Sequence and secondary structure of 5.8S rRNA in the tick, *Ixodes scapularis*

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While sequence homology among eukaryotic 5.8S rRNAs is relatively high, even among distantly related organisms (1), the secondary structure of this region, although similarly conserved, does not rely completely on sequence integrity. That is, the functional folding pattern remains the same while utilizing different rRNA base pairs achieved through compensatory mutation. Ticks in the genus *Ixodes* share 5.8S rDNA sequence homology with other arthropods from which this region has been described (2,3) (Figure 1). Parsimony analysis of bases 1-122 and 131-157 from Figure 1 (first consensus base at 5'- and 3'-end of *Drosophila* 5.8S spacer), places the *Ixodes* outgroup squarely between clusters of *Culex*, *Drosophila* and *Bombyx*, *Acyrthosiphon*.

The secondary structure of the complex of 5.8S, 2S and the 5'-end of the 28S rRNAs has been described for *Drosophila* (4). Figure 2 illustrates the probable secondary structure of this region for *Ixodes*. While the structures predicted for the Dipteran and *Ixodes* complexes are similar, three major differences in nucleotide composition are evident. The *Ixodes* bases 28-31 are involved in the first stem (A) in Figure 2; in the proposed *Drosophila* secondary structure, these bases pair externally with a portion of the 28S region. *Ixodes* bases 61-88, composing a stem (B) of nine consecutive bases, compare with a seven base stem in *Drosophila*, while the loop size is identical for the two species. Bases 114-123 in the *Ixodes* complex form an eight base stem (C) with a single mismatch ending in a four base loop. The *Drosophila* stem, of similar length with one mismatch, results in a 30 base loop which is spliced out during rRNA processing to form the Dipteran 2S fragment (5). These features of the *Ixodes* 5.8S/28S complex serve to reinforce previous observations of general conservation of secondary structure regardless of overall sequence homology.

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REFERENCES