Table 2. Characteristic features of the two new released varieties of *rajmash* in comparison to the standard checks

Traits	Description					
	New released varieties		Standard checks			
	'Baspa'	'Triloki'	'Him 1'	'Jwala'	'Hans'	'Kanchan"
Plant height (cm)	50–55	45–55	45–55	45–55	45–55	45–55
Days to maturity	110–120	98–100	90–95	90–95	90–95	95–100
Average grain yield (q/ha)	18–20	25–27	8–9	9–10	10–12	18–20
Seed size	Bold	Bold	Medium	Bold	Small	Bold
Seed Colour	Maroon with pink specks	Creamish yellow	Cream with pink specks	Maroon	White	Pink with maroon specks
Disease resistance						
i. Bacterial blight	R	R	S	S	S	MS
ii. Anthracnose	R	R	S	S	S	MR
iii. Common mosaic	R	R	S	S	S	MR
Shattering	No	No	Yes	Yes	Yes	Moderate
Cooking quality	Good	Good	Good	Good	Good	Good
Acceptability to the farmers	Acceptable	Acceptable	Acceptable	Rejected	Rejected	Rejected

R=Resistant, S=Susceptible, MS=Moderately Susceptible, MR=Moderately Resistant

whole of the winters (when the temperature regime is – 15°C to 9°C) whereas the summers are mild (10°C to 28°C) and dry (annual rainfall 25 cm). Such a naturally prevailing cold and dry climate has been utilized for the preservation of the collected germplasm as active collections for the future use in the *rajmash* breeding programme.

As per the suitability of these regions and acceptability to the farming community, different varieties are being developed for further release. Farmers are being assured for providing new potential varieties in case of failure of the old ones due to any reason. The contiguous chain has been established between the varieties released, in the adaptive trials, under preliminary screening and the related indigenous and exotic genepools, which in turn, provides sustenance to the production of *rajmash* crop. In this way, *rajmash* has become a cash crop in the dry and wet temperate zones of North-West Himalayas and the farming community fetches a good premium in the market enabling them to improve their economy.

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Characterization of Genetic Diversity of Cashew (*Anacardium occidentale* L.) in India by RAPD and AFLP Analyses

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Key Words: Cashew (*Anacardium occidentale* L.), Genetic diversity, RAPD, AFLP

Cashew was introduced in India by Portuguese during 16th century (Rao *et al.*, 1998). Existence of substantial genetic diversity in India is evident from the variation recorded in the yield and the quality of cashewnuts. Thus, crop improvement programmes can benefit greatly by germplasm collection, characterization and selection of elite lines. Genetic characterization of the cashew accessions is presently based entirely on the morphological characters (Swamy *et al.*, 1998). Although morphological characteristics are still extremely useful, these are often

quantitative in nature and influenced by environment and hence may not be very distinctive and dependable. DNA markers have been shown to complement the characterization exercise. Among the various molecular markers, PCR-based markers RAPD and AFLP could be directly employed even in the absence of prior knowledge about the sequence information. In cashew, the only molecular diversity study made thus far is of Mneney *et al.*, (1997) wherein the feasibility of RAPD for distinguishing Tanzanian cultivars has been demonstrated.

The present study aimed at identifying molecular markers for exploring the genetic diversity and developing molecular profiles for identification of cashew in India, was carried out on a small subset of National Cashew genebank collections, employing RAPD and AFLP techniques.

Soft grafts of old cultivars as well as germplasm accessions have been maintained in the National Cashew genebank at National Research Centre for Cashew, Puttur. A random subset of 18 cashew accessions was used for the study. Young leaves from single trees of each accession were collected for DNA isolation by CTAB method. Fifty RAPD primers and six fluorescent AFLP primer combinations were employed. Amplicons were scored as discrete variables. Generation of pair-wise similarity matrix, UPGMA cluster analysis and principal co-ordinate analysis were performed using the programme NTSYS-pc version 1.7 (Rohlf, 1993). Genetic diversity was estimated as mean marker diversity (Villand *et al.*, 1998).

Fifty selected random primers generated 564 bands of different sizes ranging between 220 bp and 3 kb, with a mean of 11.3 bands/primer (Fig 1). In all, 87.9% bands were polymorphic. Average Jaccard's Similarity Co-efficient (JSC) was 0.528 and the range was 0.454. In AFLP analysis, six primer pairs generated 456 bands of sizes ranging from 50 bp to 500 bp in the 19 accessions, with a mean of 76 bands/primer pair (Fig 2). All the bands were polymorphic. Average JSC was 0.346 and the range was 0.708. Significant correlation was observed when product moment correlation coefficients between similarity matrices and cophenetic matrices derived from RAPD and AFLP were statistically analysed. Both the techniques distinguished all the accessions. Mean marker diversity values of the accessions obtained by RAPD and AFLP techniques were 0.310 and 0.306 respectively and were statistically similar. The

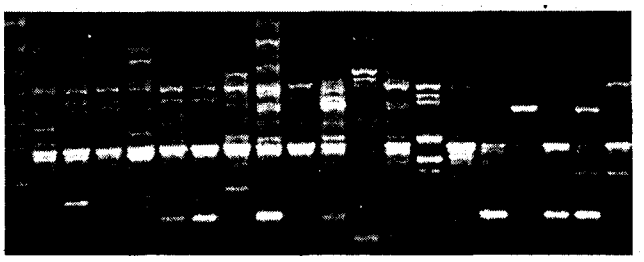

Fig. 1

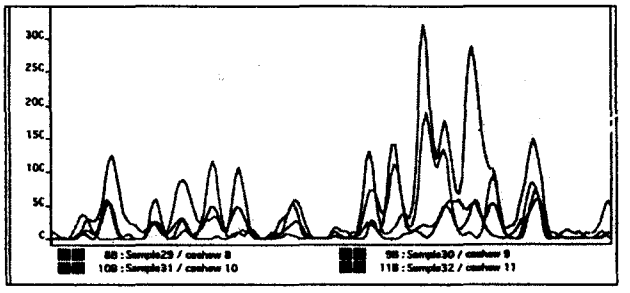

Fig. 2

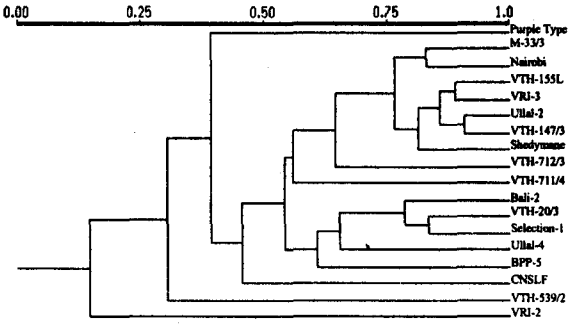

Fig. 3

dendrogram generated based on AFLP is presented (Fig 3).

The variability expressed in the form of JSC and mean marker diversity, falls in the higher bracket. This is explained as follows. Cashew is an allogamous tree species. Owing to the nature of its introduction, where the genotypes were not added from the centre of diversity constantly, only a part of genepool is expected to be present in India. However, following introduction, cashew trees were extensively planted in soil amelioration exercises of the coastal wastelands. This led to the development of natural populations of high heterozygosity and heterogeneity without any kind of human intervention. The plants were seed propagated till recently. These factors resulted in high variability between individuals within the available genepool.

Molecular genetic analysis in cashew is immediately

useful for germplasm management. However, subsequently with increased availability of characterisation data the molecular characterisation results would be valuable for trait mapping, marker assisted selection and further genomic analyses which may be useful for enhancing the efficiency of breeding efforts (Lee 1995). Result in one crop species with a set of molecular techniques cannot be extrapolated to other species (Virk *et al.*, 2000). Thus far, molecular marker studies in cashew have been scarce and inadequate *vis-à-vis* its enormous importance in commerce. In conclusion, this study provides first insights into the molecular diversity in cashew accessions employing RAPD and AFLP techniques. Primers/pairs for AFLP and RAPD are designated for identification of accessions and to carry out future experiments with larger samples.

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Evaluation of Exotic Dura Germplasm for Water Use Efficiency in Oil Palm (*Elaeis guineensis* Jacq.)

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Key Words: Dura, Oil palm (*Elaeis guineensis* L.), Exotic germplasm, Water use efficiency

Targeted area expansion of oil palm, the highest oil yielding crop in states like Andhra Pradesh, Tamil Nadu, Karnataka and Gujarat under irrigated conditions and Kerala and Andaman and Nicobar Islands under rainfed conditions, requires the genotypes having high water use efficiency. Presently available commercial plantations of tenera hybrids [dura x pisifera] necessiate more irrigation, thereby increasing the expenditure on electricity by the growers. This increases the cost of cultivation, and thus, reduces the profit margin. The potential solution to this could be the development of tenera hybrids having high water use efficiency, which can thrive well under limited moisture conditions. With this background, an exploration was carried out in Zambia, Tanzania and Guinea-Bissau to select and collect drought-tolerant genotypes. The present investigation is based on the germplasm collected from these places to screen for their response to moisture stress.

Ten exotic dura genotypes were raised in randomized complete block design with three replications under two environments namely, irrigated and stress. The plot size was four palms/genotype/treatment planted in triangular design of planting at a spacing of 9 m between palms. The irrigation was managed through drip system. Fourteen-month-old seedlings were transplanted in field. Under irrigated conditions the IW/CPE ratio was one while under stress, it was kept at 0.8. The ablation (removal of inflorescences from the palms), as recommended, was done for two years. Observations were recorded on morphological characters like plant height (m), leaflet length (cm), leaflet width (cm), number of leaflets/ leaf, petiole width (mm), petiole depth (mm), and rachis length (m). Non-destructive growth analysis was carried out as per Corley *et al.* (1971). The physiological observations like stomatal conductance (mol/m^2/s), photosynthetic rate (μmol/m^2/s), transpiration rate (mmol/m^2/s), leaf