Exploring the Role of a CENPBL Gene Family in Paramecium Genome Rearrangements

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Abstract

Paramecium tetraurelia harbors two distinct nuclei in its cytoplasm. The micronucleus (MIC, 2n) contains the germline genome that is transmitted to the offspring at each sexual cycle. The somatic macronucleus (MAC, _˜1600n), responsible for gene transcription, is destroyed during sexual processes while a new MAC differentiates from a copy of the MIC. During MAC development, _˜30% of the germline DNA is eliminated: transposable elements (TEs) and minisatellites are eliminated imprecisely, whereas 45,000 TE-derived Internal Eliminated Sequences (IESs), dispersed throughout the germline genome, are excised precisely from coding and non-coding regions to reconstitute functional genes. IES excision depends upon PiggyMac (Pgm), which cleaves DNA at IES ends, and five Pgm-like partners. We recently characterized the developmental timing of programmed DNA elimination (PDE) genome-wide and identified a distinct and reproducible elimination timing for IESs. We proposed that sequential PDE may provide *Paramecium* with a unique mechanism to fine-tune zygotic gene expression as PDE progresses. This hypothesis is illustrated by our discovery of a family of *CENPB-like* genes (*CENPBL*) which can only be expressed from the new MAC at an early stage of its development, because parts of their coding and/or regulatory sequences are excised at later stages by the IES excision machinery. *CENPBL* genes are therefore expressed only during the time window when IESs are present. CenpbL proteins share similarities with human CENP-B and its homologs, which derive from domesticated Pogo transposases and are involved in centromeric heterochromatin formation and TE silencing. Intriguingly, *Paramecium* CenpbLs have lost the DDE superfamily endonuclease domain, while retaining the CENPB-type DNA-binding HTH domain. We will present the results of RNA interference experiments designed to phenotypically characterize the effect of *CENPBL* knockdowns during MAC development and investigate their potential link with PDE.

Keywords: ciliates / programmed DNA elimination /domesticated transposases / CENPB, related proteins

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