

44. Genome analysis of the genus *Eremopyrum*

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Morphological and cytogenetical studies of *Eremopyrum*, a genus of the tribe Triticeae, were carried out in 13 different interspecific hybrids among three strains of two diploid species, *Er. buonapartis* (Spreng.) Nevski and *Er. triticeum* (Gaertn.) Nevski and nine strains of two tetraploid species, *Er. buonapartis* and *Er. orientale* (Linn.) Jaub. et Spach.

The main characteristics of the hybrids were as follows: (1) vigorous growth of hybrids, and normal tillering and flowering; (2) intermediate spikelet characters of the hybrids between parents; (3) very high pollen

Table 1. Average chromosome pairing per cell in the PMCs of interspecific *Eremopyrum* hybrids

Cross combinations (♀ × ♂)	No. of cells observed	Average chromosome pairing per cell		
		III	II	I
<i>Er. buonapartis</i> (4x) × <i>Er. buonapartis</i> (2x):				
7034 × 7035	189		6.95	7.11
<i>Er. buonapartis</i> (4x) × <i>Er. triticeum</i> (2x):				
7031* × <i>Er. trit.</i> -1	156		1.37	18.27
7032 × "	306	0.01	1.35	18.30
7033 × "	183		0.97	19.06
7034 × "	408	0.02	1.13	18.70
7034 × <i>Er. trit.</i> -2	139	0.02	1.73	17.48
7036 × <i>Er. trit.</i> -1	115		0.97	19.05
7038 × "	425	0.01	1.35	18.28
7042 × "	273		0.76	19.48
7043 × "	346		1.01	18.70
<i>Er. buonapartis</i> (4x) × <i>Er. orientale</i> (4x):				
7034 × 7037	276		6.22	15.55
<i>Er. orientale</i> (4x) × <i>Er. buonapartis</i> (4x):				
7037 × 7042	445	0.00	6.62	14.76
<i>Er. orientale</i> (4x) × <i>Er. triticeum</i> (2x):				
7037 × <i>Er. trit.</i> -1	725	0.00	6.82	7.34
<i>Er. distans</i> (2x) × <i>Er. triticeum</i> (2x)**:				
7041 × <i>Er. trit.</i> -2	263	0.01	0.70	12.59

* As to spikelet morphology this strain closely resembles *Er. orientale*.

** SAKAMOTO and MURAMATSU (1963).

sterility and complete seed sterility in all hybrid combinations.

Hybrids' average chromosome pairing per cell at MI of PMCs is shown in Table 1. From these data, the following conclusions are drawn: (1) the genome of diploid *Er. buonapartis* is found in tetraploid *Er. buonapartis*; (2) the genome of diploid *Er. triticeum* occurs in *Er. orientale*; (3) a common genome is shared by tetraploid *Er. buonapartis* and *Er. orientale*.

The morphological characteristics and chromosome pairing of F_1 hybrids between the diploid species *Er. distans* (C. Koch) Nevski and *Er. triticeum* had been previously examined (SAKAMOTO and MURAMATSU 1963). Also a karyotypical comparison had been previously carried out for diploid and tetraploid *Er. buonapartis*, *Er. distans* and *Er. orientale* (SAKAMOTO and MURAMATSU 1965). From those and the present studies, it is assumed that the tetraploid *Er. buonapartis* has originated from an amphidiploid between diploid *Er. buonapartis* and *Er. distans*, while the tetraploid *Er. orientale* was derived from an amphidiploid between *Er. distans* and *Er. triticeum*.