

CHROMOSOME PAIRING BEHAVIOUR STUDY IN ALLODIPLOID AND ALLOTRIPLOID SORGHUM HYBRIDS

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Meiotic analysis was done in a fodder sorghum variety CO-27 ($2n=20$), a wild species *Sorghum halepense* ($2n=40$) and the F_1 hybrid between them. The chromosome pairing behaviour in F_1 's revealed a greater degree of homology between the two genomes *S. bicolor* and *S. halepense*. Further laggards and bridges were found in the F_1 's which may be responsible for the partial sterility of F_1 hybrids.

Keywords: Sorghum, interspecific hybrids, meiosis.

Introduction

Sorghum (*S. bicolor*) belongs to the family Graminae which consists of many species at different ploidy levels. Several 30-chromosome hybrids between *S. bicolor* ($2n=20$) and *S. halepense* ($2n=40$) have been reported¹⁻³. Cytogenetic study of interspecific hybrid is a tool for studying the genome homology and origin of the parental species. In this context, meiosis study is a reliable method rather than karyotype analysis for understanding the genome homology. Based on the above background the present study was formulated using interspecific hybrids to study the genome homology between species and to find out the reason for partial fertility in the F_1 of the interspecific hybrid.

Materials and Methods

The experimental material consists of immature anthers from a diploid fodder sorghum variety namely CO-27 (interspecific hybrid derivative between *S. bicolor* cv. CO-11 ($2n=20$) and *S. halepense* ($2n=20$), a tetraploid wild species namely *S. halepense* ($2n=40$) and the F_1 hybrid between them. The spikelets containing immature anthers were fixed at 8.40 AM in 1:3 acetic acid - ethanol fixative. After 24 hours, the anthers were removed and squashed with 1% acetocarmine. The chromosome pairing behaviour was

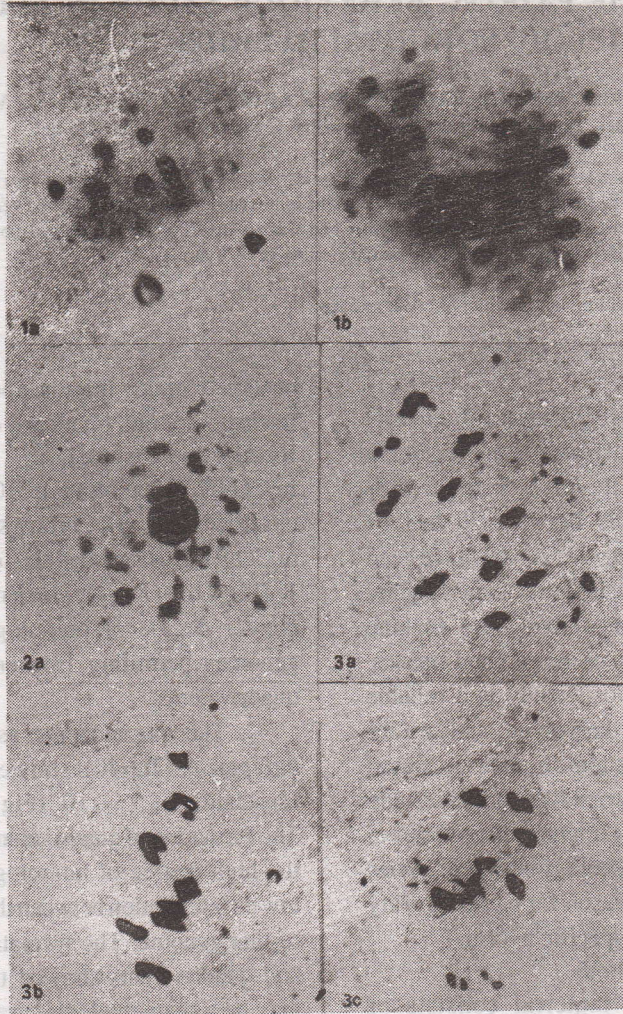
observed under microscope based on the formation of uni, bi, tri and quadrivalents.

Results and Discussion

In CO-27, a maximum of 10 bivalents were observed (Fig 1.a). Chromosome association in CO-27 also revealed the formation of $8_{ii} + 1_{iv}$ (Fig 1.b) or $3_{iv} + 4_{ii}$ which may be due to the greater degree of homology between the genomes permitting frequent formation of quadrivalents.

The chromosome association in *S. halepense* ($2n=40$) showed a maximum association of $5_{iv} + 10_{ii}$ (Fig 2.a) or $6_{ii} + 7_{iv}$. The formation of quadrivalents may be due to the high degree of homology or extremely low differentiation between the chromosomes of that genome. The formation of bivalents and quadrivalents showed that this species may be a segmental allotetraploid involving two closely related genomes which have a high degree of homology between them. The presence of homology between the chromosomes of *S. halepense* itself was reported⁴.

The allotriploid F_1 hybrid between CO-27 and *S. halepense* was found to contain 30 chromosomes⁵. The chromosome association study revealed the formation of 10_{iii} (Fig 3.a) or $7_{iv} + 1_{ii}$ (Fig 3.b) or $6_{iv} + 1_{ii} + 4_1$ (Fig 3.c). Most of the authors reported that the frequency



of trivalent formation is higher than the quadrivalent formation⁶. However in this study, the occurrence of quadrivalent formation was more which may be due to the structural homology between the genomes of the two species on the one hand and also due to the homologous nature of chromosomes in the Halepense genome itself.

Further, the occurrence of higher extent of laggards and bridges were also noticed during anaphase I (Fig 3.d) which may be

responsible for the partial fertility (26%) of the hybrids.

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