

## How to align arthropod leg segments

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**Abstract: 180 words**

10           How to align leg segments between the four groups of arthropods (insects, crustaceans, myriapods, and chelicerates) has tantalized generations of researchers, as this would answer over a century of speculation about the origins and homologies of the fascinating diversity of arthropod appendages and outgrowths. Here the expression and loss-of-function phenotypes of leg patterning genes in crustaceans, insects, and arachnids are compared using original and  
15 previously published data. All arthropod leg segments are found to correspond to each other in a one-to-one fashion. This alignment suggests that chelicerates with seven leg segments incorporated a proximal leg segment into the body wall. In addition, this alignment suggests that insect and myriapod tracheae are convergent and homologous structures: each evolved via the independent internalization of an ancestral gill (respiratory exite) on the proximal-most leg  
20 segment of their shared ancestor. A framework for understanding the homologies of any ectodermal structure in any arthropod opens up a powerful system for studying the origins of novel structures, the plasticity of morphogenetic fields across vast phylogenetic distances, and the convergent evolution of shared ancestral developmental fields.

25 **Key words**

Arthropod, appendage, homology, *Parhyale*, *Tribolium*, *Acanthoscurria*

## Research highlights

### 30 Introduction

Arthropods are the most successful animals on the planet, in part due to the diversity of their appendages. How to align the legs of all arthropods has tantalized researchers for over a century (Boxshall, 2004; Brusca & Brusca, 2003; Crampton, 1916; Hansen, 1925; Sharov, 1966; Shultz, 1989; Snodgrass, 1927; Størmer, 1944), as the solution would answer centuries of  
35 observation and speculation about arthropod structures. There are four groups of arthropods: chelicerates (spiders, etc.), myriapods (millipedes, etc.), crustaceans (shrimps, etc.), and insects (beetles, etc.). The difficulty in aligning or homologizing arthropod leg segments is due to the different numbers, shapes, and names of leg segments. Chelicerates can have either 7 or 8 leg segments, myriapods have either 6 or 7, insects have 6, and crustacean have 7 or 8 leg segments  
40 (Fig. 1) (Boxshall, 2004; Grimaldi & Engel, 2005; Schram, 1986; Shultz, 1989; Snodgrass, 1952). Since at least 1927, researchers have proposed many different theories to account for this variation, invoking leg segment deletions, duplications, and fusions to account for the different numbers of leg segments between arthropod taxa (see for example (Boxshall, 2004; Shultz, 1989; Snodgrass, 1927; Størmer, 1944)). The incredible diversity of arthropod legs even  
45 contributed to some author's conclusions that the four arthropod groups arose independently, and therefore it is not possible to homologize and align their legs (Manton, 1978). However, as molecular studies confirmed arthropod monophyly and mapped the topology of arthropod relationships with ever greater precision (Lozano-Fernandez, Giacomelli, et al., 2019; Lozano-Fernandez, Tanner, et al., 2019), and as loss-of-function studies of leg patterning genes have

50 been conducted on more branches of the arthropod tree of life, this long sought model can now  
be brought to light.

### **Aligning the leg segments of crustaceans and insects**

To align the leg segments of two arthropod groups, crustaceans and insects, Bruce and  
Patel 2020 (Bruce & Patel, 2020) compared the function of five leg patterning genes, *Distalless*  
55 (*Dll*), *dachshund (dac)*, *Sp6-9*, *extradenticle (exd)*, and *homothorax (hth)*, in the amphipod  
crustacean *Parhyale hawaiiensis* to previously published results in insects. By aligning the leg  
segment deletion phenotypes for these five genes, they found that the six distal leg segments of  
*Parhyale* and insects (leg segments 1 – 6, counting from the distal claw) corresponded to each  
other in a one-to-one fashion (Figs. 2, 3). To align the proximal leg segments, they compared the  
60 expression of *pannier (pnr)* and the *Iroquois* complex gene *araucan (ara)* in *Parhyale* and  
insects (Bruce & Patel, 2020). They found that, in both *Parhyale* and insects, the expression of  
*ara* distinguishes two proximal leg segments (leg segments 7 and 8; Fig. 2), while expression of  
*pnr* marks the true body wall (tergum; Fig. 4). These data suggested that insects had incorporated  
two ancestral proximal leg segments, 7 and 8, into the body wall (Bäcker et al., 2008; Coulcher  
65 et al., 2015; Deuve, 2001, 2018; Ewing, 1928; Heymons, 1899; Imms, 1937; Kobayashi, 2017;  
Kobayashi et al., 2013; Kukulová-Peck, 1983; Mashimo & Machida, 2017; Matsuda, 1970;  
Roonwal, 1937; Snodgrass, 1927). This work demonstrated that crustacean and insect legs had 8  
leg segments could be homologized in a straightforward, one-to-one relationship. If insect and  
crustacean legs can be homologized, this model may extend to myriapods and chelicerates as  
70 well, in a generalizable model of appendages across all four groups of arthropods.

### **Aligning the leg segments of crustaceans, insects, and chelicerates**

To align *Parhyale*, insect, and chelicerate legs, the above leg segment deletion phenotypes in *Parhyale* and insects were compared to previously published results in  
75 chelicerates. Functional experiments in chelicerates have been performed for *Dll*, *Sp6-9*, *dac*, and *hth*. Based on the leg segment deletion phenotypes of these genes, the six distal leg segments of *Parhyale*, insects, and chelicerates (leg segments 1 – 6, counting from the distal claw) correspond to each other in a one-to-one fashion, as follows.

In spiders, *Parhyale*, and insects, *Dll* is required for the development of leg segments 1 -  
80 5, counting from the distal end of the leg (Fig. 2A-F) (Angelini & Kaufman, 2004; Beermann et al., 2001; Bruce & Patel, 2020; Campbell & Tomlinson, 1998; B. Cohen et al., 1993; S. M. Cohen & Jürgens, 1989; Pechmann et al., 2011). In spiders, *Parhyale*, and insects, *Sp6-9* is required for the development of leg segments 1 – 6 (Fig. 2G – L) (Beermann et al., 2004; Bruce & Patel, 2020; Estella & Mann, 2010; Königsmann et al., 2017; Schaeper et al., 2009; Setton & Sharma, 2018). In spiders, harvestman, *Parhyale*, and insects, *dac* is required to pattern leg  
85 segments 3 – 5 (in insects, *dac* function extends partway into leg segment 2) (Bruce & Patel, 2020; Mardon et al., 1994; Sharma et al., 2013; Tavsanlı et al., 2004; Turetzek et al., 2015). In spiders, harvestman, and *Parhyale*, a weak *dac* phenotype causes leg segment 4 to be truncated and fused onto leg segment 3 (Fig. 3A - F). In harvestman, *Parhyale*, and insects, a strong *dac*  
90 phenotype affects leg segments 3 – 5 (Fig. 3G - L). In harvestman, *Parhyale*, and insects, loss of *hth* affects the proximal leg segments (Fig. 3M-R). In *Parhyale* and insects, loss of *hth* deletes the proximal leg segments, leaving only the distal 2 leg segments intact. In harvestman, reduction of *hth* shortens and fuses the proximal leg segments, leaving the distal segments unaffected (Sharma et al., 2015). It is not clear from the figures or text how many distal leg  
95 segments are unaffected - the most severely affected embryos did not survive to hatching and

their cuticle was shriveled, thus obscuring what deformities are due to loss of *hth* and what are due to the embryo not developing fully before hatching. However, leg segment 1 and at least the distal half of leg segment 2 appear unaffected. Thus, in harvestman, insects, and *Parhyale*, *hth* appears to function in all but the distal 2 leg segments. For the above comparisons, it is known that RNAi gives a range of partial knockdowns, but the above data focuses on what appear to be the null phenotypes.

To elucidate the composition of proximal leg segments in chelicerates, the expression of *pnr*, *ara*, and *Dll* was compared between *Parhyale*, *Tribolium*, and the tarantula *Acanthoscurria geniculata* (Fig. 4) (Bruce & Patel, 2020). Three orthologs of *pnr* were identified in *Acanthoscurria* that had closest homology to *Drosophila*, *Tribolium*, and *Parhyale pnr* (Fig. S1). However, only one of these was expressed at the stages examined and was therefore presumed to be *pnr*. An *Acanthoscurria Iroquois* gene was identified which was the reciprocal best BLAST hit to *Drosophila*, *Tribolium*, and *Parhyale ara*. An *Acanthoscurria Dll* gene was identified which was the reciprocal best BLAST hit to *Drosophila*, *Tribolium*, and *Parhyale Dll*.

As in *Parhyale* and *Tribolium*, *Acanthoscurria Dll* was found to be expressed in leg segment 1 – 5, and *pnr* expressed in the most dorsal tissue (Fig. 4). Thus, it appears that *pnr* marks the “true” body wall (tergum) in all arthropods. In *Parhyale* and *Tribolium*, *ara* is expressed in three domains: a dorsal armband on proximal leg segment 8 that is adjacent to the *pnr* domain; a second armband on proximal leg segment 7; and a dot of expression on the medial side of leg segment 6. *Parhyale* also expresses *ara* in the tip of the claw. In *Acanthoscurria*, at the embryonic stages examined, *ara* is expressed in three of these domains: a dorsal armband adjacent to the *pnr* domain; a second armband on proximal leg segment 7; and some expression in the tip of the claw. The dot of *ara* expression in leg segment 6 was not observed. Perhaps this

domain is expressed at embryonic stages that were not examined, or it is not expressed in the  
120 *Acanthoscurria* lineage. However, as predicted by the leg segment alignment model, the two  
armbands of *ara* expression in *Acanthoscurria* bracket a region proximal to leg segment 7  
(spider coxa) and adjacent to *pnr*. This suggests that *Acanthoscurria*, like *Parhyale* and  
*Tribolium*, also retains a remnant of an ancestral, proximal 8<sup>th</sup> leg segment.

To test this hypothesis, the expression of *odd-skipped* was examined in *Acanthoscurria*.  
125 In *Drosophila*, the *odd-skipped* family of genes are expressed in the distal edge of each leg  
segment, where it induces cells to buckle and form the flexible joint (Mirth & Akam, 2002). An  
*odd-skipped* gene was identified in *Acanthoscurria* which was the reciprocal best BLAST hit to  
*Cupiennius* (spider) *odd-related 3* (*odd-r3*) (Prpic & Damen, 2009). This *Acanthoscurria odd-r3*  
is expressed in the distal region of leg segments 1 – 7 but also in an additional ring proximal to  
130 leg segment 7 (Fig. 4G, H). This additional ring of *odd-r3* notably occurs on the distal side of a  
leg-segment-like bulge. Given that *odd-skipped* marks the distal side of leg segments (Mirth &  
Akam, 2002), the ring of *odd-r3* expression on the distal side of the leg-segment-like bulge  
suggests that it is a bona fide leg segment. Together, the expression of *pnr*, *ara* and *odd-r3* and  
the presence of a leg-segment-like bulge suggest that *Acanthoscurria* has an additional, cryptic  
135 proximal 8<sup>th</sup> leg segment.

### **Aligning the leg segments of myriapods**

No functional data for leg patterning genes is available for myriapods. However,  
morphological and embryological evidence suggests that myriapods, like insects, have  
140 incorporated proximal leg segment(s) into the body wall (Boxshall, 2004; Tiegs, 1940; Wesener,  
2014). In the embryos of both myriapods and insects, the proximal part of the developing leg

("subcoxa" in insects or "limb base" in myriapods) broadens and flattens to form the adult lateral body wall (Bitsch, 1994; Coulcher et al., 2015; Heymons, 1899; Kobayashi, 2017; Kobayashi et al., 2013; Matsuda, 1970; Roonwal, 1937; Tiegs, 1940; Uchifune & Machida, 2005; Verhoeff, 1905). In insects, this subcoxa was shown to correspond to the two proximal-most leg segments of crustaceans (Bruce & Patel, 2020), and the same may be true for myriapods (Wesener, 2014). Incorporation of proximal leg segments into the myriapod body wall would bring their leg segment count to 8, in agreement with other arthropods.

## 150 **Discussion**

The expression and embryological data shown here, in conjunction with the expression and functional data from previous publications, demonstrates that all arthropod legs can be aligned in a one-to-one fashion (Fig. 5). For example, the coxa of spiders, millipedes, and crustaceans are leg segment 7; the insect coxa, crustacean basis, and spider trochanter are leg segment 6; the insect trochanter, crustacean ischium, and spider femur are leg segment 5. In this model, arthropods ancestrally possessed a total of 8 leg segments. This fits well with the observation that arthropods in general have a maximum of 8 leg segments (Boxshall, 2004; Shultz, 1989; Snodgrass, 1952), as well as with the fossil data, where the ancestors of living arthropods also possessed 8 leg segments (Yang et al., 2018). The canonical leg segment numbers in the four groups of arthropods are proposed to be due to the incorporation of proximal leg segments into the body wall, likely to support more of the body weight on the legs. Insects, which have 6 leg segments, have incorporated two proximal leg segments into the body wall (leg segments 7 and 8). Crustaceans with 7 leg segments, like *Parhyale*, have partially incorporated

one leg segment into the body wall (leg segment 8). Myriapods with 6 or 7 leg segments  
165 incorporated 2 or 1 leg segments into the body wall, respectively.

### **Chelicerate legs**

Chelicerates with 8 free leg segments, such as sea spiders and solifugids, have not  
incorporated any leg segments into the body wall. However, in chelicerates with 7 leg segments,  
such as *Acanthoscurria*, a proximal leg segment is missing and must be accounted for. One  
170 hypothesis is that it was simply deleted. However, the expression of *Acanthoscurria pnr*, *ara*,  
and *odd-r3* presented here suggests that the proximal-most 8<sup>th</sup> leg segment of these chelicerates  
was incorporated into the body wall, similar to how insects incorporated proximal leg segments  
into their body wall (Bruce & Patel, 2020; Kobayashi, 2017, p. 201; Matsuda, 1970; Snodgrass,  
1927). Embryological evidence also supports this conclusion: a leg-like proximal 8th leg  
175 segment can be observed in embryos of the tarantula spider *Acanthoscurria* (Fig. 4G; also  
observable in (Pechmann, 2020; Pechmann et al., 2011)), as well as in *Cupiennius*  
embryos (Pechmann et al., 2010; Wolff & Hilbrant, 2011) and *Parasteatoda* embryos (Mittmann  
& Wolff, 2012; Pechmann et al., 2015). Similarly, whip spiders (amblypygids) have a  
disconnected sliver of exoskeleton dorsal to the coxa, which appear to articulate to the coxa with  
180 condyle joints (Fig. S2), that may be the remnant of the proximal 8<sup>th</sup> leg segment.

### **Myriapod legs**

When the morphological and embryological evidence in myriapods is incorporated into  
the above leg segment alignment model, two fascinating hypotheses become apparent: insect and  
myriapod respiratory systems may in fact be homologous; and insect wings may be homologous  
185 to myriapod “wings” (polydesmid paranota).

Myriapod and insect respiratory systems are astonishingly similar - a small circular spiracle associated with each leg leads to internally branching trachea (Dohle, 1998) (Fig. S3). This contributed to entrenched support for their sister relationship (Dohle, 1998). Notably, both respiratory systems appear to occur on the proximal-most leg segment (leg segment 8)(Boxshall, 190 2004; Bruce & Patel, 2020; Kobayashi et al., 2013; Tiegs, 1940). Thus, while these two systems are not homologous as tracheae (Lozano-Fernandez, Giacomelli, et al., 2019), the evidence suggests that insect and myriapod tracheae each evolved via the independent internalizing an ancestral gill (respiratory exite) on the proximal-most leg segment of their shared ancestor (Averof & Cohen, 1997; Bruce, 2021; Franch-Marro et al., 2006; Grillo et al., 2014; Wesener et 195 al., 2014).

In support of this, the genes *trachealess* (*trh*) and *ventral veins lacking* (*vvl*), which are expressed in and required for insect tracheal formation, are also expressed in the crustacean gill(Franch-Marro et al., 2006; Wilk et al., 1996), an exite on the leg. This is expected if insect tracheae are an internalized exite on the incorporated 8<sup>th</sup> leg segment. If insect tracheae are an 200 internalized exite on the 8<sup>th</sup> leg segment, then perhaps the morphologically and functionally similar myriapod tracheae are as well.

Some myriapods (polydesmid and platydesmid millepedes) have many wing-like “paranota” or “paratergites” (Fig. S3) along the side of the body. If these emerge from the proximal-most leg segment, then they may be positionally homologous to the *Parhyale* tergal 205 plate and insect wing. Thus, millipedes and insects may have convergently evolved tracheae and “wings” from the same exites on the same leg segment. These structures would therefore be bizarrely both convergent and homologous.

To test these two hypotheses, the expression of *pnr*, *Iroquois* genes like *ara*, joint-markers like *serrate* or *odd-skipped*, flat exite-patterning genes like *vestigial*, and trachea-patterning genes like *ventral veins lacking*, and *trachealess* should be examined in millipede embryos. If the tracheae and paranota are carried on leg segment 8, the following expression patterns are expected in millipede embryos: *pnr* will be expressed dorsal to the spiracle and paranota; *Iroquois* genes like *ara* will bracket the spiracle and paranota dorsally and ventrally; and joint-markers like *odd-skipped* and *serrate* will be expressed around the perimeter of the subcoxa that carries the spiracle and paranota. If millipede trachea and paranota are patterned like their proposed corresponding structures in crustacean and insect, then paranota should express *vestigial* and *scalloped*, while the tracheae should express *ventral veins lacking* and *trachealess*.

#### **A “Hox code” for proximal-distal patterning**

In the model presented here, the function of the five leg patterning genes in conjunction with the expression of the proximal patterning genes *pnr* and *ara* and the joint marker *odd* can be used as a “zip code” for understanding and homologizing along the proximal-distal axis. This is similar to the well-known “Hox code” for understanding the anterior-posterior axis. Given the conserved expression patterns of *pnr*, *ara*, and *odd* across arthropods and the ease and low cost of in situ HCR, the homologies of long-debated structures in any arthropod for which embryos can be obtained can now be elucidated in a single in situ HCR experiment using just three genes. A framework for understanding the homologies of any ectodermal structure in any arthropod opens up a powerful system for studying the origins of novel structures, the plasticity of morphogenetic fields across vast phylogenetic distances, and the convergent evolution of shared ancestral developmental fields.



## Materials and Methods

### 235 Embryo fixation

#### In situ HCR version 3.0

*Acanthoscurria* cDNA sequences were submitted to Molecular Instruments(Choi et al., 2018), and the probe sets are available from the company. In situs were performed as in Bruce et. al.  
240 2021(Bruce et al., 2021)

#### Imaging

Embryos imaged with Zeiss LSM880 confocal. Image processing done with Fiji-ImageJ. Fiji  
“Image Calculator > Subtract” method was used to remove high background from yolk  
245 autofluorescence. Figures processed using Adobe Photoshop 2020.

**Data and materials availability:** All data is available in the main text or the supplementary  
250 materials.

**Competing interests:** Authors declare no competing interests.

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provided by Mathias Pechmann (Institute for Zoology/Developmental Biology, Biocenter,  
255 University of Cologne, Germany). Images of amblypygid molt were generously provided by  
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#### **Author contributions**

HSB conceived, designed, and performed experiments and wrote manuscript. HSB would like to  
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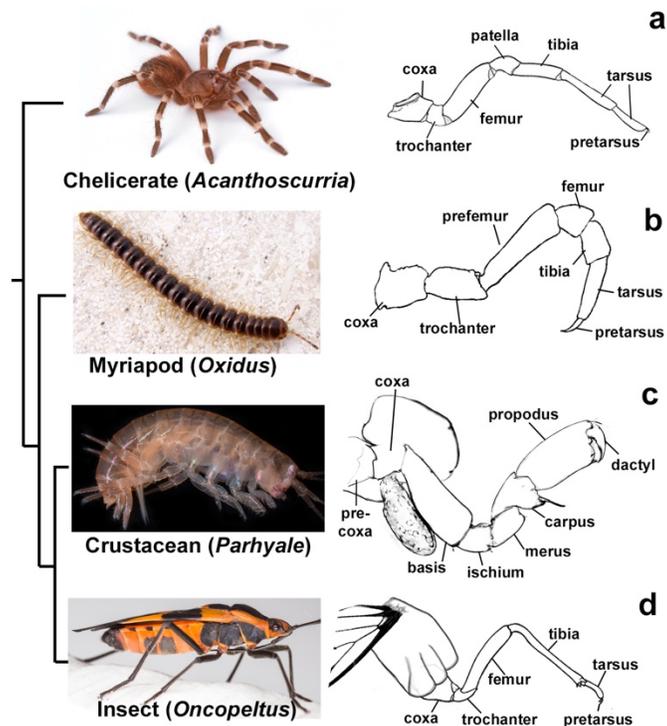
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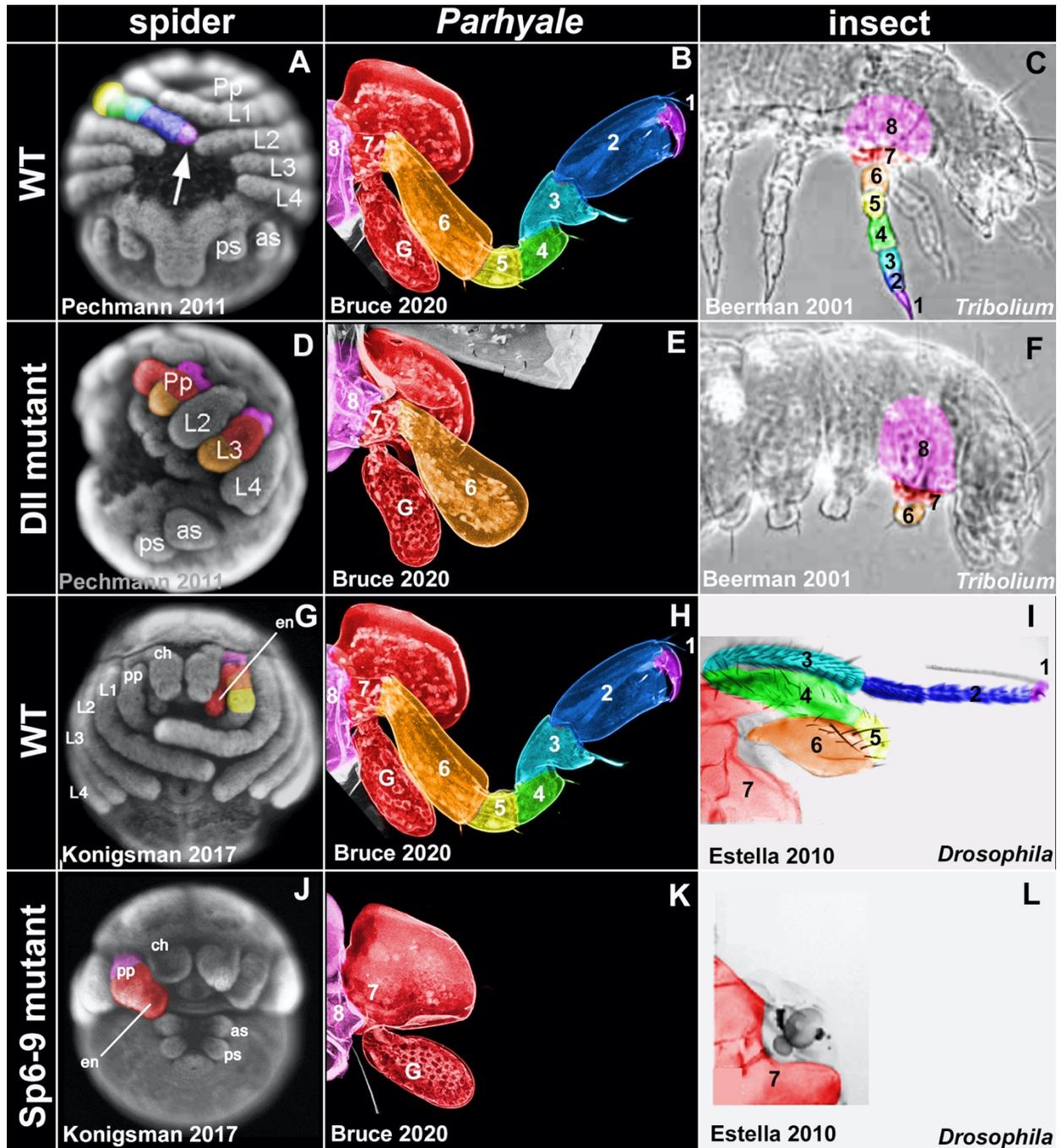
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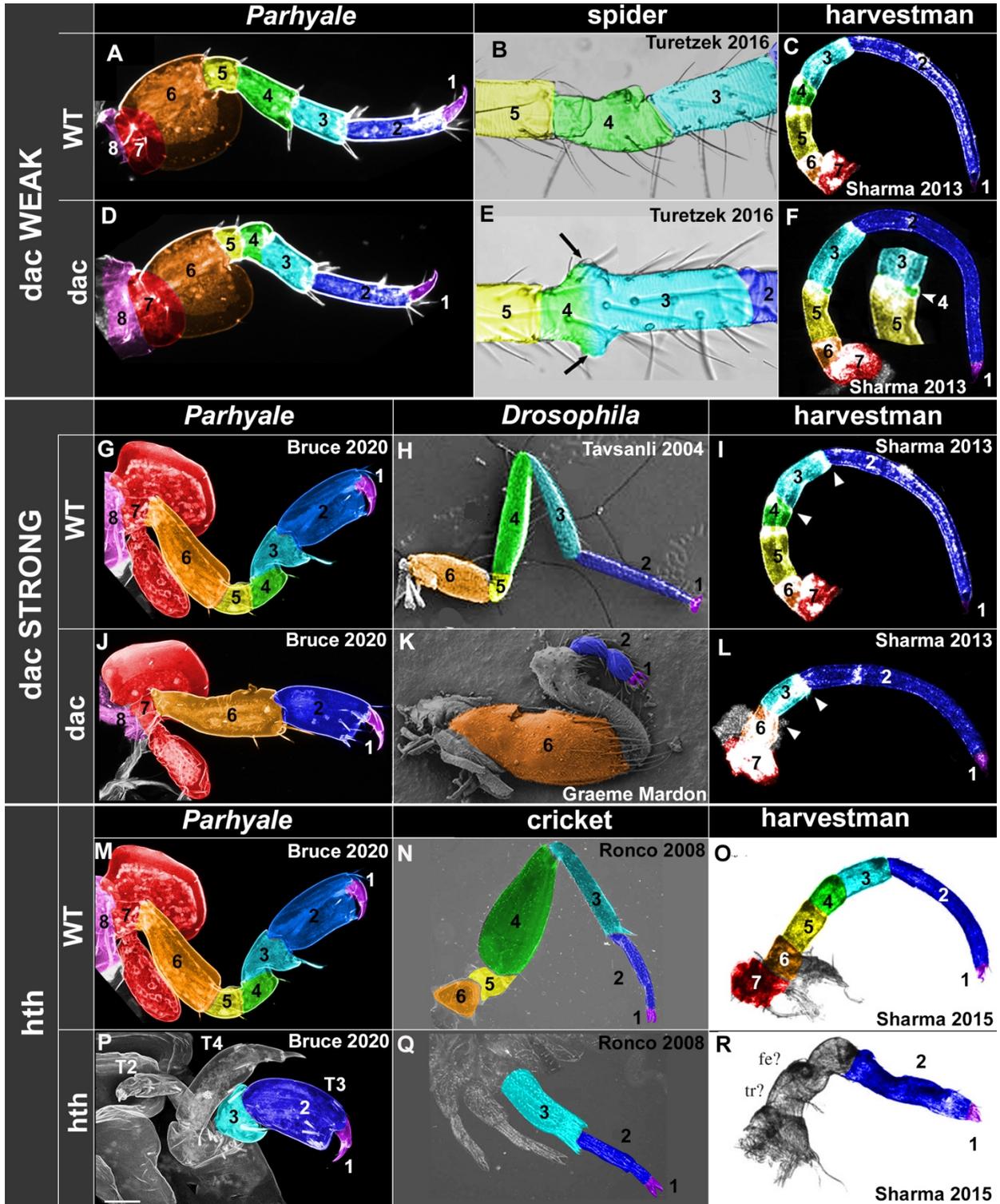
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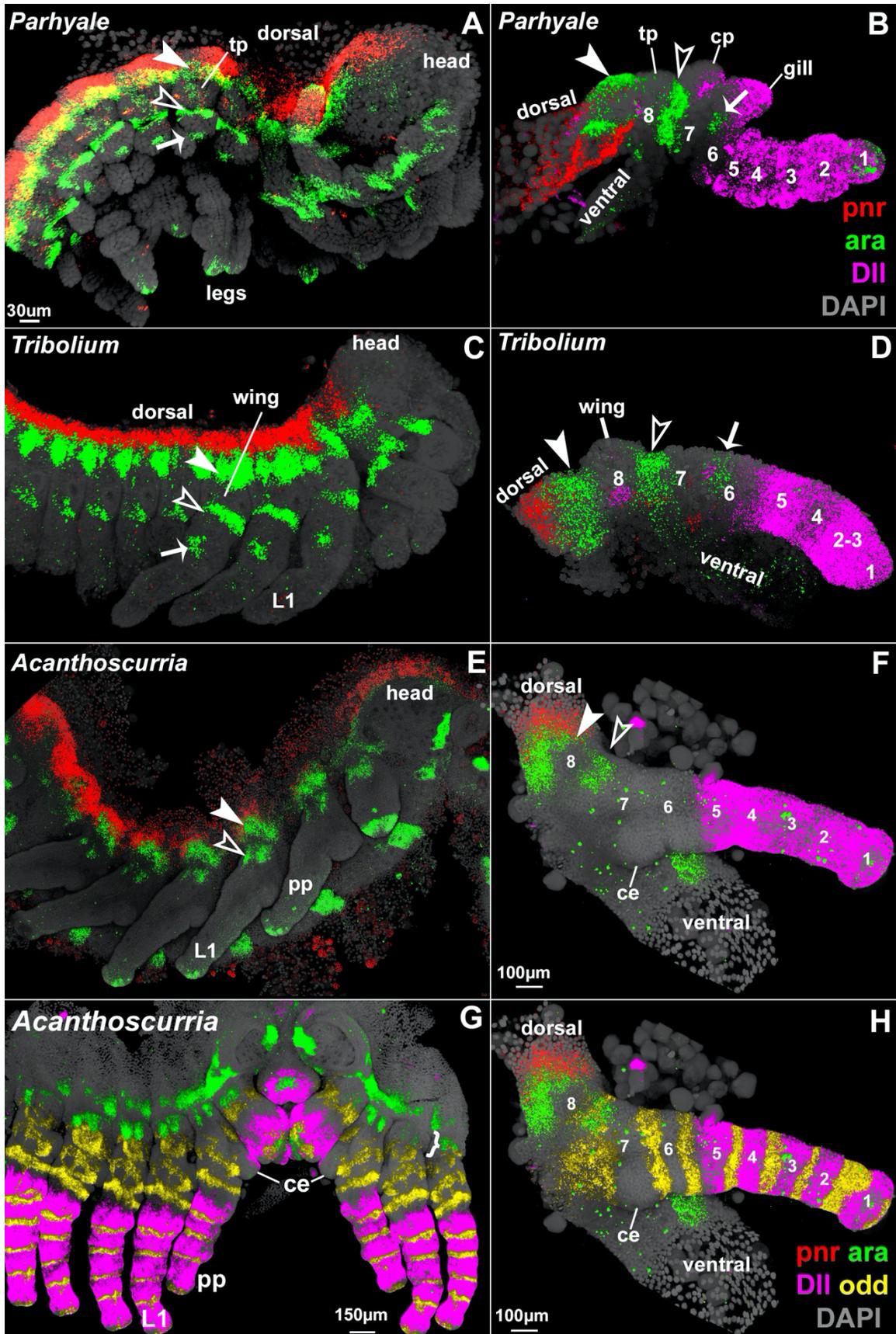
465 **Fig. 1.** Arthropod legs. Chelicerates, myriapods, crustaceans, and insects have different numbers, shapes, and names for their leg segments. Phylogeny based on Lozano 2019(Lozano-Fernandez, Giacomelli, et al., 2019). *Acanthoscurria* and *Oxidus* images from Wikipedia. Leg drawings adapted from Snodgrass 1952(Snodgrass, 1952), except *Parhyale* leg, original image.



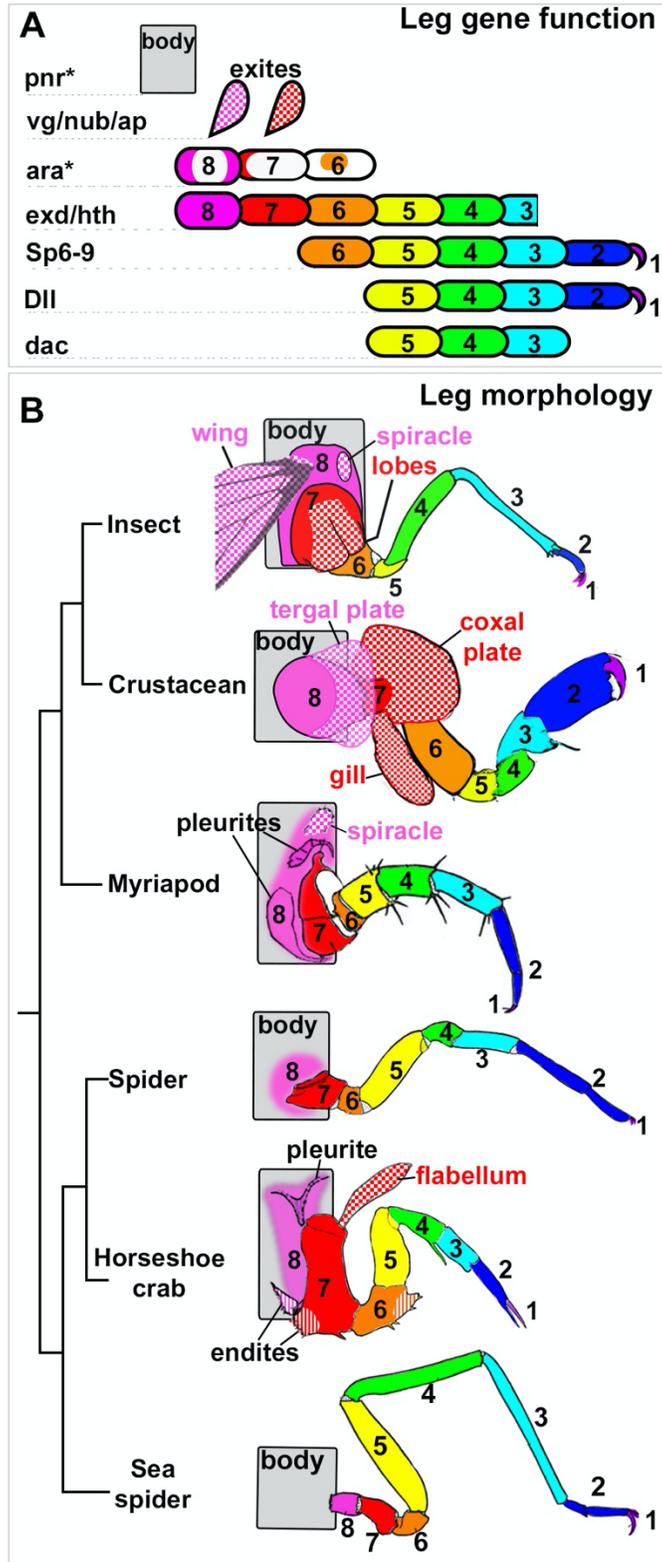
**Fig. 2.** *Dll* and *Sp6-9* function in arthropods. In spiders, *Parhyale*, and insects, *Dll* is required for the development of leg segments 1 - 5, counting from the distal end of the leg. In spiders, *Parhyale*, and insects, *Sp6-9* is required for the development of leg segments 1 – 6. A, D from Pechmann 2011. B, E, H, K from Bruce and Patel 2020. C, F from Beerman 2001. G, J from Konigsman 2017. I, L from Estella 2010.



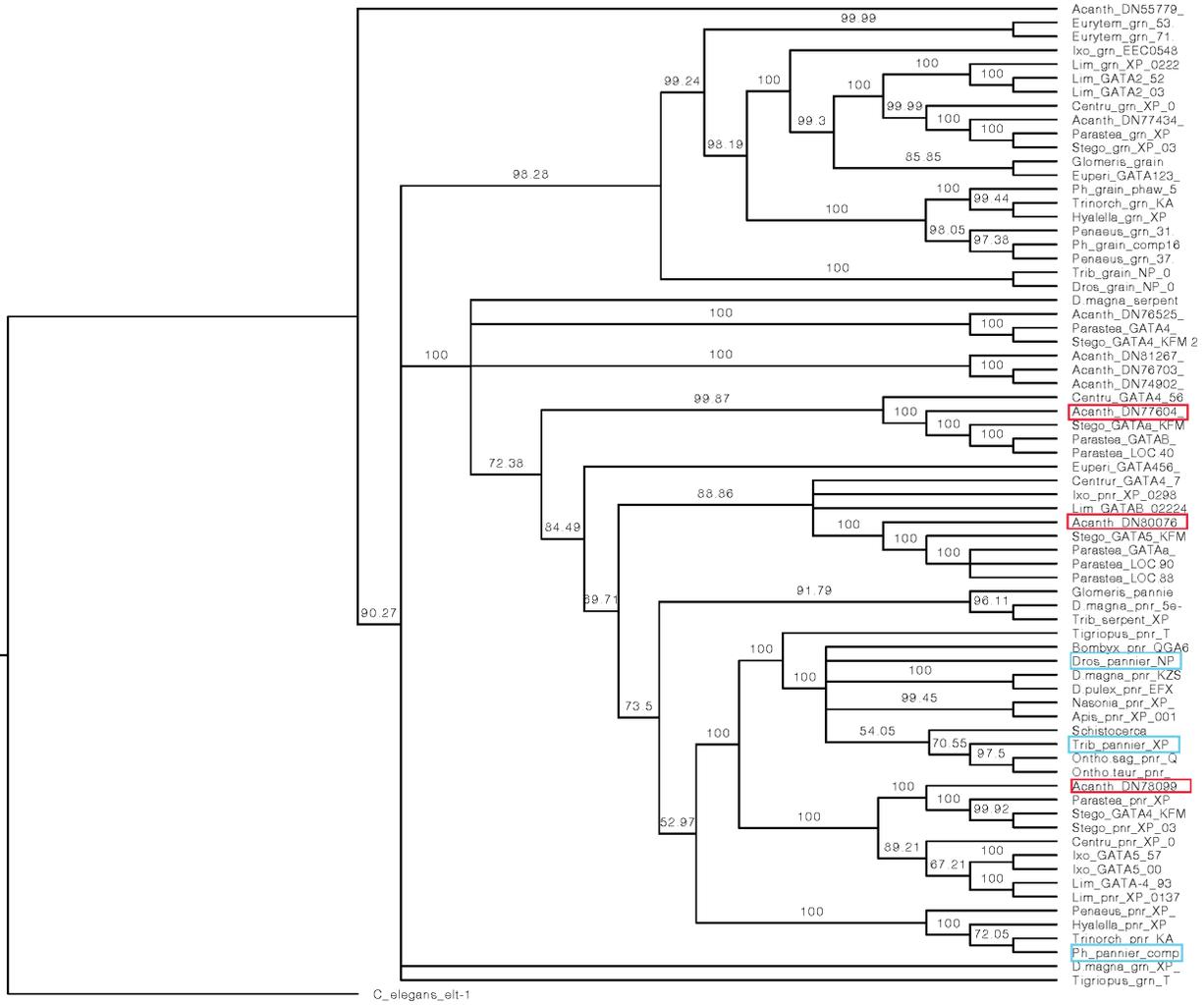
**Fig. 3.** *dac* and *hth* function in arthropods. In spiders, harvestman, and *Parhyale*, a weak *dac2* phenotype causes green leg segment 4 to be truncated and fused onto cyan leg segment 3. In harvestman, *Parhyale*, and *Drosophila*, a strong *dac2* phenotype affects leg segments 3 – 5. In *Parhyale* and insects, loss of *hth* deletes the proximal leg segments, leaving only the distal 2 leg segments intact. In harvestman, reduction of *hth* shortens and fuses the proximal leg segments, leaving the distal segments unaffected. A, D, original work. B, E, Turetzek 2016. C, F, Sharma 2013. G, J, Bruce and Patel 2020. H, Tavsanlı 2004. I, L, Sharma 2013. K, Graeme Mardon, unpublished. M, P, Bruce and Patel 2020. N, Q, Ronco 2008. O, R, Sharma 2015



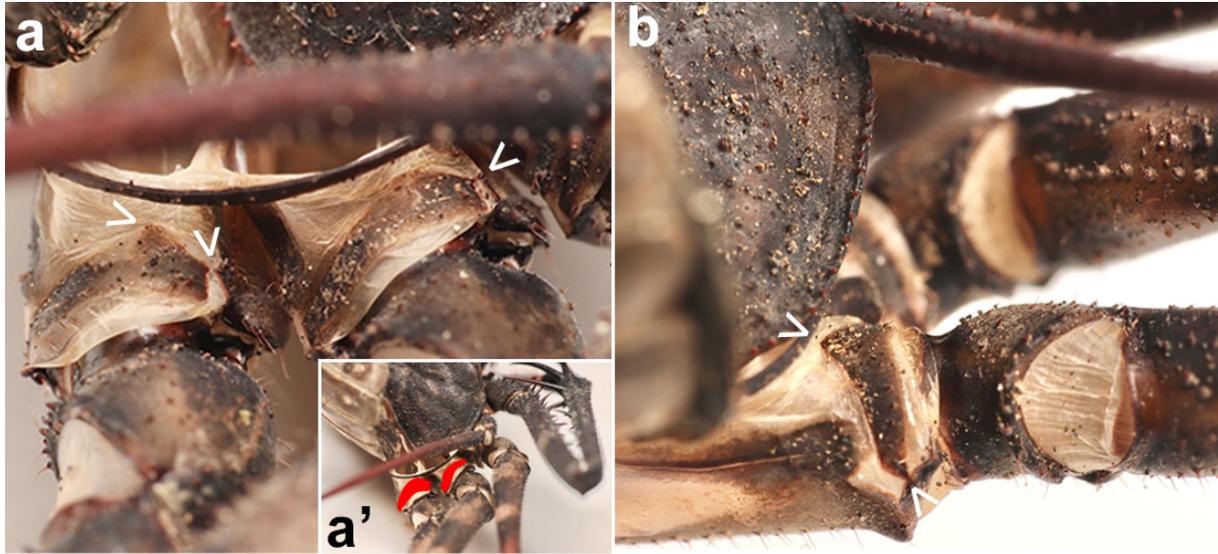
**Fig. 4.** Elucidating proximal leg segments in arthropods. Dissected right half of *Parhyale* (A), *Tribolium* (C), and *Acanthoscurria* (E) embryos. Dissected leg of *Parhyale* (B), *Tribolium* (D), and *Acanthoscurria* (F) embryos. *pnr* (red), *ara* (green), *Dll* (pink), DAPI (grey). In all three arthropods, leg segments 1 through 5 are identified by *Dll* expression. *Dll* also expressed in *Parhyale* gill, coxal plate (cp) and tergal plate(tp). In all three arthropods, the two *ara* armband domains bracket a region proximal to leg segment 7. In all three arthropods, *pnr* marks the most dorsal domain and is adjacent to and partially overlapping the dorsal *ara* domain. *ara* is also expressed in a smattering of ventral non-leg cells, and in *Parhyale* and *Acanthoscurria*, in the distal tip of the leg. *Tribolium* larvae have a fused tibia and tarsus, the tibiotarsus, here labelled 2-3(Coulcher et al., 2015). In *Acanthoscurria*, leg segment 7 is easily identified by the coxal endite (ce) that bulges medially. Large dorsal cells in *Parhyale* and *Acanthoscurria* are yolk or extra-embryonic cells that exist prior to dorsal closure. (G – H) *Acanthoscurria odd-r3* (yellow) is expressed in the distal region of each leg segment where the joint will later form. (G) Stage 12.5 *Acanthoscurria* embryos dissected away from yolk mass. Leg segment 7 is readily identified by the coxal endite. Proximal to leg segment 7, there is a leg-segment-like bulge (white curly brace), which expresses *odd-r3* in its distal region. By St 12.5, *pnr* expression in the walking legs and head is reduced and not visible through the other colors (compare with St 11.5 embryo in G). (H) dissected walking leg 1 from Stage 11.5 embryo where morphological bulges and subdivisions of the leg segments have not yet begun. *odd-r3* encircles the distal region of each leg segment, including the hypothesized proximal 8<sup>th</sup> leg segment.



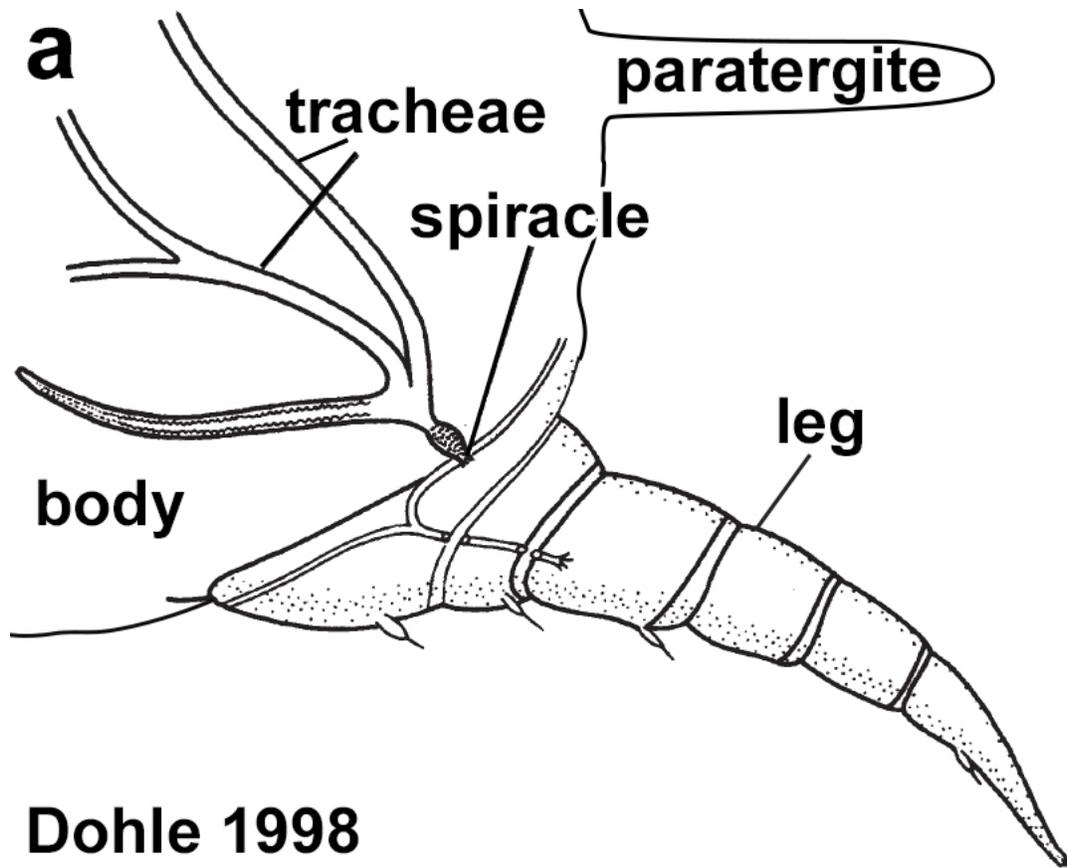
520 **Fig. 5.** Model of how to align all arthropod legs. A. Schematic of which genes function is related to (specific) leg segments. B. Morphology and homologies of arthropod leg segments based on leg gene function in insects, *Parhyale*, and chelicerates. Colors and patterns indicate proposed homologies. Exites (checker pattern); endites (stripe pattern). Drawings in B modified from Snodgrass 1952.



525 **Fig. S1.** Three orthologs of *pnr* were identified in *Acanthoscurria* with closest homology to *Drosophila*, *Tribolium*, and *Parhyale* *pnr* (Fig. S1-2). However, only one of these was expressed at the stages examined, Acanth\_DN78099, and was presumed to be *pnr*. Consensus tree generated using Mafft, which gave similar topology to Clustal consensus tree.



530 **Fig. S2.** Proposed precoxa in whip scorpions. Day-old molted exoskeleton. Condyles (points of articulation of joints between adjacent leg segments) of proposed precoxa indicated by >. **a**, dorsal view of molt. **a'**, zoomed out view of a. **b**, posterior view.



**Dohle 1998**

**Fig. S3.** Respiratory system of myriapod. Modified from Dohle 1998.