

Estimation of the coefficient of double-reduction in autotetraploid lucerne

R. Ayadi, P. Barre, C. Huyghe and B. Julier

INRA, Unité de Génétique et d'Amélioration des Plantes Fourragères, 86600 Lusignan, France

E-mail: julier@lusignan.inra.fr

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Introduction Polyploidy plays an important role in the evolution of species and many cultivated species, particularly in angiosperms, are polyploids (Bever and Felber, 1992; Gallais, 2003). Autopolyploid species that show a tetrasomic inheritance have complex genetics. However, some theoretical models were built for: (1) genetic mapping (Hackett *et al.*, 1998), (2) quantitative genetics (Gallais, 2003) and (3) population genetics (Ronfort *et al.*, 1998). But in practice, most data analyses ignore one essential feature of tetrasomic inheritance that is double-reduction. Indeed, in an autotetraploid species, homologous chromosomes can form tetravalents at meiosis. In this case, a double-reduction is observed if crossing-over occurs between a locus and its centromere, and if the sister chromatids migrate to the same pole at anaphase I. The gametes may, thus, carry a pair of sister alleles. Double-reduction frequency is represented by the index of separation (α) (Demarly, 1963; Mather, 1935; Mather, 1936). The parameter α is considered as a product of four probabilities: $\alpha = q e a s$ (Gallais, 2003) in which “q” is the probability of multivalent formation, “e” the probability of first equational division, related to the frequency of crossing-over, “a” is the probability of non-disjunction at first anaphase and “s” is the probability of having two sister chromatids in the same gamete. If separation during anaphase II is random, $s = 1/2$. Consequently, α will be low for a gene located in the vicinity of the centromere and will increase with distance between the gene and the centromere. It was demonstrated that double-reduction events alter the rate of progression towards equilibrium under inbreeding or under random mating, modify the recombination rate between loci and also alter the rate of decay of linkage disequilibrium under random mating (Bever and Felber, 1992). Current theoretical models allow drawing genetic maps taking into account double-reduction (Luo *et al.*, 2004). Thus, it is possible to estimate α for codominant loci in tetraploid species. To date, we have few estimates of the double-reduction frequency. Haynes and Douches (1993) on potato and Julier *et al.* (2003) on lucerne found that double-reduction occurs sporadically. In both studies, the low number of progenies hampered a precise estimation of α . The aim of our study was to estimate the frequency of double-reduction in a mapping population of lucerne that includes a large number of individuals.

Materials and methods A mapping population (Julier *et al.*, 2003) containing more than 1000 F1 individuals resulting from a cross between two parental genotypes (Magali 2 and Mercedes 4-11) was obtained. Four microsatellite markers were selected with two of them (MTIC103 and MAA660870) located at the ends of chromosome 8 and two others (AFct45 and MTIC289) located in the vicinity of the centromere of chromosome 7. Theoretical models for double-reduction estimation were applied (Hackett *et al.*, 1998; Luo *et al.*, 2004).

Results and conclusions Three of the microsatellite markers (AFct45, MTIC289 and MTIC103) showed four alleles and one null allele in the population, the fourth marker (MAA660870) had five alleles and one null allele. Detailed information was obtained on the double-reduction for these markers. The results are relevant to the low number of tetravalents observed at meioses (Armstrong, 1954) and the determination of double-reduction frequency allows a better understanding of the functioning of *Medicago sativa*.

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