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MEIOTIC ANALYSIS OF F1 HYBRIDS AMONG TEOSINTES

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The association of homologous or homeologous chromosomes in the meiotic behaviour of F1 hybrids reveals the relative affinity between genomes of parental species. Chromosomal rearrangements and genetic incompatibilities producing abnormal meiosis (abnormal spindle, laggard chromosomes, among others) acting as reproductive isolation mechanisms, could also be detected. In the present work the genome affinities based on the chromosome association of seven artificial hybrids among teosintes are discussed. Moreover, pollen stainability is reported.

Artificial crossings between teosintes were carried out in the greenhouse to obtain the F1 hybrid plants. The taxa using as parental differs in chromosome sizes and total DNA amounts: *Zea mays* ssp. *mexicana* ($2n=20$; $2C=6.79\text{pg}$), *Zea mays* ssp. *parviglumis* ($2n=20$; $2C=5.86\text{pg}$), *Zea luxurians* ($2n=20$; $2C=8.83\text{pg}$), *Zea diploperennis* ($2n=20$; $2C=6.36\text{pg}$) and *Zea perennis* ($2n=40$; $2C=11.36\text{pg}$) (Tito *et al.*, 1991, TAG 83:58-64). Young panicles from each F1 hybrid were fixed in a 3:1 solution of absolute ethanol: acetic acid and squashed in 2% acetic haematoxylin. Normal (stained) and aborted (unstained) pollen grains were distinguished using Alexander's stain (Alexander 1969, *Biotech Histochem* 44:117-122).

Table 1 shows the meiotic configurations and pollen stainability of the studied F1 hybrids.

The hybrids with $2n=20$ involving *Z. luxurians* as one of the parental presented: heterozygosity for heterochromatic blocks at pachytene; 5 to 10 heteromorphic bivalents,

univalents with different sizes and two asynchronous groups of 5 bivalents each at diplotene-metaphase I. At anaphase I, a maximum of 10 laggard chromosomes were observed, some of them with early separation of their chromatids. Particularly, the meiotic behaviour of the F1 hybrids *Z. luxurians* x *Z. m. ssp. parviglumis* revealed differences in paracentric inversions among parentals, since up to 3 bridges with fragments were recorded at anaphase I. The lack of pairing and the presence of heteromorphic bivalents are probably due to partial homology among chromosomes, and/or differences in DNA content and chromosome sizes between the parental species.

Z. m. ssp. parviglumis x *Z. diploperennis* hybrids show, at diakinesis-metaphase I, 10 bivalents as the most frequent configuration and two asynchronous groups of 5 bivalents each. Moreover, evidences of abnormal spindles at anaphase I and citomixis (cell fusion) were frequently detected. The low viability of pollen, jointly with evidence of citomixis detected suggests the existence of genetic incompatibility between the two parent species.

The hybrids with $2n=30$, *Z. perennis* x *Z. luxurians* and *Z. perennis* x *Z. diploperennis*, showed 5III+5II+5I as the more frequent meiotic configuration, with trivalents type "fry-pan" and homomorphic bivalents.

Summarizing, the variation in total genomic DNA content among the progenitor species of the analyzed hybrids, which reflects differences in chromosome sizes, explains the high frequency of heteromorphic bivalents and univalents of different sizes detected, particularly when *Z. luxurians* is involved as one of the parental species. The presence of bridges and fragments in the hybrids indicate differences in structural rearrangements (paracentric inversions) between parents. The low pollen viability is probably due to structural/genic differences between parents, responsible for the postcigotic reproductive isolation detected among them.

These results show that the genomic relationships between teosintes, revealed through of meiotic behavior of their F1 hybrids, are relevant in the study of genome organization and diversification of the genus *Zea*.

Hybrids	(2n)	III (X±SD) (range)	II (X±SD) (range)	I (X±SD) (range)	Most frequent configurations (%)	N° of cells	Pollen stainability (%)
<i>Z. m. ssp. parviglumis</i> x <i>Z. m. ssp. mexicana</i>	20	-	9.83 ± 0.38 (9-10)	0.33 ± 0.0 (0-1)	10 II (83%)	77	84%
<i>Z. luxurians</i> x <i>Z. diploperennis</i> (1)	20	-	8.65 ± 0.12 (7-10)	2.7 ± 0.23 (0-6)	9 II + 2 I (38%) 8 II + 4 I (45%)	84	5%
<i>Z. luxurians</i> x <i>Z. m. ssp. parviglumis</i>	20	-	9.16 ± 0.96 (5-10)	1.68 ± 1.59 (0-10)	10 II (45%) 9 II + 2 I (33%)	145	7%
<i>Z. luxurians</i> x <i>Z. m. ssp. mexicana</i>	20	-	7.5± 1.34 (5-10)	5 ± 2.44 (0-10)	8II + 4 I (36%)	67	7.25 %
<i>Z. m. ssp. parviglumis</i> x <i>Z. diploperennis</i>	20	-	9.49± 0.56 (8-10)	1.01 ± 0.51 (0-4)	10 II (52%) 9 II + 2 I (44%)	63	6%
<i>Z. diploperennis</i> x <i>Z. perennis</i> (2)	30	4.91 (1-8)	5.25 (2-10)	4.73 (2-8)	5 III + 5 II + 5 I (40%)	168	2%
<i>Z. luxurians</i> x <i>Z. perennis</i> (1)	30	5.26 ± 0.19 (3-8)	4.76 ± 0.23 (2-8)	4.70 ± 0.20 (2-7)	5 III + 5 II + 5 I (37%)	46	2%

Table 1: Meiotic configurations of the F1 artificial hybrids. I: Univalents. II: Bivalents. SD: Standard deviation. III: Trivalents. (1): From Poggio *et al.*, *Genome* 42:993-1000, 1999. (2): From Naranjo *et al.*, *Acad. Nac. Cs. Ex. Fis. Nat.*, Buenos Aires, Monogr. 5:43-53, 1990.