Supporting Information

Sim and Denlinger 10.1073/pnas.0802067105

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 cInR   ----------MKQFNTNHVVRLLGVVSQGDPTLVIMELMANGDLKGYLRRHRPDYEN---
aeInR   KDSFLLEASVMKQFNTHHVVRLLGVVSQGDPTLVIMELMANGDLKSYLRRHRPDYEN---
asInR   RDSFLIEATIMKEFHTHHVVRLYGVVSVGQPTLVIMELMANGDLKSYLRRHRPDYEN---
agInR   RDSFLIEATIMKEFHTHHVVRLYGVVSVGQPTLVIMELMANGDLKSYLRRHRPDYEN---
 dInR   RTNFLSEASVMKEFDTYHVVRLLGVCSRGQPALVVMELMKKGDLKSYLRAHRPEERDEAM

 cInR   -------GNEPSPQPPTLRQIYQMAIEIADGMAYLSAKKFVHRDLAARNCMVADDLTVKI
aeInR   -------GEDPSPQPPTLRQIIQMAIEIADGMAYLSAKKFVHRDLAARNCMVADDMTVKI
asInR   -------GEESSPQPPTLKQIYQMAIEIADGMAYLSAKKFVHRDLAARNCMVAEDLTVKI
agInR   -------GEESSPQPPTLKQIYQMAIEIADGMAYLAAKKFVHRDLAARNCMVAEDLTVKI
 dInR   MTYLNRIGVTGNVQPPTYGRIYQMAIEIADGMAYLAAKKFVHRDLAARNCMVADDLTVKI

 cInR   GDFGMTRD----------------------------------------------------
aeInR   GDFGMTRDIYETDYYRKGTKGFLPVRWMAPESLKDGIFSSSSDVFSYGVVLWEMATLASQ
asInR   GDFGMTRDIYETDYYRKGTKGFLPVRWMAPESLKDGMFSSSSDVFSYGVVLWEMATLASQ
agInR   GDFGMTRDIYETDYYRKGTKGFLPVRWMAPESLKDGMFSSSSDVFSYGVVLWEMATLASQ
 dInR   GDFGMTRDIYETDYYRKGTKGLLPVRWMPPESLRDGVYSSASDVFSFGVVLWEMATLAAQ
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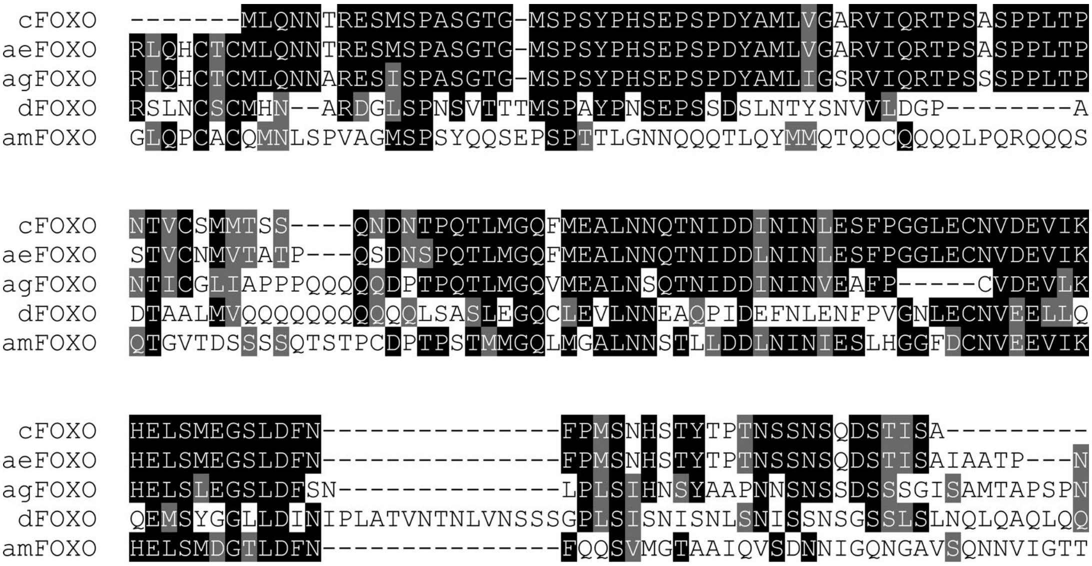
Fig. S1. Multiple sequence alignment of the deduced *C. pipiens* insulin receptor (InR) with other insect InRs retrieved from the GenBank database. Amino acids identical to *C. pipiens* are black, and conserved and semiconserved substitutions are in gray. cInR, *C. pipiens*, EU442282; aeInR, *A. aegypti*, EAT46545; asInR, *Anopheles stephensi*, AAU06124; agInR, *A. gambiae*, XP_320130; dInR, *D. melanogaster*, AAC47458.



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cFOXO   -------MLQNNTRESMSPASGTG-MSPSYPHSEPSPDYAMLVGARVIQRTPSASPPLTP
aeFOXO  RLQHCTCMLQNNTRESMSPASGTG-MSPSYPHSEPSPDYAMLVGARVIQRTPSASPPLTP
agFOXO  RIQHCTCMLQNNARESISPASGTG-MSPSYPHSEPSPDYAMLIGSRVIQRTPSSSPPLTP
dFOXO   RSLNCSCMHN--ARDGLSPNSVTTTMSPAYPNSEPSSDSLNTYSNVVLDGP--------A
amFOXO  GLQPCACQMNLSPVAGMSPSYQQSEPSPTTLGNNQQQTLQYMMQTQQCQQQQLPQRQQQS

cFOXO   NTVCSMMTSS----QNDNTPQTLMGQFMEALNNQTNIDDININLESFPGGLECNVDEVIK
aeFOXO  STVCNMVTATP---QSDNSPQTLMGQFMEALNNQTNIDDLNINLESFPGGLECNVDEVIK
agFOXO  NTICGLIAPPPQQQQQDPTPQTLMGQVMEALNSQTNIDDININVEAFP-----CVDEVLK
dFOXO   DTAALMVQQQQQQQQQQQLSASLEGQCLEVLNNEAQPIDEFNLENFPVGNLECNVEELLQ
amFOXO  QTGVTDSSSSQTSTPCDPTPSTMMGQLMGALNNSTLLDDLNINIESLHGGFDCNVEEVIK

cFOXO   HELSMEGSLDFN---------------FPMSNHSTYTPTNSSNSQDSTISA---------
aeFOXO  HELSMEGSLDFN---------------FPMSNHSTYTPTNSSNSQDSTISAIAATP---N
agFOXO  HELSLEGSLDFSN--------------LPLSIHNSYAAPNNSNSSDSSSGISAMTAPSPN
dFOXO   QEMSYGGLLDINIPLATVNTNLVNSSSGPLSISNISNLSNISSNSGSSLSLNQLQAQLQQ
amFOXO  HELSMDGTLDFN---------------FQQSVMGTAAIQVSDNNIGQNGAVSQNNVIGTT
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Fig. S2. Multiple sequence alignment of the deduced *C. pipiens* forkhead transcription factor with other insect FOXOs retrieved from the GenBank database. Amino acids identical to *C. pipiens* are black, and conserved and semiconserved substitutions are in gray. cFOXO, *C. pipiens*, EU442283; aeFOXO, *A. aegypti*, EAT34955; agFOXO, *A. gambiae*, XP_321536; dFOXO, *D. melanogaster*, NP_996204; amFOXO, *A. mellifera*, XP_001122804.