

neurogenes synteny project

1.

Paper notes

Moroz et al., 2014 [1]

Table 34S -structure of figure shows that it is from bilaterian perspective (closer to bilateria more rectangles filled in)

-remember there are also random absences in cnidaria; the mirror of bilateria, but all the proteins are characterized from bilateria

-no examples where ctenophores or sponges don't have something present in fungi, capsaspora, monosiga

-Suppl Table 12as - it's possible didn't use Amphimedon genome, but Amphimedon was covered by the other papers and I crossreferenced them.

Mentioned in text:

Not in ctenophores:

neurogenin

NeuroD

Achaete-scute

REST

HOX

Otx

-not that much overlap in genes looked at by Riesgo vs Moroz

Ryan et al., 2013 [2]

netrin, slit, unc-5 (axon guidance) not in Mnemiopsis or Amphimedon

-used genomes, since based on Alie and Manuel 2010

Supplementary Table S17: Presence and absence of post-synaptic genes - pretty much Alie and Manuel 2010

Supplementary Table S19: Presence and absence of Dopamine / Norepinephrine /Epinephrine Biosynthetic Pathway components

-are seqs of the animals in S17 genomes? Unsure, but all animals in table have genomes (and the Mle seqs are from the genome)

-AMPA iGluR and NMDA iGluR included as iGluR

Alie and Manuel, 2010 [3]

-used genomes

-Ryan built on Fig. 1. Cross ref with current data to make sure have everything.

-Only use Monosiga, Trichoplax, Amphimedon, Nematostella, Hydra, Homo

Capitella (3 absences), Drosophila (2 absences), Homo very similar with few differences

Unicellular animals mostly missing everything (except B-cat and PMCA). Start with Monosiga which has more things. B-cat and PMCA are ancient - interesting?

AMPA and NMDAR collapsed into iGluR in table; presence of one of these trumped absence of the other
PKC alpha-beta-gamma = PKC on table

Table

Table abbreviations

DBH - dopamine-B-hydroxylase

DDC - DOPA decarboxylase

TH - tyrosine hydroxylase

TPH - tryptophan hydroxylase

PAH - phenylalanine hydroxylase

GAD - glutamate decarboxylase

Qdpr - quinoid dihydropteridine reductase,

Slc18A2 = Homo sapiens solute carrier family 18 member 2,

Pnmt = phenylethanolamine N-methyltransferase

Missing domains

Piccolo - Pleurobrachia - missing ZF (Moroz et al., 2014)

Erbin - Pleurobrachia - missing PDZ (Moroz et al., 2014)

Species names written to the broadest level - eg. *Monosiga brevicollis* in Riesgo et al but only *Monosiga* in Moroz, so put *Monosiga* only

Many entries have NA but if combine:

Salpingoeca + *Monosiga* = Choanoflagellida

Pleurobrachia + Mnemiopsis = Ctenophora

Amphimedon + Ooscarella = Porifera

Nematostella + Hydra = Cnidaria

Get only 4 entries that have an NA.

(What about 0/1s (conflicting info?) >> decided to transform 0/1s into NA

Loss_Status: P1C0: present in Porifera, absent in Ctenophora - 6 instances

C1P0: present in Ctenophora, absent in Porifera - 3 instances

T0: absent in Trichoplax but present in Ctenophora or Porifera - 5 instances

There is only 2 instances where Capsaspora has a 1 while choanoflagellates have 0: GABAR and DDC. Don't use column in second iteration

'Fungi' is very vaguely defined - don't use column in second iteration

Stopped at Delta catenin

Make new table where all 0/1s or missing_domains (i.e. not 0,1,NA) into NA

Create a new table where species for Ctenophora, Porifera combined: <https://stackoverflow.com/questions/14563531/combine-column-to-remove-nas>

Papers+Links

Riesgo et al., 2014

<https://academic.oup.com/mbe/article/31/5/1102/993377>

Neural genes Fig

<https://academic.oup.com/view-large/figure/74385341/msu057f3p.jpeg>

Moroz et al., 2014

<https://www.nature.com/articles/nature13400>

Table 34S:

<https://media.nature.com/original/nature-assets/nature/journal/v510/n7503/extref/nature13400-s1.pdf>

Ryan et al, 2013

<http://science.sciencemag.org/content/342/6164/1242592>

Suppl Mat:

<http://science.sciencemag.org/content/sci/suppl/2013/12/11/342.6164.1242592.DC1/Ryan.SM.pdf>

Alie and Manuel, 2010

<https://bmcevolbiol.biomedcentral.com/articles/10.1186/1471-2148-10-34>

Srivastava et al., 2010

Suppl.S8.9 <https://media.nature.com/original/nature-assets/nature/journal/v466/n7307/extref/nature09201-s1.pdf>

2. Should we be expecting these genes in these animals?
Why should they use similar genes?
How misguided is this approach? What is the true question implied by this approach?

References

1. Leonid L. Moroz MRC Kevin M. Kocot. The ctenophore genome and the evolutionary origins of neural systems. *Nature*. Nature Publishing Group; 2014;510: 109–114. doi:10.1038/nature13400
2. Joseph F. Ryan CES Kevin Pang. The genome of the ctenophore *mnemiopsis leidyi* and its implications for cell type evolution. *Science*. American Association for the Advancement of Science; 2013;342: 1242592. doi:10.1126/science.1242592
3. Alié A, Manuel M. The backbone of the post-synaptic density originated in a unicellular ancestor of choanoflagellates and metazoans. *BMC Evolutionary Biology*. 2010;10: 34. doi:10.1186/1471-2148-10-34