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Corrigendum

Corrigendum to "A molecular analysis of neurogenic placode and cranial sensory ganglion development in the shark, *Scyliorhinus canicula*" [Dev. Biol. 304 (2007) 156–181]

P. O'Neill, R.B. McCole, C.V.H. Baker*

Department of Physiology, Development and Neuroscience, Anatomy Building, Downing Street, Cambridge CB2 3DY, UK

It has come to the attention of the authors that, owing to a computer file mix-up, the partial cDNA sequence submitted to GenBank as *Scyliorhinus canicula Eya4* (accession number EF185886) was incorrect. Although the text of the article and the *Eya4* expression data are unaffected, this sequence was used to prepare the *Eya4*-related information presented in Fig. 1, Tables 1 and 2, and Supplementary Fig. 5. The GenBank submission has been corrected (accession number EF185886.2) and corrected versions of the above-named figures and tables are provided here. The authors sincerely apologise for this mistake and for any inconvenience this may have caused.

The authors would like to acknowledge the invaluable assistance of James Blundell in preparing the corrected figures and tables.

^{*} Corresponding author. Fax: +44 1223 333786. E-mail address: cvhb1@cam.ac.uk (C.V.H. Baker).

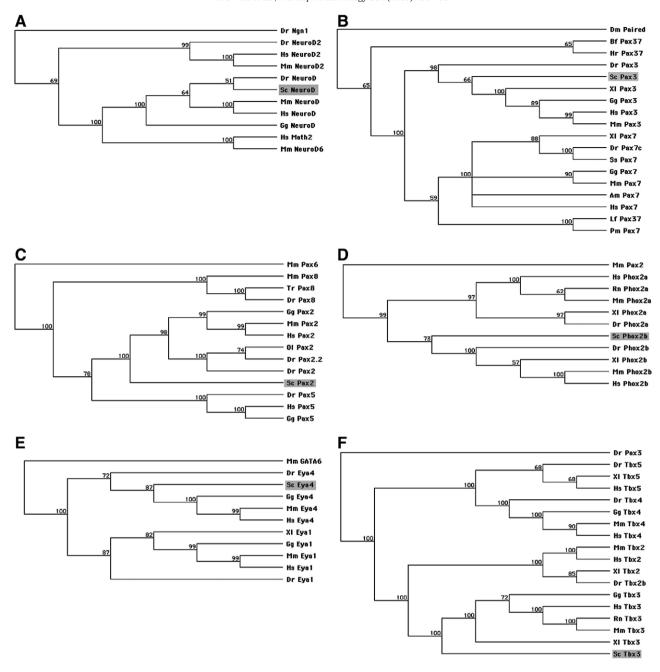


Fig. 1. Phylogenetic trees, constructed in MacVector using the neighbor-joining method, of predicted protein sequences confirming the identity of cloned fragments of six *S. canicula* transcription factors (shaded box in each tree). Figures adjacent to nodes indicate percentage bootstrap support values. (A) NeuroD. (B) Pax3. (C) Pax2. (D) Phox2b. (E) Eya4. (F) Tbx3. Species abbreviations: Am, Ambystoma mexicanum; Bf, Branchiostoma floridae; Cf, Canis familiaris; Ci, Ciona intestinalis; Dm, Drosophila melanogaster; Dr, Danio rerio; Fr, Fugu rubripes; Gg, Gallus gallus; Hr, Halocynthia roretzi; Hs, Homo sapiens; Lf, Lampetra fluviatilis; Mm, Mus musculus; Ol, Oryzias latipes; Pm, Petromyzon marinus; Rn, Rattus norvegicus; Sc, Scyliorhinus canicula; Ss, Salmo salar; Tr, Takifugu rubripes; Xl, Xenopus laevis.

 Table 1

 Degenerate primer sequences used to isolate fragments of S. canicula cDNAs.

Gene	Forward primer	Reverse primer	Annealing temp. °C
NeuroD	AAACGACGAGGACCTAAGAAGAARAARATGAC	TCGAACTCAGCAGATGGCTCRTGYTTRAA	61
Pax3	AGGAGACAGGCTCCATCAGA	GGGACAGAGCGTAATCAGTCTGNGGYTGRTG	55
Pax2	CACGGNGGNGTGAACCAGC	TYCCRGGNACCATKCCNGC	55
Phox2b	CAGGCTTCCGGATTCCARTAYAAYCC	GGAGGACAGCACGGAAGCRAANGGNCC	50
Eya4	ATGGAAATGCAGGATCTA	TAATACTGNGCRTACTG	55
Tbx3	CATCAGCCGCCRTTTTTCCC	CCATCGCCAACTTACTGGGG	55

Table 2 Putative placodal marker genes cloned for expression analysis in *S. canicula*.

Gene	Expected expression	Size (bp)	Equivalent amino acids of mouse homologue	Predicted amino acid identity to mouse homologue	GenBank Accession Number
NeuroD	Pan-neuronal	626	83–293	91% overall 98% in bHLH domain	EF185882
Pax3	Ophthalmic trigeminal placodes	944	92–415	82% overall 84% over partial Pax domain 98% in homeodomain	EF185883
Pax2	Otic and epibranchial placodes	898	24–344	78% overall 99% over partial Pax domain	EF185884
Phox2b	Epibranchial placode-derived neurons	691	38–297	75% overall 97% in homeodomain	EF185885
Eya4	Isolated in attempt to isolate <i>Eya1</i> as a pan-placodal marker	647	30-256	72% overall (59% to mouse Eya1)	EF185886
Tbx	Lateral line placodes	1435	35–506	65% overall 96% in T-box	EF185887

See Supplementary Figs. 1–6 for protein alignments. References: *NeuroD*: Chae et al. (2004). *Pax3*: Stark et al. (1997). *Pax2*: Baker and Bronner-Fraser (2000); Ohyama and Groves (2004); Schlosser and Ahrens (2004). *Phox2b*: reviewed in Brunet and Pattyn (2002). *Eya1/4*: reviewed in Bailey and Streit (2006); Schlosser (2006). *Tbx3*: reviewed in Schlosser and Ahrens (2004).

Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4	1 1 1 1		21 50 50 50 49
Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4	22 51 51 51 50	SKLDKANLSNSSIISNGTAVKT SKLDKSGLSSTSVTINGTGVSLLAVKT SKLEKSNLSSTSVTINGTGGENMTVLNIADWLLSCNTPSSATMSLLAVKT SKLDKNLSSTSVTINGTGGENMTVLNTADWLLSCSTPSSATMSLLAVKT SKLDKNILSSTSVTINGTGGONMTVLNTADWLLSCSTPSSATMSLLAVKT SKLDKNILSN-NTTNGTGVKS *** * ***	43 77 100 100 70
Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4	78 101	EPMSSSDTATTTOGGLDNYTGSVITSGGYSPRGIHQYSPQLYPSKPYPH EPLHSSESTITTGDGALDTFTGSVITSSGYSPRSAQQYSPQLYPSKPYPH EPLNSSETTATTGDGALDTFTGSVITSSGYSPRSAHQYSPQLYPSKPYPH EPMNSNETTTTTGDGSLDTFTGSVITSSGYSPRSAHQYSPQIYPSKPYPH EPLNSSEAVSSACDSGLDTYTGSVISSGYSPRPAHQYSPPLYPSKPYPH ** **********************************	93 127 150 150 120
Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4	94 128 151 151 121	ILSTPAVQSMTPYAGQTQYSGMQQPAVYAAYSQTGQHYGLPTY ILSTPAAQTMSAYAGGTQYSGMQQPAVYTAYSQTGQPYSLPAYDLGVM ILSTPAAQTMSAYAGGTQYSGMQQPAVYTAYSQTGQPYSLPTYDLGVM ILSTPAAQTMSAYAGGTQYSGMQQPAVYTAYSQTGQPYSLPTYDLGVM ILSTPAAQTMSAYAGGTQYSGMQQPAVYTAYSQTGPYSLPTYDLGVM ILSTPVAPPMSAYTGQSQFSSMQQSTVYTPYSQTTPPYGLSTYATDLGVM ** * * * * * * * * * * * * * * * * * *	198 198
Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4	176 199 199	GIKTEGGLPQAQSALQTGCLSYSPGFAAPQPGQTAYSYQMQGSSFTPS LPAKKTESGLSQTQSPLQSGCLSYSPGFSTPQPGQTTYSYQMPGSSFAPS LPAIKTESGLSQTQSPLQSGCLSYSPGFSTPQPGQTTYSYQMPGSSFAPS LPGIKTESGLSQTQSPLQSGCLSYSPGFSTPQPGQTTYSYQMPGSSFTPS LPGIKTEGGLTQTQSTLQSG-LSYSPGFTHPIRCQQVQVLQPLLVSTLPT **** ** * * * * * * * * * * * * * * *	184 225 248 248 219
Mm Hs Gg	Eya4 Eya4 Eya4 Eya4 Eya4			216 274 297 297 241

Supplementary Fig. 5. Alignment of the predicted protein sequence encoded by the clone fragment of *S. canicula Eya4* cDNA, with mouse, human, chick and zebrafish Eya4 proteins. Asterisks indicate residues identical in all aligned sequences. Species abbreviations: Dr, *Danio rerio*; Gg, *Gallus gallus*; Hs, *Homo sapiens*; Mm, *Mus musculus*; Sc, *Scyliorhinus canicula*.