

Head patterning and Hox gene expression in an onychophoran and its implications for the arthropod head problem

Bo Joakim Eriksson^{1,4,*}, Noel N. Tait², Graham E. Budd³, Ralf Janssen³, Michael Akam¹

1. University Museum of Zoology and Department of Zoology, Downing Street, Cambridge, CB2 3EJ, UK

2. Department of Biological Sciences, Macquarie University, Sydney 2109 NSW, Australia

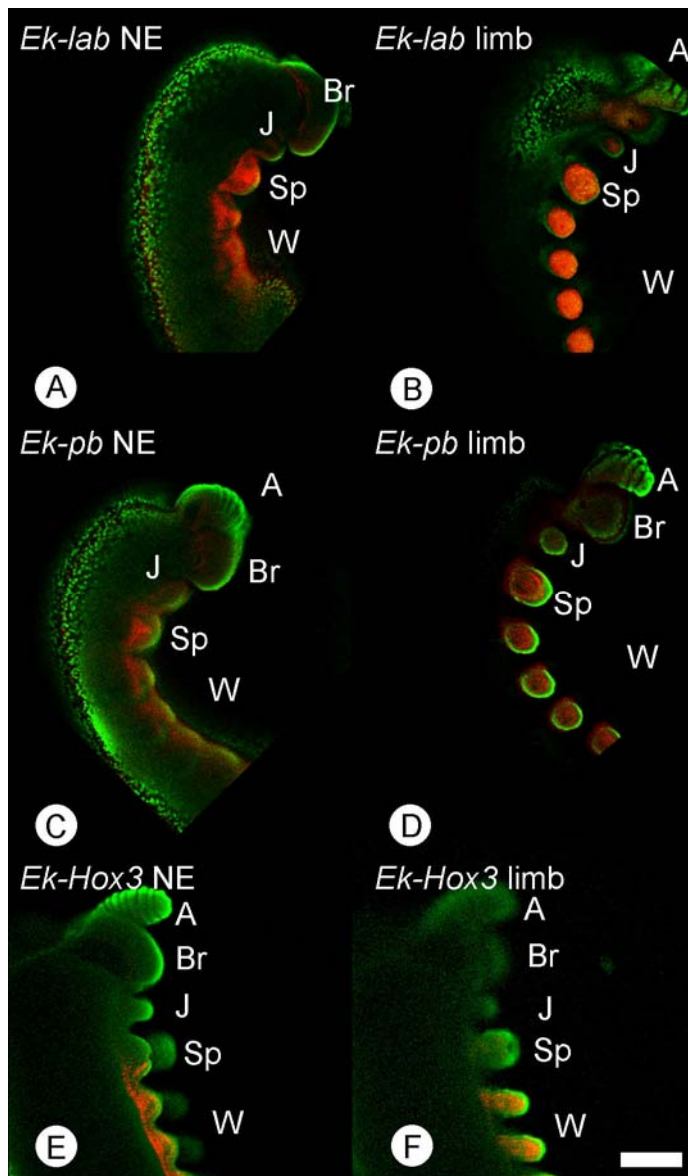
3. Dept Earth Sciences, Paleobiology, Uppsala University, Villavägen 16, Uppsala, SE-752 36, Sweden.

4. Current Address: School of Biological and Chemical Sciences, Queen Mary, University of London, Mile End Road, London E1 4NS.

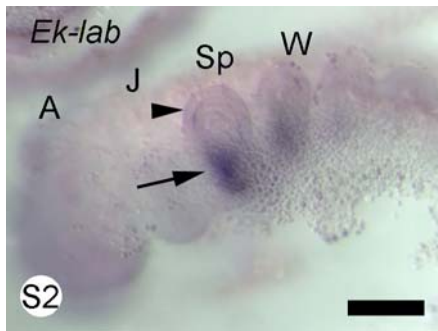
* Corresponding: j.eriksson@qmul.ac.uk
peripatus@live.se

Development Genes and evolution, supplementary data

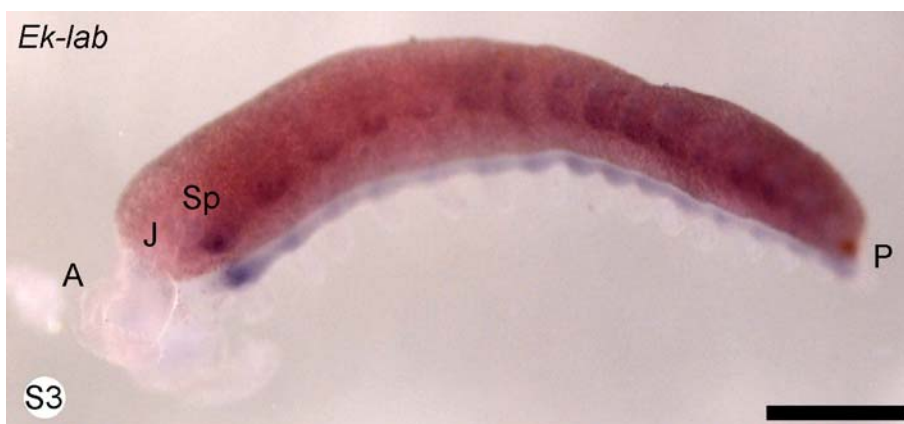
Supplementary figures



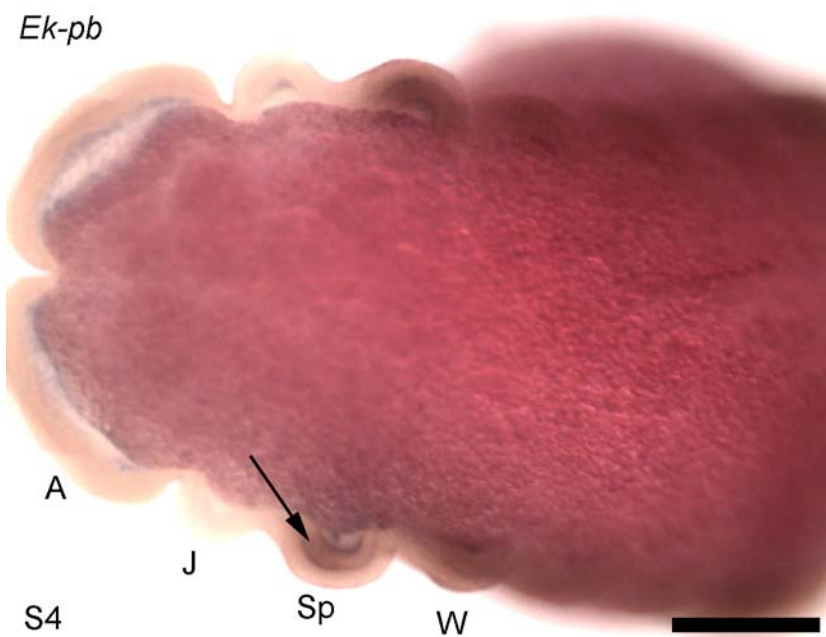
S. 1 Optical sections from CLSM showing embryos of *Euperipatoides kanangrensis* at stage V stained for: *lab*, *pb* and *Hox3*. Lateral view, anterior is up. A, Section through the neuroectoderm showing *lab* expression in the mesoderm beneath as well as the basal and apical ectoderm of segments from the slime papilla (Sp) and continuing posteriorly. B, Same embryo as in A with a section through the limbs showing expression of *lab* in the mesoderm as well as basal and apical ectoderm of segments from the slime papilla and continuing posteriorly. C, Section through the neuroectoderm showing expression of *pb* in the mesoderm and basal ectoderm but lacking in the apical ectoderm of segments from the slime papilla and continuing posteriorly. D, Same embryo as in C with a section through the limbs showing expression of *pb* in the mesoderm and basal ectoderm but lacking in the apical ectodermal layer of segments from the slime papilla and continuing posteriorly. E, section through the neuroectoderm showing expression of *Hox3* in the mesoderm and basal ectoderm of the posterior half of the slime papilla segment and continuing posteriorly. F, Same embryo as in C with a section through the limbs showing expression of *Hox3* in the interior starting with the first walking (W) leg and continuing posteriorly. A = antenna, Br = brain rudiment, J = jaw, scale bar = 500 μ m.



S. 2 The anterior of a whole mount of *Euperipatoides kanangrensis* embryo at stage III stained for the presence of *lab* mRNA. Lateral view, anterior is to the left. Arrow points at the neuroectoderm of the slime papilla segment (Sp) and the arrowhead indicates the expression in the limb. A = antenna, W = walking leg, scale bar = 200 μ m.



S. 3 Whole mount of *Euperipatoides kanangrensis* embryo at stage V stained for the presence of *lab* mRNA. Lateral view, anterior is to the left. The mRNA of *lab* can be seen from the slime papilla (Sp) segment and posteriorly to the proctodeum (P). A = antenna, J = jaw, scale bar = 500 μ m.



S. 4 Whole mount of *Euperipatoides kanangrensis* embryo at stage III stained for the presence of *pb* mRNA. Dorsal view, anterior is to the left. The expression has its anterior border in the slime papilla segment (sp) and the arrow indicates its presence in the mesoderm of the limb bud. A = antenna, J = jaw, scale bar = 200 μ m.

Chelicerates	Oc	Ch	Pp	L1	L2	L3	L4	Op1	Op2	Op3
<i>labial</i>										
<i>pb</i>										
<i>Hox3</i>										
<i>Dfd</i>										
Myriapods*	Oc	Ant	Int	Mn	Mx1	Mx2	Mxpd	L1	L2	L3
<i>labial</i>										
<i>pb</i>										
<i>Hox3</i>										
<i>Dfd</i>										
Crustaceans	Oc	Ant1	Ant2	Mn	Mx1	Mx2	T1	T2	T3	T4
<i>labial</i>										
<i>pb</i>										
<i>Hox3</i>										
<i>Dfd</i>										
Insects	Oc	Ant	Int	Mn	Mx	Lab	T1	T2	T3	A1
<i>labial</i>										
<i>pb</i>										
<i>bicoid*/zen*</i>	Anterior blastoderm									
<i>Dfd</i>										
Onychophora	Ant/Oc	Jaw	Sp	L1	L2	L3	L4	L5	L6	L7
<i>labial</i>										
<i>pb</i>										
<i>Hox3</i>										
<i>Dfd</i>										

S. 5 Scheme of the expression of the anterior *Hox* genes *lab* (purple), *pb* (orange), *Hox3* (yellow) and *Dfd* (green) in relation to segment borders in different arthropod groups and onychophorans. The anterior expression borders of the four anterior *Hox* genes are conserved between onychophorans and arthropods suggesting that the head segments can be aligned from anterior to posterior, see main text. The star at Myriapods indicates that a more recent investigation in myriapods show a slightly different expression pattern, however, the anterior expression border is the same (Janssen and Damen 2006). The star at bicoid/zen indicates that these genes have gained different functions in insects. For some of the original data on the expression of *Hox* genes and other genes relevant for the question of head segmentation in arthropods see: Abzhanov A, Kaufman T C (1999); Damen et al. (1998); Haas et al. (2001); Hughes and Kaufman (2002); Jager et al. (2006); Kimm and Prpic (2006); Posnien et al. (2009); Rogers and Kaufman (1996); Rogers et al. (2002); Schmidt-Ott and Technau (1992); Schmidt-Ott et al. (1994); Telford and Thomas (1998).

Supplementary material no. 6

The orthology assignment of the anterior *Hox* genes was based on phylogenetic analysis. The phylogenetic analyses were carried out using amino acid sequences. We compiled a *Hox* gene alignment including anterior *Hox* genes of representatives of bilaterians. The species names and their abbreviations used in phylogenetic analysis are provided in Table S 1. Sequences were aligned using the program ClustalX v.2.0.10. First the homeobox region was aligned, and then using the homeobox as anchor, the flanking regions were aligned with subsequent trimming carried out manually. Bayesian likelihood analyses were conducted using MrBayes version 3.1.1 with four simultaneous Markov chains per run and two independent runs per analysis. Chains were run for one million generations with a sampling frequency of 1000 generations and burnin of 1000. The clear classification of the *E. kanangrensis Hox* genes into

their orthology groups is apparent from phylogenetic analyses (S 6). Although our phylogenetic analysis clearly assigns the *E. kanangrensis* *Hox* genes to their paralog class with high support values, the internal grouping remains unclear.

Table S. 1 List of the species used in phylogenetic analysis

Abbreviation	Species name	Common name	phylum or class
<i>Bfl</i>	<i>Branchiostoma floridae</i>	amphioxus	Cephalochordata
<i>Btu</i>	<i>Bugula turrita</i>	bryozoan	Bryozoa
<i>Cel</i>	<i>Caenorhabditis elegans</i>	nematode	Nematoda
<i>Cin</i>	<i>Ciona intestinalis</i>	tunicate	Tunicata
<i>Dja</i>	<i>Dugesia japonica</i>	flatworm	Platyhelminthes
<i>Dme</i>	<i>Drosophila melanogaster</i>	fruit fly	Insecta
<i>Esc</i>	<i>Euprymna scolopes</i>	squid	Cephalopoda
<i>Eka</i>	<i>Euperipatoides kanangrensis</i>	velvet worm	Onychophora
<i>Fen</i>	<i>Flaccisagitta enflata</i>	arrow worm	Chaetognatha
<i>Lan</i>	<i>Lingula anatina</i>	brachiopod	Brachiopoda
<i>Lat</i>	<i>Lithobius atkinsoni</i>	centiped	Myriapoda
<i>Lgi</i>	<i>Lottia gigantea</i>	limpet	Gastropoda
<i>Lsa</i>	<i>Lineus sanguineus</i>	ribbon worms	Nemertea
<i>Mmu</i>	<i>Mus musculus</i>	house mouse	Vertebrata
<i>Ngr</i>	<i>Nymphon gracile</i>	sea spider	Pycnogonida
<i>Nvi</i>	<i>Nereis virens</i>	segmented worm	Polychaeta
<i>Pca</i>	<i>Priapulid caudatus</i>	Priapulid	Priapulida
<i>Pdu</i>	<i>Platynereis dumerilii</i>	segmented worms	Polychaeta
<i>Sca</i>	<i>Sacculina carcini</i>	crustacean	Cirripedia
<i>Sko</i>	<i>Saccoglossus kowalevskii</i>	hemichordate	Hemichordata
<i>Sro</i>	<i>Symsagittifera roscoffensis</i>	flatworm	Acoelomorpha
<i>Tca</i>	<i>Tribolium castaneum</i>	beetle	Insecta

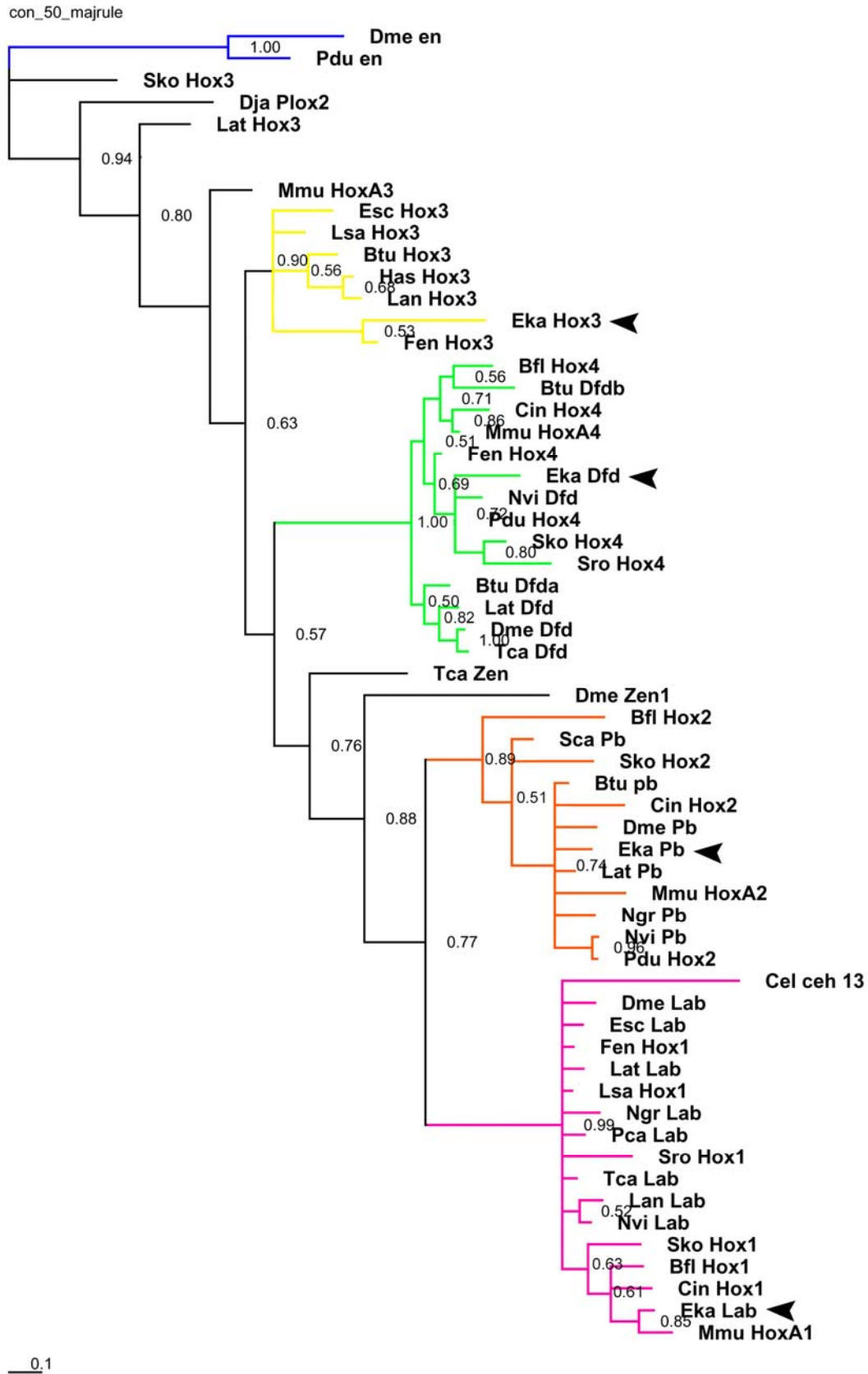


Figure S 6 Phylogenetic reconstruction of Hox paralogs group 1 (purple), paralogs group 2 (orange), and paralogs group 3 (yellow), and paralogs group 4 (green) relationships. *Engrailed (en)* is used as outgroup (blue). Arrow heads point *E. kanangrensis* Hox sequences.

Supplementary references

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