanical types namely, Virginia bunch (VB), Virginia runner (VR), Valencia (VL), and Spanish bunch (SB) are exclusively cultivated by the farmers owing to their agronomic attributes and market value. Kochert et al. (1996) suggested that A. hypogaea might have arisen as the result of single polyploidization event and the dramatic shifts in the morphology of plant organ arose as a result of changes in one or two major genes and a few modifier loci. The possible role of spontaneous and induced mutations in the evolution of abundant morphological variation in groundnut was also evident from various sub-specific changes brought about by mutations in a few breeding programmes (Mouli and Kale, 1982b; Prasad, 1989). Despite tremendous variation in morphology, physiology and agronomical traits, groundnut has shown limited variation at molecular level, isozyme and seed protein (Stalker et al., 1994); RFLP and RAPD (Paik – Ro et al., 1992). However, recent studies revealed polymorphism in the