

THE STABILITY OF INSTABILITY: OCCURRENCE OF A FUNCTIONAL TELOMERASE IN THE HOLOCENTRIC CHROMOSOMES OF APHIDS

MONTI V.*, MANDRIOLI M.*, RIVI M.**, BIZZARO D.***, MANICARDI G.C.**

*) Dip. Biologia, Università di Modena e Reggio Emilia, Modena (Italy)

**) Dip. Scienze Agrarie e degli Alimenti, Università di Modena e Reggio Emilia, Reggio Emilia (Italy)

***) Dip. Scienze della Vita e dell'Ambiente, Ancona (Italy)

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The structure of the telomeres of four aphid species (*Acyrtosiphon pisum*, *Megoura viciae*, *Myzus persicae* and *Rhopalosiphum padi*), evaluated by Southern blotting and fluorescent *in situ* hybridization, revealed that each chromosomal end consists of the (TTAGG)_n repeat. The presence and the sequence composition of a telomerase coding gene has been verified in *A. pisum* genome, revealing that aphid telomerase presents about 20% sequence identity with the invertebrate and vertebrate homologues and possesses the two main domains involved in telomerase activity thus demonstrating that it is a functional enzyme. Interestingly, telomerase expression has been observed in different somatic tissues suggesting that in aphids the telomerase activity could be not restricted as in human cells. The study of telomeres in a *M. persicae* clone with chromosome number ranging from 12 to 17 even within each embryo, evidenced that aphid telomerase can initiate the *de novo* synthesis of telomere sequences at internal breakpoints resulting in the stabilization of the chromosomal fragments. Chromosome instability is a peculiar feature of malignant cells, whereas it is a very rare phenomenon in physiological situations and even more in whole organisms. The observed rearrangements involved prevalently X chromosome, but also autosomes 1 and 3. Literature data revealed that autosomes 3 and, more rarely, 1 are the chromosomes mostly involved in *M. persicae* karyotype variations. On the contrary fragmentations occurring at the X chromosomes are absolutely rare in aphids not only in natural populations, but also in X-ray irradiated specimens.

The random-breakage model of chromosome evolution has been the dominant paradigm for several years. However, further analyses suggested that recurrent breaks are found in fragile regions or hotspots so that the random breakage model required substantial reassessment in favour of models that put the architecture of the chromosomes in a pivotal position for revealing the molecular basis of chromosomal evolution among species. Several comparative mapping studies in a wide variety of closely related eukaryotes showed a relationship between large-scale chromosomal rearrangement and repetitive DNA. The nature of the repetitive DNA within these breakpoint regions varies significantly, from clusters of rRNA and satellite DNAs to various mobile elements. The *M. persicae* clone analysed showed chromosome fragmentations generally located within satellite DNAs clusters, which seem therefore to represent fragile sites that could be at the basis of the intraindividual chromosome fissions.

Experiments of male induction assessed that this *M. persicae* clone is an obligate parthenogenetic population. The holocentric nature of aphid chromosome could justify karyotype variations, whereas the reproduction by apomictic parthenogenesis, together with a higher

telomerase expression level, favoured the stabilization of the observed intraindividual chromosome instability.