with 0.1 percentage Mercuric chloride (2 minute) seeds were then inoculated with different concentrations of 2,4-D (1, 1.5, 2, 2.5 and 3 mg/l) and 0.5 mg/l kinetin. Contaminations were removed and callus induction percentage for different treatments was noted. From the study it was noted that percentage of callus induction varied with different concentrations of 2,4-D. callusing was obtained with all combinations of 2,4-D and kinetin but maximum callus induction was obtained when MS media was supplemented with 2 mg/l 2,4-D along with 0.5 mg/l kinetin. For genotypic variation in callusing was respond. It was noticed that the variety Vaishak (76% callusing response) responded well to *in vitro* conditions than variety Swarna prabha (61% callusing response).

B 8

Evaluation of microsatellite markers for genetic diversity analysis among different accessions of arecanut (*Areca catechu* L.)

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Betel nut (Areca nut, *Areca catechu* L.) is one of the important commercial cultivated crops of tropical and subtropical habitats throughout Southeast Asia and Oceania. In India, it is cultivated in South, Konkan, North East region and Andaman and Nicobar group of Islands of the country. Arecanut is a monocot, belongs to family Palmae mainly grown for its masticatory nuts, having economic, religious, cultural and medicinal importance. So far, arecanut accessions have been characterized for morphological and yield parameters. But these parameters offer limited information about relatedness, diversifications and are also subjected to environmental and physiological influences. With this perspective, the present investigation attempt was made on utilizing molecular markers to understand the genetic diversity. Nine different microsatellite markers specific to arecanut, were used to evaluate the variation in the different accession of arecanut germplasm which includes indigenous and exotic collection maintained at CPCRI (RS) Vittal, Dakshina Kannada. Among the nine microsatellite, all displayed polymorphism except one. Cluster analysis revealed two major clusters- the Konkan collections clustering separately in a distinct cluster, while the collections form NE and Exotic collections clustered separately. Indigenous Konkan collections batch I and batch II share genotypes corresponding to their geographical region.