Figures and figure supplements

Ancient origins of arthropod moulting pathway components

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Figure 1. Simplified overview of the neuropeptide/hormone signalling pathway at moulting. PTTH initiates a signalling cascade that results in the biosynthesis of ecdysone. The decline of the ecdysone titre triggers the release of ETH that, in turn, causes the release of EH. These two hormones mutually enhance one another in a positive feedback loop to control and regulate pre-ecdyssis behaviour. With the ensuing release of CCAP, caused by EH, pre-ecdyssis ceases and the ecdysis motor program is started. Finally, bursicon responds to the increasing levels of CCAP and initiates post-ecdyssis behaviour and cuticle tanning. This figure is based on the studies of McNabb et al. (1997) and Clark et al. (2004). Animal silhouettes were obtained under Public Domain licence at phylopic (http://phylopic.org/), unless otherwise indicated. Beetle: T. Michael Keesey after Ponomarenko (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); moth: by Gareth Monger (available for reuse under https://creativecommons.org/licenses/by/3.0/); Drosophila: Thomas Hegna (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/).

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Figure 2. Origin and distribution of the key ligand-receptor components of the arthropod moulting signalling pathway across Metazoa. (A) Simplified phylogeny (based on Dunn et al., 2014) of Metazoa showing the lineages in which the key components of the arthropod moulting signalling pathway are present. Note that Porifera and Placozoa, that lack the moulting pathway components investigated here, are omitted for clarity. Coloured lines indicate the presence of a given ligand and/or receptor in a given lineage. Eclosion hormone and bursicon peptidergic systems originated prior to the cnidarian-bilaterian split, whereas the ecdysis-triggering hormone and crustacean cardioactive peptide trace back to the last common ancestor of Bilateria. PTTH is an insect-specific neuropeptide. (B) Expanded phylogeny of Metazoa with Porifera as the earliest branching clade (adapted from Dunn et al., 2014). Coloured lines indicate the presence of a given ligand (right side) and receptor (left side) in a given lineage. Phylum name in bold indicates the availability of genomic data. Note that although the trunk ortholog was not retrieved from the genomes of Nematostella vectensis and Caenorhabditis elegans, similarity searches against publicly available protein databases identified this gene in other cnidarian and nematode species. Animal silhouettes were obtained under Public Domain licence at phylopic (http://phylopic.org/), unless otherwise indicated. Credited images: Ctenophora: Martini (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Cnidaria: Jack Warner (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Xenacoelomorpha: Andreas Hejnol (available for reuse under https://creativecommons.org/licenses/by-nc/3.0/); Chordata: Jake Warner (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Ambulacraria: Noah Schlottman (photograph from Casey Dunn available for reuse under https://creativecommons.org/licenses/by-sa/3.0/); Ecdysozoa: Thomas Hegna based on picture by Nicolas Gompel (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Lophotrochozoa: Fernando Carezzano (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/). DOI: https://doi.org/10.7554/eLife.46113.004
Figure 2—figure supplement 1. 2D cluster maps of trunk/PTTH, EH, CCAP and bursicon ligands reflecting the evolutionary relatedness of the key arthropod moulting components among metazoans. Colour shapes and nodes are based on the different metazoan phyla investigated (circles = protostome animals; triangles = deuterostome animals; crosses = cnidarians and ctenophores; square = xenacoelomorphs). Edges correspond to BLAST connections. The ctenophore trunk sequence (A) is circled and marked with a white arrow.
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Figure 2—figure supplement 2. Phylogenetic analysis of the PTTH/trunk receptor tyrosine kinase torso showing the presence of torso receptor in cnidarians, lophotrochozoans, ecdysozoans and deuterostomes. Support values for the tree nodes obtained from mrbayes, RAxML and PhyML are shown as percentage. Tree topology obtained from RAxML was used as a backbone, and conflicting topology branches from mrbayes and PhyML inferred trees are marked by brackets ([]) around the support values.

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Figure 2—figure supplement 3. Phylogenetic analysis of the ecdysis-triggering hormone receptor showing the presence of ETH-receptor in bilaterians. Note a substantial expansion of the eth-receptor homologs in the genomes of the Branchiostoma floridae and B. belcheri. Support values for the tree nodes obtained from mrbayes, RAxML and PhyML are shown as percentage. Tree topology obtained from RaXML was used as a backbone, and conflicting topology branches from RAxML and PhyML inferred trees are marked by brackets ([]) around the support values.

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Figure 2—figure supplement 4. Phylogenetic analysis of the guanylyl cyclase eclosion hormone receptor showing the presence of EH-receptor in ecdysozoans, lophotrochozoans, ambulacrarians and cephalochordates. Support values for the tree nodes obtained from mrbayes, RAxML and PhyML are shown as percentage. Tree topology obtained from mrbayes was used as a backbone, and conflicting topology branches from RAxML and PhyML inferred trees are marked by brackets [ ] around the support values.

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Figure 2—figure supplement 5. Phylogenetic analysis of the G protein-coupled CCAP receptor showing the presence of CCAP-receptor in ecdysozoans, lophotrochozoans, deuterostomes (including vertebrates) and acellos. Support values for the tree nodes obtained from mrbayes, RAxML and PhyML are shown as percentage. Tree topology obtained from RAxML was used as a backbone, and conflicting topology branches from mrbayes and PhyML inferred trees are marked by brackets \( [\] \) around the support values.

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Figure 2—figure supplement 6. Phylogenetic analysis of the bursicon G protein-coupled receptor rickets showing the presence of rickets receptor in arthropods and lophotrochozoans. Note the restriction of the rickets receptor to arthropods and lophotrochozoans, while its ligand is also present in cnidarians and various deuterostomes. Support values for the tree nodes obtained from mrbayes, RAxML and PhyML are shown as percentage. Tree topology obtained from RAxML was used as a backbone, and conflicting topology branches from mrbayes and PhyML inferred trees are marked by brackets ([ ]) around the support values.

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Figure 3. Cluster analysis of prothoracicotropic hormone (ptth), trunk, noggin orthologs and multiple sequence alignment of the ctenophore trunk-like peptide and the metazoan ortholog sequences. (A) 2D cluster map of ptth, trunk and noggin genes. Red triangles correspond to ptth homologs, green parallelograms correspond to noggin homologs and red circles correspond to trunk homologs. The ctenophore trunk gene sequence is represented by the pink star. Edges represent BLAST connections of P value > 1e-05. Note that the ctenophore trunk peptide is indirectly connected to insect PTTH sequences via transitive BLAST connections. (B) Multiple sequence alignment representation of ctenophore trunk sequence and its metazoan orthologs produced by Jalview 2 (Waterhouse et al., 2009). Only the sequences directly connected to the ctenophore sequence in the 2D cluster map are included in the multiple sequence alignment. The conservation histogram corresponds to the number of conserved amino acid physico-chemical properties for each column of the alignment.

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Figure 4. Distribution of the arthropod peptidergic system components throughout Metazoa. (A) Simplified phylogeny of Metazoa with Porifera as the most basally branching clade (adapted from Dunn et al., 2014) showing the origin of the trunk/PTTH, eclosion-hormone (EH), bursicon, crustacean cardioactive peptide (CCAP) and ecdysis-triggering hormone (ETH) peptigeric systems. (B) Distribution of the arthropod peptigeric system components within Panarthropoda. Secondary losses are depicted by the red crosses followed by the name of the peptide system absent in the lineage. Note that ETH and bursicon, two vital components underlying molting in insects, were possibly secondarily lost in the Onychophora and Tardigrada (indicated by the red cross), respectively. Genomic and transcriptomic homology searches within the Kinorhyncha, Priapulida and Loricifera (condensed into the clade Scalidophora in Figure 1B) were not performed in this study (indicated by the question mark). Animal silhouettes were obtained under Public Domain licence at phylopic (http://phylopic.org/), unless otherwise indicated. Arthropoda: T. Michael Keesey after Ponomarenko (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Onychophora: Noah Schlottman, photo by Adam G. Clause (available for reuse under https://creativecommons.org/licenses/by-sa/3.0/); Tardigrada: Fernando Carezzano (available for reuse under https://creativecommons.org/publicdomain/zero/1.0/); Nematoida: Malo Kodos, image from the Smithsonian Institution (available for reuse under https://creativecommons.org/licenses/by-nc-sa/3.0/); Scalidophora: Noah Schlottman, photo by Martin V. Sørensen (available for reuse under https://creativecommons.org/licenses/by-sa/3.0/). DOI: https://doi.org/10.7554/eLife.46113.018