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Karyotype diversity in five new brinjal varieties

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ABSTRACT

Somatic chromosome number and karyotype analysis in five new varieties of brinjal (*Solanum melongena* var. *esculentum*) namely var. Utkal Anushree, Utkal Jyoti, Utkal Madhuri, Utkal Keshari and Utkal Tarini were reported for the first time. Diploid chromosome number 2n = 24 was recorded in all the varieties with structural variation in chromosome morphology in the genomic compliment. Total chromosome length varied from 82.5 to 94.2 µm and 42.5 to 48.5 µm^3 in var. Utkal Anushree and Utkal Jyoti respectively. Total F% revealed mostly with median constricted chromosomes. Karyotype analysis helped in distinguishing purple coloured skin fruit type var. Utkal Tarini and Utkal Kehari with green colour skin fruit type vars. Utkal Anushree and Utkal Madhuri, which will be helpful for further crop improvement through breeding.

Key words: Brinjal, chromosome number, diversity analysis, karyotype analysis.

INTRODUCTION

Brinjal (*Solanum melongena* L.), of the family Solanaceae is the most common, popular and principal vegetable crop grown in many parts in India. Brinjal is of considerable economic importance to India, Nigeria and across West African Sub-region (Olatunji, 6). The area under cultivation of brinjal is estimated at 0.51 m. ha with total production of 8,200,000 Mt (FAO, 2005, http:/ faostat.fao.org). Brinjal is usually self-pollinated, but as high as 48% cross-pollination has been reported and hence it is often known as a cross-pollinated crop, cross-pollination take place by insects due to heteromorphic flower structure called as heterostyly. There are three main botanical varieties under the species *melongena*. The round or egg-shaped cultivars are grouped under var. *esculentum.* The long, slender types are included under var. *serpentinum* and the dwarf brinjal plants are put under var. *depressum.* The common brinjal, to which the large fruited forms belong, is known under the name S. *melongena* var. *esculentum.* Among the 22 Indian species in the genus *Solanum,* there is a group of 5 related ones, all prickly and diploids *viz*., S. *melongena* L., *S. coagulans* (syn: *S. incanum* L.), *S. xanthocarpum, S. indicum* L. and *S. maccani.* It appears that *S. melongena* is more closely related to *S. incanum* as compared to any other species. *S. melongena* is readily crossable with *S. incanum.*

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Varietal identification and techniques to assess cultivar homogeneity are important for seed production, germplasm maintenance, crop certification and registration. The new brinjal varieties created from the restricted gene pool are likely to be genetically quite similar and hence difficult to differentiate morphologically. Therefore, genetic identity of varieties is necessary for maintaining germplasm and planning of breeding programme to suit to varied environments.

Somatic chromosome number 2*n* = 24, 48, 58, 60 (Okoli, 5) established aneuploids 2*n* = 54, 66 or *n* = 18, 36 (Bir and Neelam, 1). However, the detail karyotype and RAPD analysis of brinjal of Indian origin is meager. Several chromosome reports described both the somatic and gametic counts without detailed karyotypic study. Ugborogho and Oyelana (13), and Omidiji (7) opined that the dearth of information on emerging structural differences in genomes of different varieties of brinjal may have been responsible for hybridization failures recorded among few species within the genus.

Consequently, that lack of sufficient information about the nature and extent of structural changes in chromosomes make this study imperative. In this paper an attempt has been made for studying detailed karyotype and somatic chromosomes number as well as randomly amplified polymorphic DNA (RAPD) in five varieties of brinjal developed at the Orissa University of Agriculture and Technology, Bhubaneswar to delineate the structural differences if any at varietal level so as to facilitate crossing of genetically superior genotypes in

crop improvement programmes through conventional breeding.

MATERIALS AND METHODS

Seeds of five new brinjal varieties namely var. Utkal Tarini, Utkal Keshari, Utkal Madhuri, Utkal Jyoti and Utkal Anushree (released at National or State levels) developed at OUA&T, Bhubaneswar were grown in the experimental greenhouse following the recommended cultural practices (Table 1). Fresh healthy root tips from each variety were pretreated in saturated solution of para-dichlorobenzene with aesculine at 18°C for 3h followed by overnight fixation in 1:3 acetic acid: alcohol. Chromosomes were stained overnight in 2% aceto-orceine after cold hydrolysis in 5N HCl for 5 min. and were squashed in 45% propionic acid. Ten well scattered metaphase plates from each genotype were selected for karyotype analysis. Detail karyotype analysis was made following Das and Mallick (3). A general description of the representative types of chromosomes (Fig. 1) were rated as; Type A: Chromosomes are medium sized with two constrictions in nearly median to median and nearly sub median to sub median in position respectively; Type A': Medium sized chromosomes with two constrictions comprised with nearly sub-median and another is on nearly terminal positions respectively; Type B: Chromosomes are medium to small with nearly median to median primary constrictions; and Type C: Medium to small chromosomes with nearly sub median to sub terminal primary constrictions.

The mean values of total genomic chromosome length and total genomic chromosome volume with standard error were calculated.

RESULTS AND DISCUSSION

Detailed analysis of five brinjal varieties showed 2*n* = 24 somatic chromosome numbers in all the genotypes (Figs. 2 to 6). On the basis of the size of the chromosome and the position of the constrictions, a number of chromosome types were found to be common with the genotypes studied though they differed from each other in the minute structural details of the karyotype. Though all the four types of chromosomes were present, numerical differences were most prominent among the studied genotypes. The karyotype formula of all the genotypes revealed definite differences in the chromosome structure. Type A chromosomes with secondary constrictions were present in all the genotypes except var. Utkal Madhuri, which had 4 Type A chromosomes. Two additional secondary constricted Type A' chromosomes were present in var. Utkal Tarini and Utkal Madhuri. Type B were present in all the varieties but the dose difference was very much evident; the maximum number of Type B chromosomes were recorded in var. Utkal Jyoti (20 in number) followed by var. Utkal Anushree (18 in number), var. Utkal Madhuri (16 in number), var. Utkal Keshari (14 in number) and var. Keshari (8 in number). Furthermore, the number of Type C of chromosomes were very less in all the genotype as compared to Type B chromosomes that was 4 in var. Utkal Anushree and Utkal Madhuri a green pigmented fruit bearer where as the number of Type C chromosomes were 8 in var. Utkal Keshari and 12 in var. Utkal Tarini having light purple fruit colour (Table 1).

Detailed analysis of the somatic complements and the different genomic characteristics showed genotype specific variations in chromosome structure (Table 1). The total genomic chromosome length and volume varied from 82.54 to 94.24 µm and 42.51to 48.53 µm^3 in var. Utkal Anushree and Utkal Tarini, respectively. The average length and volume of chromosomes varied from 3.44 to 3.93 and 1.77 to 2.02 µm accordingly (Table 1). The centromeric index in the chromosomes of all the genotypes varied from 42.22% in var. Utkal Tarini to 48.45% in var. Utkal Jyoti. Significant variations in chromosome length, volume and TF% were observed among the studied brinjal genotypes as per the analysis of variance.

Table 1. Comparative genomic parameters and genome characteristics in five varieties of brinjal.

Variety	2n	Karyotype formula	NSC	Genomic chrom-osome length (mm ± SE)	Genomic chrom-osome volume (mm^3 ± SE)	Total form perce-ntage (m± SE)	Average chrom-osome length (mm)	Average chrom-osome volume (mm^3)
Utlakal Anushree	24	2A+18B+4C	2	82.54±0.25	42.51±0.11	47.24±0.09	3.44	1.77
Utkal Jyoti	24	2A+20B+2C	4	92.62±0.22	47.70±0.22	48.45±0.11	3.86	1.99
Utkal Madhuri	24	4A+2A'+16B+4C	6	84.52±0.27	43.52±0.20	46.34±0.08	3.52	1.81
Utkal Keshari	24	2A+14B+8C	4	90.26±0.32	46.48±0.19	43.25±0.13	3.76	1.93
Utkal Tarini	24	2A+2A'+8B+12C	4	94.24±0.14	48.53±0.15	42.22±0.12	3.93	2.02

NSC= Number of secondary constricted chromosomes.

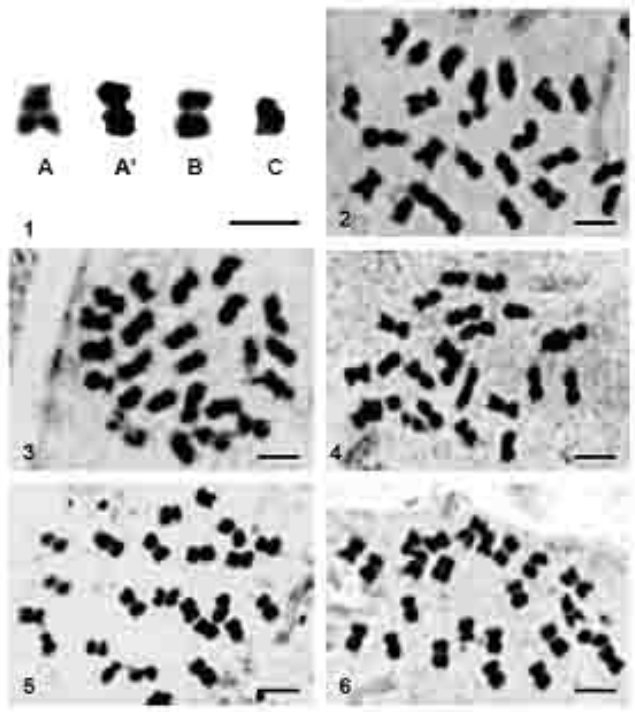

Fig. 1. Standard type of chromosomes in genomic setup of *Solanum melongena*.

Fig. 2-6. Metaphase chromosomes of different brinjal varieties showing 2*n* = 24 chromosomes.
(2.var. Utkal Anushree, 3. var. Utkal Jyoti, 4. var. Utkal Madhuri, 5. var. Utkal Keshari, and 6. var. Utkal Tarini, (Bar=10 ìm)

Patterns of karyotype are increasingly being used in assessing phylogenetic relationships among different species (Pringle and Murray, 9; Pandit and Babu, 8). Basically, the karyotype of these species consisted mostly metacentric and submetacentric chromosomes. However, few subt-elocentric chromos-omes were encountered. The total chromosome length and volume varied significantly among the varieties. Detailed karyotype analysis revealed the highest number of Type B chromosomes and lowest number of Type C chromosomes in var. Utkal Jyoti which might be a typical varietal character which distinguish this variety from other. Total F% analysis showed asymmetric karyotype having median to nearly median chromosomes with a moderate fluctuation of F% values from 42.22 to 43.25% in var. Utkal Tarini and Utkal Jyoti. The gradual alterations and shifting of TF% values might be due to the chromosomal alteration in the genome. It was suggested from the karyotype that var. Utkal Anushree and Utkal Madhuri having green colour fruit might have originated from a same progenitor with much more similarity in genomic setup which got reflected in the morphological characters. Where as var. Tarini and Keshari showed closeness with their genomic setup with purple colour fruits and var. Utkal Jyoti might have developed from any of these two varieties. The structural alterations in the chromosome morphology as well as variations of secondary constricted chromosomes in the genotypes might be due to duplication of chromosomes or translocations between the chromosomes with or without secondary constrictions at a very early stage of evolution (Pringle and Murray, 9; Saghai-Maroof *et al*., 12). Total chromosome length and volume differed markedly among the genotypes. Minute observations showed a proportional increase in chromosome length with an increase in chromosome volume. A correlation coefficient of 0.72 was found between the total chromosome length and total chromosome volume suggesting a high interdependence between them at the varietal level. These facts indicate the predetermined genetic control of chromosome coiling. Evidently, differences in chromosome length or chromosome volume were due to differential condensation and spiralization of the chromosome arms. In addition, the variety specific compaction of DNA threads along with nucleosomes or the additional gene sequences with altered non-histone proteins in the chromosome played an important role in the chromosomal architecture of the genotypes (Chattopadhyay and Sharma). Ugborogho and Oyelana (13), and Omidiji (7) shared the same view. As a consequence, the unredu-ced gametes that may have arisen from irregular meiosis gave rise to series of aneuploids, and hence, evolution of new chromosome races. This was achie-ved as unreduced pollen became successfully incorp-orated into any of the regular diploids through hybrid-ization. Several workers including Ugborogho and Oyelana (14) studied various chromos-ome configurations at meiosis to establish relation-ship among related species of angiosperms. Knapp (4 had earlier identified a number of hybrid swamps and concluded that this was a comm-on occurrence in the genus. It is pertinent to draw attention to the several ongoing attempts at improving the agronomic qualities of few domesticated species through intraspecific hybridization. This practice will continue to bring about changes in chromosome forms and unstable genomes in the genus.

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