Gene expression pattern

Isolation of three zebrafish *dachshund* homologues and their expression in sensory organs, the central nervous system and pectoral fin buds

Katherine L. Hammond\(^{a,b,*}\), Robert E. Hill\(^a\), Tanya T. Whitfield\(^b\), Peter D. Currie\(^a\)

\(^{a}\)MRC Human Genetics Unit, Western General Hospital, Crewe Road, Edinburgh, EH4 2XU, UK

\(^{b}\)Centre for Developmental Genetics, University of Sheffield School of Medicine and Biomedical Science, Firth Court, Western Bank, Sheffield, S10 2TN, UK

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Abstract

*Drosophila dachshund* (dac) interacts with *sine oculis* (so), *eyes absent* (eya) and *eyeless* (ey) to control compound eye development. We have cloned three zebrafish dac homologues, *dachA*, *dachB* and *dachC*, which are expressed widely, in distinct but overlapping patterns. Expression of all three is found in sensory organs, the central nervous system and pectoral fin buds. *dachA* is also expressed strongly in the somites and *dachC* in the neural crest and pronephros. These expression domains overlap extensively with those of zebrafish *pax*, *eya* and *six* family members, the homologues of *Drosophila eya*, *eya* and *so*, respectively. This is consistent with the proposal that *Dach*, *Eya*, *Six* and *Pax* family members may form networks, similar to that found in the *fly* eye, in the development of many vertebrate organs. © 2002 Elsevier Science Ireland Ltd. All rights reserved.

Keywords: Eye; Ear; Otic vesicle; Sensory patch; Lateral line; Sensory ridge; Neuromast; Lateral line; Sensory ridge; Neuromast; Forebrain; Hypothalamus; Diencephalon; Midbrain; Habenula; Dorsal thalamus; Hindbrain; Rhombomere; Trigeminal ganglion; Spinal neuron; Spinal cord; Pronephros; Pectoral fin bud; Somite; Branchial arch; Neural crest; dachshund; dac; dach; pax; eya; six; Zebrafish

1. Results and discussion

*Drosophila* Dachshund (Dac) is fundamental to compound eye development and functions as part of an interacting network with Eyeless (Ey), Sine oculis (So) and Eyes absent (Eya; Treisman, 1999). Vertebrate homologues of *dac* have been isolated from mouse (*Dach1* and *Dach2*), human (*DACH1*) and chick (*Dach2*) and these are thought to act in networks similar to that found in the fly (Hammond et al., 1998; Caubit et al., 1999; Kozmik et al., 1999; Davis et al., 1999; Heanue et al., 1999; Davis et al., 2001). The vertebrate networks also include members of the Pax, Eya and Six gene families, the vertebrate counterparts of ey, eya and so, respectively.

In vertebrates, a Pax/Eya/Six/Dach network seems to be important in the development of a variety of organs, with a different selection of the Dach, Pax, Eya and Six family genes active in each tissue. Dach2, for instance, interacts with Pax3, Eya2 and Six1 in the developing chick somite (Heanue et al., 1999) and evidence is consistent with a similar network, including Dach1, Pax6, Eya1, 2, 3 and Six3, in the vertebrate eye (Hill et al., 1991; Xu et al., 1997; Loosli et al., 1999; Chow et al., 1999). Expression of members of all four gene families overlaps in many other areas including the pronephros, central nervous system (CNS), and otic vesicle, raising the possibility that a Dach/Eya/Pax/Six ‘cassette’ is important in all these tissues.

Here we report the isolation and characterization of three zebrafish *dachshund* genes, *dachA*, *dachB* and *dachC*. These genes are expressed extensively in the CNS, the pronephros and in the sensory organs of the lateral line, eye and ear, where many members of the zebrafish *pax*, *six* and *eya* families are also detected (Kobayashi et al., 2000; Nornes et al., 1998; Pfeffer et al., 1998; Riley et al., 1999; Sahly et al., 1999; Seo et al., 1998).

1.1. Isolation of *dachA*, *dachB* and *dachC*

We isolated *dachA*, *B*, and *C* by screening a zebrafish 15–19 h cDNA library with the dach-box N region (see below) of murine *Dach1*. These clones are 2883, 2357 and 2055 bp long, respectively and contain full length open reading frames of 602, 564 and 576 amino acids (Fig.
1a). DachC has the most similar amino acid sequence to murine Dach1, while DachA and DachB are more similar to chick and murine Dach2. Of the two, DachA is the most similar to Dach2 (Fig. 1b). Two regions highly conserved between mammalian and Drosophila Dachshund, Dach-box C and Dach-box N (also known as DD1 and DD2; Davis et al., 1999), are found in all three zebrafish proteins (Fig. 1b).

1.2. Expression analysis

We analyzed expression of dachA, B and C by whole-mount in situ hybridization between the 10 somite (s) stage and 72 h post-fertilization (hpf). All three genes are expressed widely, in distinct but overlapping patterns. dachA and dachC show significant expression similarity to mammalian Dach1 and Dach2, but dachB is less similar, being predominantly expressed in the lateral line system, which has no mammalian counterpart (Hammond et al., 1998; Caubit et al., 1999; Kozmik et al., 1999; Davis et al., 1999, 2001).

1.2.1. Sense organs

1.2.1.1. Eye. Only dachA is expressed in the developing eye. It is detected throughout the optic vesicle by 12s, and then is restricted to the lens from 20s to 34 hpf (Fig. 2A). Lens expression disappears by 48 hpf when strong retinal expression is seen in the ganglion cell layer (Fig. 2B). Retinal expression remains weakly detectable at 72 hpf.

1.2.1.2. Ear. dachA, dachB and dachC are all expressed in the ear. dachA is seen at 14s in two medial domains, one at each end of the otic vesicle (Fig. 2C). These are likely to be the areas where sensory hair cells of the maculae are developing (Haddon et al., 1998; Riley et al., 1997). From 20s (Fig. 2D,E) to 34 hpf (Fig. 2F), expression is seen in a dorso-medial band which encompasses the two original domains. In addition, at 34 hpf, expression is seen in the anterior macula and in an adjacent ventral epithelial region (Fig. 2F). At 48 hpf, weak expression is seen in both maculae. From 48 to 72 hpf, dorsal expression includes a duct-like
structure, believed to be the presumptive endolymphatic duct (Fig. 2G,H). Expression is also detected in the semicircular canal projections (Fig. 2G,H).

dachB is expressed in the maculae at 34 hpf and in all sensory patches from 48 to 72 hpf (Fig. 2I,J).

dachC is expressed in a ventral epithelial region from 34 to 42 hpf (Fig. 2K,L).

1.2.1.3. Lateral line system. Only dachB is strongly expressed in the lateral line system, although dachA is
expressed weakly in the migrating midbody lateral line primordium and neuromasts (not shown).

*dachB* is expressed in the pre-otic lateral line placode from 15s (Fig. 4B, E—shown at 20s) and continues to be expressed in the sensory ridges (Fig. 4D) and, until 72 hpf, in the neuromasts derived from these (Fig. 4G, H). The midbody lateral line primordium expresses *dachB* strongly as it migrates the length of the body from 20s until 48 hpf (Fig. 4C, F—shown at 24 hpf). The neuromasts it deposits also express *dachB* until 72 hpf (data not shown).

1.2.2. CNS

All three fish genes are expressed in the CNS.

1.2.2.1. dachA. *dachA* is first detected in early somitogenesis in the forebrain and spinal cord (Fig. 3A—shown at 14s). Hindbrain expression, in rhombomeres 3, 5, and 7, is seen at 16s and is maintained until 34 hpf (Fig. 3B, C). By 48 hpf, hindbrain expression remains but is not obviously restricted to specific rhombomeres (Fig. 3G). Forebrain expression is seen in a dorsal region and in the hypothalamus by 20s (Fig. 3B–D—shown at 24 hpf); the

1.2.2.2. dachB. At 10s, ventro-medial expression is seen in the spinal cord and lateral, punctate expression, representing individual neurons, is seen in the rostral embryo (Fig. 4A). At 20s, punctate expression throughout the caudal neural tube is seen but ventro-medial expression has disappeared (Fig. 4B, E). At 24 hpf, the hindbrain and the nucleus of the post-optic commissure express *dachB* (Fig. 4C, F) and at 48 hpf, expression is detected in the hindbrain and neurons of the midbrain tegmentum (Fig. 4G–I).

1.2.2.3. dachC. Forebrain expression begins to appear at 20s and is strong in the diencephalon by 24 hpf (Fig. 5B, C). Expression is now also seen in the cerebellum, rhombomere 4 of the hindbrain and spinal neurons (Fig. 5B, C). By 34 hpf, the trigeminal ganglion expresses
Fig. 4. Expression of \textit{dachB} in 10s to 48 hpf zebrafish embryos. Anterior is to the left. Scale bar, 100 $\mu$m, except in (J) where it is 50 $\mu$m. (A) 10s, lateral view: expression is seen in a ventro-medial domain of spinal cord (wide arrow) and in individual, lateral neurons in the rostral part of the embryo. (B) 19s, lateral view; (E), 19s, dorsal view: expression is seen in individual neurons throughout the neural tube and in the pre-otic lateral line placode (thin arrow) which is seen just beginning to split to form dorsal and ventral sensory ridges. Ventro-medial expression has now disappeared (wide arrow). (C) 24 hpf, lateral view; (F), 24 hpf, dorsal view: expression remains in discrete, lateral regions of the hindbrain and anterior spinal cord (wide arrow) and is seen in the migrating midbody lateral line primordium (arrowhead) and the nucleus of the post-optic commissure (thin arrow). (D) 34 hpf, lateral view: the three sensory ridges (arrows) derived from the pre-otic lateral line placode all express \textit{dachB}. Expression is also seen in one branchial arch (arrowhead). (G) 48 hpf, lateral view; (H), 48 hpf, dorsal view; (I), 48 hpf dorsal view: expression is seen in the nascent neuromasts deposited around the periphery of the eye by the sensory ridges (thin arrows (G,H)), the hindbrain (hb) and in individual neurons of the midbrain tegmentum (I). (J) 48 hpf, pectoral fin bud, dorsal view (distal to bottom): expression is seen weakly in the developing muscle masses.

Fig. 5. Expression of \textit{dachC} in 20s to 72 hpf zebrafish embryos. Anterior is to the left. Scale bar, 100 $\mu$m, except (E) where it is 50 $\mu$m. (A) 20s, lateral view (dorsal to top): expression is strong in the neural crest, seen migrating ventrally (black arrow). At 10–15s expression is similar although migration has yet to occur (not shown). This is very similar to murine \textit{Dach1} expression, which is seen in premigratory and migratory neural crest. (B) 24 hpf, dorsal view; (C), 24 hpf, lateral view (dorsal to top): expression is seen in the cerebellum (black arrow), pronephric duct (black arrowhead), spinal neurons (white arrow), neural crest, diencephalon (*) and deep within rhombomere 4 of the hindbrain (white arrowhead). Just posterior to rhombomere 4 (below focal plane), branchial arch expression is seen. (D) 34 hpf, lateral view: shows trigeminal ganglion expression (black arrow) between the eye and the ear. (E) Pectoral fin bud, 48 hpf, dorsal view (distal to top): The developing muscles express \textit{dachC} strongly at 48 hpf. (F) 48 hpf, lateral view; (G), 48 hpf dorsal view: expression is seen in the habenula and dorsal thalams (white arrow), rhombomeres of the hindbrain, and in the midbrain tectum and tegmentum. (H) 72 hpf, lateral view; (I), 72 hpf, dorsal view: expression is mainly restricted to two longitudinal hindbrain regions either side of the midline.
dachC (Fig. 5D). At 48 hpf, dachC is seen in the habenula, dorsal thalamus, midbrain tectum and tegmentum, cerebellum and rhombomeres of the hindbrain (Fig. 5F,G). At 72 hpf, expression is mainly restricted to two longitudinal hindbrain stripes (Fig. 5H,I).

1.2.3. Other domains of expression

1.2.3.1. Pectoral fin buds. All three dach genes are expressed in the pectoral fin buds. dachA is seen throughout the bud at 24 hpf but is restricted to a larger anterior and smaller posterior domain by 48 hpf (Fig. 3E,F). dachB and dachC are both found in the distal bud at 30 hpf. dachC is strongly expressed in the developing fin muscle at 48 hpf (Fig. 5E), while dachB is weakly expressed in a similar region (Fig. 4J). A small ventral region between the pectoral fin buds expresses all three genes strongly at 24 hpf (data not shown).

1.2.3.2. Somites. dachA is expressed transiently in the most anterior 4–5 somites from 12s to 16s (Fig. 3A).

1.2.3.3. Branchial arches. dachB is expressed in a single branchial arch at 34 hpf (Fig. 4D) and dachC is expressed in two at 24 hpf (Fig. 5B).

1.2.3.4. Pronephros. dachC is strongly expressed in the pronephros at 24 hpf (Fig. 5B,C).

1.2.3.5. Neural crest. dachC is expressed strongly in the pronephros at 24 hpf (Fig. 5B,C). At 72 hpf, expression is mainly restricted to two at 48 hpf (Fig. 5B). A small ventral region between the pectoral fin buds expresses all three genes strongly at 24 hpf (data not shown).

2. Materials and methods

dachA was isolated by screening a zebrfish 15–19 h (28.5 °C) polyA+ cDNA library in Uni-Zap XR lambda vector (a gift from Bruce Appel, University of Oregon) with a template produced by PCR amplification of the Dach-box N conserved region of murine Dach1, using primers GCT TTC GAC CTG TTC CTG AAG and CTG TGA GTC CTC TTA GGA GGC. Hybridization was carried out as in Nehls et al. (1994), after which positive clones were excised from the Uni-Zap phage vector (Stratagene) to produce pBluescript SK+ phagemid.

dachB and dachC were isolated by re-screening the library with probe amplified from the Dach-box N region of dachA using primers AAC TGG CAT TGG TGC AGT CG and GTG AAA GTG GCC TCG TTC AC.

Sequencing was carried out using an ABI 373A automated fluorescent sequencer and an ABI Prism dRhodamine terminator cycle sequencing ready reaction kit (Perkin-Elmer Applied Biosystems). Sequences were analyzed using Applied Biosystems 377A software and programs available through http://workbench.sdsc.edu.

2.1. In situ hybridization

Whole-mount in situ hybridization was carried out as in Oxtoby and Jowett (1993). Probes were labelled using a DIG labelling kit (Roche). Embryos used were either WIK or gol+/- and some embryos were treated with 0.0035% 1-phenyl-2-thiourea (Sigma), to prevent pigment formation (Westerfield, 1994).

For microscopy, embryos were cleared and mounted in glycerol or were dehydrated through an ethanol series, cleared in 2:1 benzyl alcohol/benzyl benzoate, and mounted in DePeX (BDH).

3. Note

Sequence data for dachA, dachB and dachC have been deposited with GenBank, accession numbers AF427108, AF427109 and AF207110.

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References


