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Cytogenetic Studies In Interspecific Derivatives Of Sunflower (*Helianthus* Spp.)

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ABSTRACT

Wild sunflower species are potential sources of desirable genes in breeding for resistance to pathogens as well as high protein and oleic acid content. The possibility of using them in sunflower breeding was studied by the analysis of meiosis and pollen viability in the interspecific derivatives (prebred sunflower lines) of wild diploid annual *Helianthus* species (2n=34) with cultivated sunflower (*Helianthus annuus* L.). Twenty four prebred lines derived from interspecific hybridization between four wild annual diploid *Helianthus* species *viz., H. argophyllus, H. petiolaris, H. annuus* and *H. debilis* and cultivated sunflower were characterized using cytogenetic tools. The prebred lines showed morphological similarity with cultivated sunflower for several quantitative characters, but exhibited a wide range of pollen fertility (80.2% - 96.2%). The somatic chromosome number of all the lines was 34 (diploid). Most of the meiocytes showed predominantly bivalents (15-17). Univalents (0-6), trivalents (0-2) and quadrivalents (0-3) were also recorded in addition to normal bivalents during diakinesis and metaphase I. Some unique shaped bivalents were noticed in addition to frequent ring and rod shaped bivalents. Presence of chromosome bridges, laggards and micronuclei in the later stages of meiosis were observed in a few meiocytes.

INTRODUCTION

Interspecific hybridization offers a lot of scope for broadening the genetic base of cultivated sunflower. Wild sunflowers are distantly related to cultivated sunflower and possess considerable genetic variability for most economic and agronomic characters, insect and disease resistance and seed quality factors Seiler (1992). The genus *Helianthus* includes 49 species and represents a polyploid complex that contains diploid (2n=34), tetraploid (2n=68) and hexaploid (2n=102) species and among them 12 were annual and 37 were perennial species (Rogers *et al*., 1982). The diploid group is particularly interesting as a potential source of resistance to several sunflower diseases, cytoplasmic male sterility, high protein and oil content Prabakaran and Sujatha (2000). The use of wild sunflower species in sunflower improvement is frequently obstructed by genome incompatibility, genetic distance, increased chromosome number and aberrations in tetraploid and hexaploid species during meiosis leading to sterility. Cytogenetic analysis should reveal some of the problems occurring in interspecific hybridization including different ploidy levels of the species used and intraspecific chromosome structural differences.

MATERIALS AND METHODS

The materials for the present investigation comprised of 24 prebred sunflower lines derived from the interspecific crosses between cultivated sunflower (*Helianthus annuus* L.) and four wild diploid annual species *viz., H. argophyllus, H. petiolaris, H. annuus* (wild), *H. debilis* and trispecific crosses involving *H. argophyllus, H. annuus* (wild) and *H. annuus* (cultivated). These lines were developed through interspecific hybridization followed by a limited number of backcrosses with cultivated sunflower to eliminate the undesirable wild characters and intermating of desirable plants in each family to avoid further loss of desirable genes of wild species. The experimental material was socon in the research farm of Directorate of Oil Seed Research, Hydrabad, During Rabi 2001.

Pollen viability was studied by the method of Alexander (1969). The method was based on the differential staining property of fertile and sterile pollen grains. Pollen from non-dehiscent anthers were taken from randomly selected prebred lines and suspended in a drop of stain. Fertile and sterile pollen grains were counted and pollen fertility was expressed as percentage of total pollen grains.

Meiosis was studied at diakinesis, metaphase I, anaphase I and telophase II in acetocarmine preparations of pollen mother cells (PMC). Anthers were fixed in Carnoy's II (6:3:1 : Ethyl alcohol, chloroform and glacial acetic acid) solution. Staining was performed in 1 per cent acetocarmine stain. Observations were made on squash preparations. Meiotic chromosome associations were recorded and their weighted average was calculated in relation to total number of PMC's studied. Meiotic irregularities were observed and expressed in per cent.

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