



A report on a paracentric inversion in *Withania somnifera* (L.) Dun.

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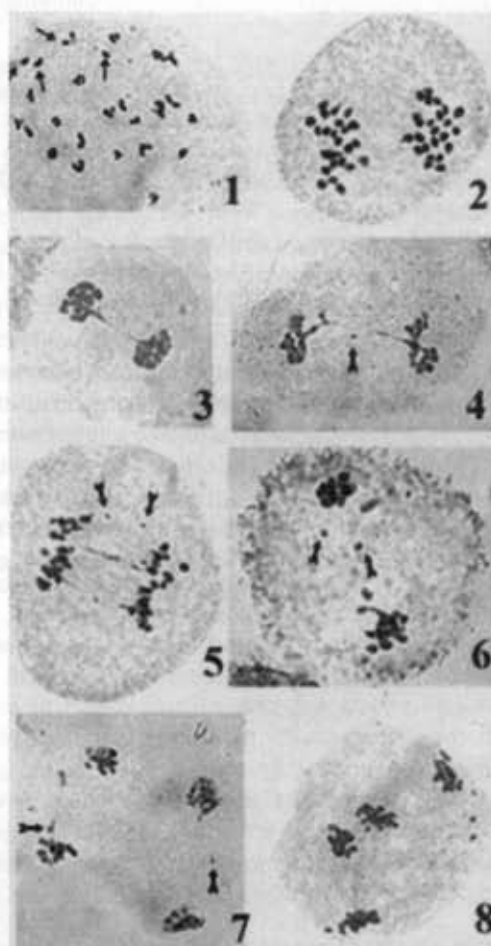
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Cytogenetical studies in *Withania somnifera* (L.) Dun., an important evergreen tomentose shrub belonging to the family Solanaceae with immense therapeutic uses including anticancerous [1] and antioxidant [2] properties, is restricted to chromosome counts only and has been reported to be variable as $2n = 24$ [3], 48 [4] and 72 [5]. From the seed stock of *Withania somnifera* (L.) Dun. (Neemuch cultivar : MPST No. NH-II/ XVIII/946, obtained from Agri-Horticultural Society of India) plants were raised in the experimental field of Kalyani University and a plant possessing characteristic configurations of paracentric inversion [6] at anaphase I and II was identified (1 out of 26 plants scored cytologically) and has been described in the text.

The marked plant attaining a height of 78.0 cm at maturity bore higher number of fruits (464 berries with 6.47% abortive ones, standard normal: 218.8 ± 35.6 berries per plant, abortive - 0.0%) but these fruits yielded ($t = 9.61$ at 33 DF, p value > 0.001) lower number of seeds (range: 5 to 14, mean: 8.1 ± 0.6) as compared to standard normal (range: 14 to 28, mean: 20.5 ± 1.2).

Meiotic analysis (flower buds fixed between 5:30 to 6:30 A.M. in Carnoy's fluid for 48 to 72 h and preserved in 70% alcohol; PMCs and pollens stained in 1% propionocarmine solution; fully stained pollen grains considered as fertile) in the marked plant ($2n = 48$) revealed mostly the formation of bivalents ($22.7 \text{ II} + 2.6 \text{ I/cell}$, 56 cells scored) at diplotene (Fig. 1) and metaphase I as was observed in standard normals ($23.8 \text{ II} + 0.30 \text{ I/cell}$, 496 PMCs assessed; data pooled over 5 randomly selected plants). In standard normal plants, about 95.9% (492 cells scored) of AI cells were cytologically (Fig. 2) balanced (24/24) with rare formation of bridges (0.81%) and lagging (1-2) chromosomes (3.2%); however, pollen fertility was very low (34.7%, 985 pollen grains examined). The marked plant demonstrated relatively high frequency of formation of bridges and fragment(s) at AI (Figs. 3-6) and AII (Figs.



Figs. 1-8. Meiotic chromosomes in *Withania somnifera*. 1. 22 II + 4 I at diplotene ($2n = 48$), 2-6. AI configurations, 2. 24/24 segregation of chromosomes, 3. Bridge formation, 4. Bridge with a fragment, 5. Double bridge with two fragments, 6. Double fragments, 7-8. AII configurations, 7. Double bridge with 2 fragments, 8. Two fragments. Univalents (\rightarrow) and fragments (\dashrightarrow) are marked.

7-8) stages and was characterized as an inversion heterozygote. Different configurations have arisen at anaphase I as a consequence of the possibility and

number of chiasma formation within the inversion loop and in the region between inverted segment and the centromere [7].

In the heterozygote, single bridge with an acentric fragment was predominant both at AI and AII stages followed by cells with single and double fragment(s). Fragments were consistent in sizes ($2.0\mu \times 1.98\mu$). The AI configurations (Table 1) have been used to estimate expected pollen abortion frequency in the heterozygote reflecting the amount and kind of crossing over within the inversion loop [8] and was calculated to be 12.1%. However, very high observed pollen abortion frequency (68.34%; 319 pollens examined) depicted the possible influence of some genetical and/or environmental factors.

Table 1. Types and frequency of AI and AII configurations in the inversion heterozygote in *Withania somnifera*

Meiotic divisions	No. of cells scored	Configurations (%)					
		NB	B	BF	F	BBFF	FF
Anaphase I	442	80.3	3.2	8.4	3.6	0.5	4.1
Anaphase II	268	82.8	1.5	6.7	5.2	0.7	3.0

NB = No bridge; B = bridge; BF = bridge with a fragment; F = single fragment; BBFF = double bridge with 2 fragments; FF = double fragments.

In *Withania somnifera* there is an extreme degree of variability with respect to growth habit and morphological characteristics [9]. Intrachromosomal gene rearrangement through paracentric inversion may account for such widespread intraspecific variability and polymorphism. Further, paracentric inversion may be exploited for designing wide varieties of genetical experiments in the species.

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