

# A Double Segment Periodicity Underlies Segment Generation in Centipede Development

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Dmsob HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKCAECGKGFCSRTLAVHKIL
Stmodr1 HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKCECGKGFCSRTLAVHKIL
Agodr1 HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKCECGKGFCSRTLAVHKIL
Dmbowl HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKCECGKGFCSRTLAVHKIL
Agodr2 HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKCECGKGFCSRTLAVHKIL
Dmodd HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKDKPFKSDCGKGFCSRTLAVHKVT
Agodd HERTHTDERPYSCDICGKAFRRQDHLRDHRYIHSKEKPFKSDCGKGFCSRTLAVHKVT
DmKr HERTHTGKPFECPECDKRFRTRDHHLKTHMLHTGKPFYHCSHCDRQFVQVANLRRHLRV
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Dmsob HMEESPCHKPVCNRSFNQRSNLKTHLLTHTDIKPYNCASCGKVFRRNCDLRRHSLTH
Stmodr1 HMEESPCHKPVCNRSFNQRSNLKTHLLTHTDIKPYNCPCGKVFRRNCDLRRHSLTH
Agodr1 HMEESPCHKPVCNRSFNQRSNLKTHLLTHTDIKPYNCIACGKVFRRNCDLRRHSLTH
Dmbowl HMEESPCHKPVCNRSFNQRSNLKTHLLTHTDHKPYECSSCGKVFRRNCDLRRHALTH
Agodr2 HMEESPCHKPVCNRSFNQRSNLKTHLLTHTDHKPYECNSCGKVFRRNCDLRRHALTH
Dmodd HLEEGPHKPIQRSFNQANLKSHLQSHSEQSTKEVVVTTSPATSHSVNQLSSP
Agodd HLEEAPHKTIQNRNFRANLKTHTMOSHSPQGSAGLPLGGSIPEQLDLEGDGDG
DmKr HTGERPYTCEICDGKFSNQLKSHMLVHTGKPFECERCHMKFRRRHMLMNHKCGI
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Figure S1. Amino Acid Alignment of the Three *odd-skipped* Related Genes from *Drosophila melanogaster* and from *Anopheles gambiae* with *Strigamia maritime odr1*; *Drosophila Krüppel* Is Shown as an Outgroup

To identify the orthology of the *Strigamia maritime odd-skipped* related gene, we collected amino acid sequences from public databases for genes of the *odd-skipped* family. These include *Drosophila melanogaster odd*, *sob*, and *bow1* and three previously unannotated genes from the *Anopheles gambiae* genome database (Ensembl accession numbers ENSANGP00000007133, ENSANGP00000016384, and ENSANGG00000023975). We used *Drosophila Krüppel* as an outgroup for the analysis.

The alignment shows that all of the *odd-skipped* family of genes include a highly conserved region encompassing four zinc finger motifs (highlighted in yellow; the sequence begins in the middle of the first zinc finger), whereas *Drosophila odd* (*Dmodd*) and one of the *Anopheles* genes (#16384, hereafter referred to as *Agodd*) lack the fifth zinc finger motif that is shared by the *Strigamia* gene and the remaining *Anopheles* and *Drosophila* genes (highlighted in pink). Residues unique to the *Strigamia* gene are highlighted in blue.

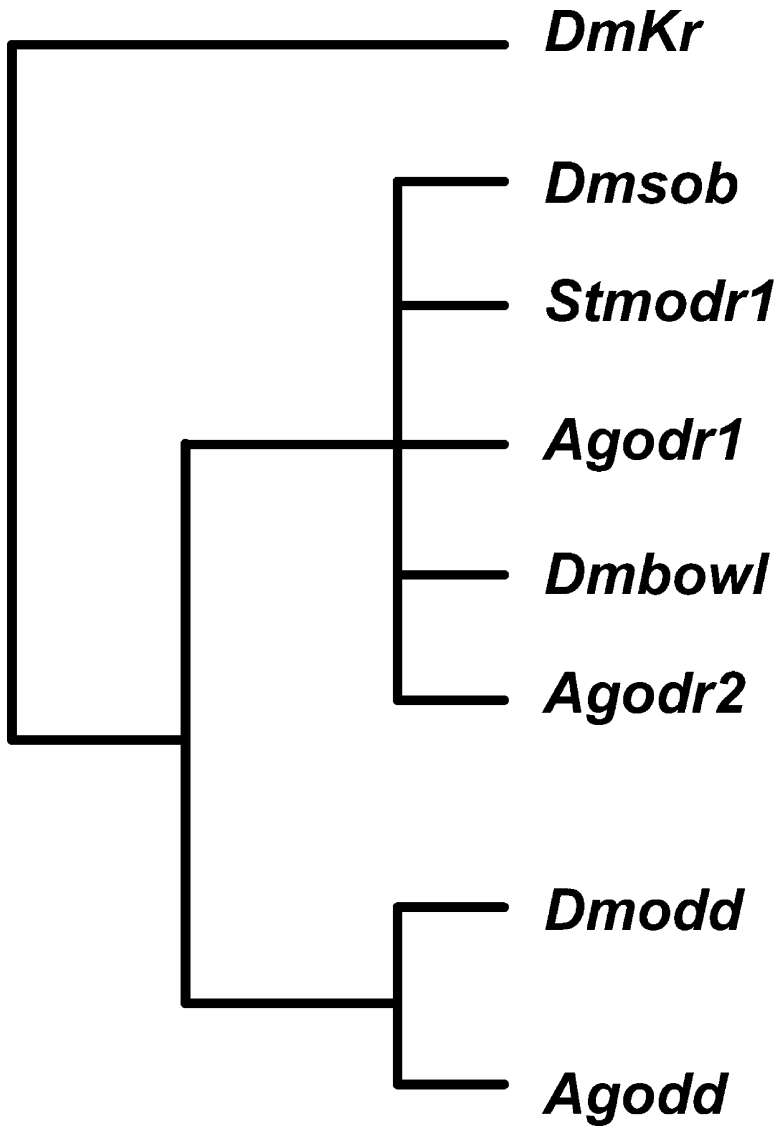


Figure S2. A Maximum Likelihood Tree Showing the Putative Relationships between the Different Members of the *odd-skipped* Gene Family

We generated a maximum likelihood tree, using Tree-Puzzle version 5.1. In the tree that was generated, *Dmodd* and *Agodd* are clearly seen to form one group, with *Drosophila sob* and *bowl* (*Dmsob*, *Dmbowl*), two of the *Anopheles* genes (#7133 and #23975, referred to as *Agodr1* and *Agodr2*, respectively), and the *Strigamia* gene (*Stmodr1*) forming a second group. The resulting tree is presented. It is important to point out that this is not a thorough phylogenetic analysis and the relations shown should be taken as tentative. Specifically, we do not know whether the *Anopheles* and *Drosophila odd-skipped* genes derive from a duplication that predates the insect-myriapod split or are simply a highly derived sequence, emerging relatively late within the *odd/bowl/sob* family of genes.