

neurogenes synteny project

1.

Paper notes - neural genes presence/absences

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>

Synteny programs/papers

ghost locus hypothesis:

Ramos et al., 2012 [4]

<https://www.sciencedirect.com/science/article/pii/S0960982212009888>

-first ghost locus paper - parahox, Amphimedon + Trichoplax

Fortunato et al, 2014 [5] - sycon Parahox

<https://www.nature.com/articles/nature13881>

-second ghost locus paper?

Ferrier 2015 [6] (review)

<https://academic.oup.com/bfg/article/15/5/333/1741867>

Reviews:

Liu et al 2018 [7]

<https://bmcbioinformatics.biomedcentral.com/articles/10.1186/s12859-018-2026-4>

-most synteny programs designed with assumption working on complete high quality genomes.

-need N50 of at least 1Mb for robust synteny analysis

-Fig. 5 - Below 0.5 Mb error rate skyrockets - looks like close to 20-30% for ~100-200 kbs N50s -This can represent a major source of systemic bias in my analysis

Scaffold N50s of my genomes

Mnemiopsis (from orig [2]): 187 kb

Pleurobachia (Suppl Table 5S from [1]): 20.607 kb

Amphimedon orig, Ensembl (https://metazoa.ensembl.org/Amphimedon_queenslandica/Info/Annotation/):

120 kb >> likely improved, looking for Aqu2.1 (or is this only a re-annotation not reassembly?)

- Slightly confused with scaffold N50 stats in [8] suppl Table S2.3.2

Oscarella carmela (Suppl from [9]): 5.897 kb!! :O

Data/downloads

Pleurobachia genome: https://www.ncbi.nlm.nih.gov/assembly/GCA_000695325.1

P.bachei_draft_genome_v.1.1

Organism: Pleurobrachia bachei (ctenophores)

Submitter: University of Florida

Date: 2014/05/21

Assembly level: Scaffold

Genome representation: full

RefSeq category: representative genome

GenBank assembly accession: GCA_000695325.1 (latest)

RefSeq assembly accession: n/a

IDs: 180401 [UID] 1073948 [GenBank]

-paper said deposited at Moroz's website; links don't work on website.

Mnemiopsis leidyi: https://www.ncbi.nlm.nih.gov/assembly/GCA_000226015.1/

MneLei_Aug2011

Organism name: Mnemiopsis leidyi (sea walnut)

BioSample: SAMN02953801 BioProject: PRJNA64405

Submitter: National Human Genome Research Institute, National Institutes of Health

Date: 2011/09/19

Assembly level: Scaffold

Genome representation: full

RefSeq category: representative genome

GenBank assembly accession: GCA_000226015.1 (latest)

RefSeq assembly accession: n/a

RefSeq assembly and GenBank assembly identical: n/a

WGS Project: AGCP01

Assembly method: Phusion v. 1.02

Genome coverage: 12xSequencing technology: 454 GS-FLX Titanium; Illumina GA IIX

IDs: 304208 [UID] 304208 [GenBank]

Amphimedon queenslandica: v1.0: https://www.ncbi.nlm.nih.gov/assembly/GCF_000090795.1

Organism: Amphimedon queenslandica (sponges)

Submitter: US DOE Joint Genome Institute (JGI-PGF)

Date: 2010/05/28

Assembly level: Scaffold

Genome representation: full

RefSeq category: representative genome
GenBank assembly accession: GCA_000090795.1 (latest)
RefSeq assembly accession: GCF_000090795.1 (latest)
IDs: 293608 [UID] 111438 [GenBank] 293608 [RefSeq]

Oscarella carmela: <http://www.compagen.org/datasets.html> OCAR not *Oscarella* sp.

-added .fna and gzipped

-*Oscarella carmela* (this assembly) renamed *Oscarella pearsei*; *Oscarella* sp. in Compagen redescribed *Oscarella carmela*. See <https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0183002> - old *O. carmela* papers based on two species (*carmela* + *pearsei*). Both in compagen, but although there is press release compagen didn't change their names in db. *Can't find annotation file*.

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: neural genes

<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 - neural genes <https://media.nature.com/original/nature-assets/nature/journal/v466/n7307/extref/nature09201-s1.pdf>

Nichols et al., 2012

<https://www.pnas.org/content/109/32/13046>

Suppl

<https://www.pnas.org/content/pnas/suppl/2012/07/25/1120685109.DCSupplemental/sapp.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

4. Ramos OM, Barker D, Ferrier DE. Ghost loci imply hox and parahox existence in the last common ancestor of animals. *Current biology*. Elsevier; 2012;22: 1951–1956.

5. Fortunato SA, Adamski M, Ramos OM, Leininger S, Liu J, Ferrier DE, et al. Calcisponges have a parahox gene and dynamic expression of dispersed nk homeobox genes. *Nature*. Nature Publishing Group; 2014;514: 620.

6. Ferrier DE. The origin of the hox/parahox genes, the ghost locus hypothesis and the complexity of the first animal. *Briefings in functional genomics*. Oxford University Press; 2015;15: 333–341.

7. Liu D, Hunt M, Tsai IJ. Inferring synteny between genome assemblies: A systematic evaluation. *BMC bioinformatics*. BioMed Central; 2018;19: 26.

8. Srivastava M, Simakov O, Chapman J, Fahey B, Gauthier ME, Mitros T, et al. The amphimedon queenslandica genome and the evolution of animal complexity. *Nature*. Nature Publishing Group; 2010;466: 720.

9. Nichols SA, Roberts BW, Richter DJ, Fairclough SR, King N. Origin of metazoan cadherin diversity and the antiquity of the classical cadherin/ β -catenin complex. *Proceedings of the National Academy of Sciences*. National Acad Sciences; 2012;109: 13046–13051.