

Toll Evolution: A Perspective from Regulatory Regions

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Toll Evolution: A Perspective from Regulatory Regions

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Abstract:

Background: Toll and Toll-related proteins play an important role in antibacterial innate immunity and are widespread in insects, plants, and mammals. The completion of new genomes such as *Anopheles gambiae* has provided an avenue for a deeper understanding of Toll evolution. While most evolutionary analyses are performed on protein sequences, here, we present a unique phylogenetic analysis of Toll genes from the perspective of upstream regulatory regions so as to study the importance of evolutionary information inherited in such sequences. Results: In a comparative study, phylogeny on the protein products of Toll like genes showed consistency with earlier literature except for the single point of divergence between insects and mammals. On the other hand, the phylogeny based on upstream regulatory sequences (-3000 to +10) showed a broader distinction between the plants and the rest, though the tree was not well resolved probably due to poor alignment of these sequences. The phylogeny based on TFBS necessitated the development of a supervised statistical approach to determine their "evolutionary informativeness". Employing the frequency of evolutionarily informative TFBS, a phylogeny was derived using pair-wise distances. It suggested a closer relationship between *Anopheles* and plants than to *Drosophila* and a significant homology among mammalian TLRs. Conclusions: A unique approach of using TFBS in studying evolution of Toll genes has been developed. Broadly, this approach showed results similar to the protein phylogeny. The inclusion of the evolutionary information from TFBS may be relevant to such analyses due to the selective pressure of conservation in upstream sequences.

Description:

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