

**S1 Fig. Alignment of tryptophan 2,3-dioxygenase (TO) polypeptide sequences from various insect species.** TO polypeptide sequences from *Heliothis virescens* (PCG74852.1), *Spodoptera litura* (XP\_022823393.1), *Plodia interpunctella* (AAR24625.1), *Bicyclus anynana* (XP\_023952864.1), *Papilio polytes* (XP\_013141355.1), *Bombyx mori* (XP\_004922659.1), *Anopheles darlingi* (ETN63322.1), *Anopheles gambiae* (XP\_312204.2), *Aedes aegypti* (AAL37360.1), *Neodiprion lecontei* (XP\_015514842.1), and *Zootermopsis nevadensis* (XP\_021924784.1) were downloaded from National Center for Biotechnology Information and aligned using AlignX module of Vector NTI Advance 11.5 suite (Invitrogen). Identical amino acids are indicated by red text with yellow background. A block of similar amino acids are shown in black text with green background, conservative amino acids are shown in dark blue text, and non-similar amino acids are shown in black text. Alignment gaps are indicated by a hyphen (-). Tryptophan dioxygenase domain is underlined.

	1		80
<i>H. zea</i>	(1)	-MACPMRSALDESMACQEGDCILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>S. litura</i>	(1)	-MACPMRSMMDSSAQQEGNHILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>B. mori</i>	(1)	-MACPMRSALDEINGQEGAHILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>H. virescens</i>	(1)	-MACPMRSVMDDSTAQEGNHILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>P. interpunctella</i>	(1)	-MACPMRSMNDS--QGGSCILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-AHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>P. polytes</i>	(1)	-MACPMRSVMDDSGAQEGSHILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>B. anynana</i>	(1)	-MACPMRSVTDSSAQEGDHLILGNEAGMLYGEYLMLDKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFEVDS	
<i>A. aegypti</i>	(1)	-MSCPVGHNHGDP--QGGQRLGSEAGMLYGEYLMLDKLLSAQRMLSVESNKP-VHDEHLFIVTHQAYELWFKQIIFELDS	
<i>A. darlingi</i>	(1)	-MSCPVRSCFVDS-VQGGHHLGSEAGMLYGEYLMLDKLLSAQRMLSVEGKKP-VHDEHLFIVTHQAYELWFKQIIFELDS	
<i>A. gambiae</i>	(1)	-MSCPMRSCFVDS-VQGGHHLGSEAGMLYGEYLMLDKLLSAQRMLSVEGKKP-VHDEHLFIVTHQAYELWFKQIIFELDS	
<i>Z. navadensis</i>	(1)	MNSCVFTNGTDIS--QGEDQLDQGAGMLYGEYLQLDKILNQAQRMLSARTNHP-VHDEHLFIVTHQAYELWFKQIIFELDS	
<i>N. lecontei</i>	(1)	-MACPMRNGGEGDTSCQEGDQLTEGPMGLYGEYLRLLKLLSAQRMLSAESSKP-VHDEHLFIVTHQAYELWFKQIIFELDS	
	81		160
<i>H. zea</i>	(79)	<u>VRALLDVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRNYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>S. litura</i>	(79)	<u>VRALLDVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRNYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>B. mori</i>	(79)	<u>VRALLNVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRHYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>H. virescens</i>	(79)	<u>VRALLDVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRNYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>P. interpunctella</i>	(77)	<u>VRSLLDVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRNYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>P. polytes</i>	(79)	<u>VRSLLDVE--GLDEGHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRHYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>B. anynana</i>	(78)	<u>VRTLLDVE--GLDESHTMEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRHYLRPASGFQSLQFRLLFNKLGKQAL</u>	
<i>A. aegypti</i>	(77)	<u>IRSLFSTE--HMEESRTLEILKRLNRIVMILKLLVDQVPILETMTPLDFMDFRDYLRPASGFQSLQFRLLFNKLGKTEH</u>	
<i>A. darlingi</i>	(78)	<u>IRVLFSTE--HIEESRTLEILKRLNRIVMILKLLVDQVPILETMTPLDFMDFRDYLRPASGFQSLQFRLLFNKLGKSEH</u>	
<i>A. gambiae</i>	(78)	<u>IRDLFSTE--HIEESRTLEILKRLNRIVMILKLLVDQVPILETMTPLDFMDFRDYLRPASGFQSLQFRLLFNKLGKSEH</u>	
<i>Z. navadensis</i>	(78)	<u>IRAKFNTEDLVDESQSEIILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRNYLRPASGFQSLQFRLLFNKLGKQEH</u>	
<i>N. lecontei</i>	(80)	<u>VRALFNTE--GLDESRTLEILKRLNRIVLILKLLVDQVMILETMTPLDFMDFRDYLRPASGFQSLQFRLLFNKLGKQEH</u>	
	161		240
<i>H. zea</i>	(157)	<u>RVKYNQSYQTVFGDDPEAMDALQKSEGEPAALLALIERWLERTPGLITHGFNFWGKFOAAVNKLIKDDIDAAARETNETVR</u>	
<i>S. litura</i>	(157)	<u>RVKYNQSYQTVFGDDPEAMALHKSSEGEPAALLALIERWLERTPGLNTHGFNFWGKFOAAVSKLIKDDIDAAASHETNETVR</u>	
<i>B. mori</i>	(157)	<u>RVKYNQNYQTVFGDDPEAMDALQKSEGEPAALLALIERWLERTPGLNTHGFNFWGKFOATVNKMLKIDIEATANLESIIVAVR</u>	
<i>H. virescens</i>	(157)	<u>RVKYNQSYQNVFGDDPEAMDALQKSEGEPAALLALIERWLERTPGLTRGFNFWGKFOAAVTKLIKDDIDAAANETNETVR</u>	
<i>P. interpunctella</i>	(155)	<u>RVKYNQNYQTVFGDDPEAMDALHKSSEEPALLALIERWLERTPGLQTHGFNFWGKFOAAVNKLIKDDIDAAAMTEPNETVR</u>	
<i>P. polytes</i>	(157)	<u>RVKYNQNYQTVFGDDPEAMESLHKSEEPALLALIERWLERTPGLNTHGFNFWGKFOANVTMIKDDIDEAAMLEPNEVVR</u>	
<i>B. anynana</i>	(156)	<u>RVKYNQNYQTVFGDDPEAMDALHKSSEEPALLALIERWLERTPGLITHGFDFWGKFOAAVVKMIRSVVEAMREPNETVR</u>	
<i>A. aegypti</i>	(155)	<u>RVKYNQKYSVFAASDPCATIERLSITESEPSLADLVQKWLERTPGLTNGFNFWGKFEESVQQLADQEAASAMEEHEENVK</u>	
<i>A. darlingi</i>	(156)	<u>RVKYNQKYTEVFAASDPSAIDRIAVTEEPSLADLVQKWLERTPGLLEDGFNFWGKQESVQKLLSDQEAASAMKEEHEHVR</u>	
<i>A. gambiae</i>	(156)	<u>RVKYNQKYTEVFAASDPAIERTIGTETEPSLADLVQKWLERTPGLQDGFNFWGKQESVQQLAQAQEAASAMEEHEENVR</u>	
<i>Z. navadensis</i>	(158)	<u>RVKYNQKYSVFGNDPEAIKAKAEKSENEPPLAHLVQRWLERTPGLQDGFNFWGKQKQAVETLLAKQRKTAEEAVNETLR</u>	
<i>N. lecontei</i>	(158)	<u>RVKYNQSYTRVFGDDPEAMTALGLAENEPSLSCLVQRWLERTPGLQDGFNFWGKQKQAVETLLAKQRKTAEEAVNETLR</u>	
	241		320
<i>H. zea</i>	(237)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>S. litura</i>	(237)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>B. mori</i>	(237)	<u>RHRLQDVENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>H. virescens</i>	(237)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>P. interpunctella</i>	(235)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>P. polytes</i>	(237)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>B. anynana</i>	(236)	<u>RHRLQDAENRREIYRSIFDPAVHDALRSRGERRLSHRALQGAIMITFYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>A. aegypti</i>	(235)	<u>NYRLMDIEKRREIVYSIFDAVVDALVARGERRFTHRALQGAIMITFYRDEPRFSQPHRLMLLMDIDSLITKWRYNHVI</u>	
<i>A. darlingi</i>	(236)	<u>EYRLMDIEKRREIVYSIFDAVVDALVARGERRFTHRALQGAIMITFYRDEPRFSQPHQLMLLMDIDSLITKWRYNHVI</u>	
<i>A. gambiae</i>	(236)	<u>EYRLMDIEKRREIVYSIFDAVVDALVARGERRFTHRALQGAIMITFYRDEPRFSQPHQLMLLMDIDSLITKWRYNHVI</u>	
<i>Z. navadensis</i>	(238)	<u>QHRFMDYEKRREIENSIFDPTTHAALVSRGERRFSHRALQGAIMITFYRDEPRFNQPHQLTLLMIDSLITKWRYNHVI</u>	
<i>N. lecontei</i>	(238)	<u>NHRLSDISSRAVEEITIFNEALHDALVSRGERRFTHAALQGAIMITLYRDEPRFSQPHQLTLLMIDSLITKWRYNHVI</u>	

	321		400
<i>H. zea</i>	(317)	MVORMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDGMKRSLNLTWGD	SVK----ENGQNGD
<i>S. litura</i>	(317)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDNMKKS	LTWGDKENG---QNMQNGA
<i>B. mori</i>	(317)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDGMKRS	LNLTWGDNVR-----ENGD
<i>H. virescens</i>	(317)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDGMKRS	LNLTWGDIVK----ENGQNGD
<i>P. interpunctella</i>	(315)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDGMKRS	LNLTWGDNAR-----ENGK
<i>P. polytes</i>	(317)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDGMKRS	LNLTWGDNIK----ENSQNGQ
<i>B. anynana</i>	(316)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLPRSLIPPLDDG	IKRDLSLTWGDHIFENGHSAKENG
<i>A. aegypti</i>	(315)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLIPRGSIPPLTC	EMQKALNLAWGSPVH-----Q
<i>A. darlingi</i>	(316)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLIPRNTIPPLTNE	MQKALNLAWGSPAHE-----T
<i>A. gambiae</i>	(316)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLIPRQSIPLTNE	MQKALNLAWGSPAHE-----F
<i>Z. navadensis</i>	(318)	MVQRMIGSAQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLIPRGYIPPLTRH	MKSKLSLSRDLIRN---WNDATDS
<i>N. lecontei</i>	(318)	MVQRMIGSQQLGTGGSSGYQYLRSTLSDRYKVFLDLFNLSTFLIPRNLIPLSR	DMKAKLSGAWGCWGA-----D

	401		425
<i>H. zea</i>	(393)	NAQNGDNAQNGIESSL-----	
<i>S. litura</i>	(394)	HSQNSQKETNGEGPETTLWQ----	
<i>B. mori</i>	(390)	ETTPQNGLEASL-----	
<i>H. virescens</i>	(393)	NEQNGIESSF-----	
<i>P. interpunctella</i>	(388)	ETHDGELNNCMLKLELA-----	
<i>P. polytes</i>	(393)	NSQNGLEFL-----	
<i>B. anynana</i>	(396)	NKKNGENHQNGLDEFSKLSLNEKKS	
<i>A. aegypti</i>	(385)	AKQINYAAK-----	
<i>A. darlingi</i>	(386)	ATRNGTLH-----	
<i>A. gambiae</i>	(386)	ARNGSLH-----	
<i>Z. navadensis</i>	(395)	EVDKPLERSVEASI-----	
<i>N. lecontei</i>	(388)	DDQNNLESSAEASM-----	