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Research Article

Spliced-Leader *trans*-Splicing in Freshwater Planarians

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trans-Splicing, in which a spliced-leader (SL) RNA is appended to the most 5' exon of independently transcribed pre-mRNAs, has been described in a wide range of eukaryotes, from protozoans to chordates. Here we describe *trans*-splicing in the freshwater planarian *Schmidtea mediterranea*, a free-living member of the phylum Platyhelminthes. Analysis of an expressed sequence tag (EST) collection from this organism showed that over 300 transcripts shared one of two ~35-base sequences (Smed SL-1 and

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SL-2) at their 5' ends. Examination of genomic sequences encoding representatives of these transcripts revealed that these shared sequences were transcribed elsewhere in the genome. RNA blot analysis, 5' and 3' rapid amplification of cDNA ends, as well as genomic sequence data showed that 42-nt SL sequences were derived from small RNAs of ≈ 110 nt. Similar sequences were also found at the 5' ends of ESTs from the planarian *Dugesia japonica*. *trans*-Splicing has already been described in numerous representatives of the phylum Platyhelminthes (trematodes, cestodes, and polyclads); its presence in two representatives of the triclads supports the hypothesis that this mode of RNA processing is ancestral within this group. The upcoming complete genome sequence of *S. mediterranea*, combined with this animal's experimental accessibility and susceptibility to RNAi, provide another model organism in which to study the function of the still-enigmatic *trans*-splicing.

Key Words: spliced-leader RNA • *trans*-splicing • planarian • Platyhelminthes • *Schmidtea mediterranea* • *Dugesia japonica*

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