ESTIMATION OF ALLELE FREQUENCIES IN TETRAPLOID POPULATIONS UNDER PREFERENTIAL PAIRING AND DOUBLE REDUCTION

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Recently, we presented a method for estimating allele frequencies in polyploids under disomic or polysomic inheritance (De Silva et al. 2005). This method, under polysomy, considered only the simple case where inheritance is by random chromosome segregation. While disomy and polysomy are the two extremes, a number of polyploids display a combination of both pairing behaviours. In genetic models this is described by the 'preferential pairing factor'. Even when pairing between arms of a set of more than two chromosomes are equally likely, chance alone can result in both bivalent and multivalent pairing. For instance, in a tetraploid with no preferential pairing one would expect equal numbers of bivalents and tetravalents. Furthermore, when polyvalents are formed cross-overs can happen between the locus and the centromere resulting in double-reduction gametes. The consequence of double-reduction is an increase in homozygous combinations of alleles both in the gametes and genotypes. Therefore, especially when the locus under consideration is away from the centromere, 'double-reduction' needs to be factored in to ensure allele frequency estimates are unbiased. In this paper we will present extensions of our estimation method to situations of preferential pairing and double reduction. We will verify the method, for the case of a tetraploid, by simulation.

De Silva HN, Hall AJ, Rikkerink E, McNeilage MA and Fraser LG (2005). Estimation of allele frequencies in polyploids under certain patterns of inheritance. Heredity 95: 327-334.