

Phenoscape

Informatics to reason across evolutionary and developmental biology

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Jim Balhoff, Peter Midford

Two problems:

- We need a way to find **candidate genes** (**networks**) for evolutionary **morphology**
- We need a way to **aggregate comparable phenotypic data** across studies

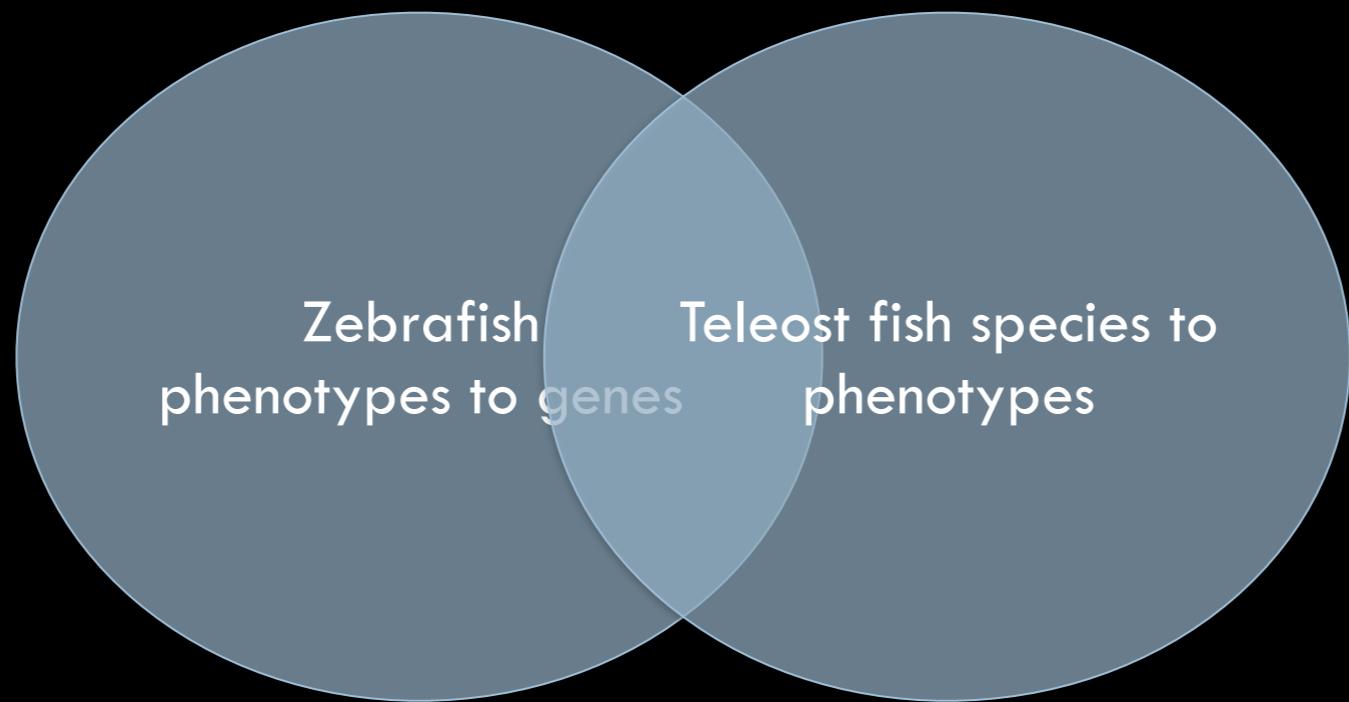
candidate genes for evolutionary novelties?



Pimelodus maculatus

photo J. Lundberg, ANSP 2002

Ontologies bring together diverse data around **phenotype**:



Candidate genes
Broad-scale view of phenotypes

Zebrafish \longleftrightarrow Human

Conservation of gene sequence & function and phenotype



slc24a5 involved in pigmentation similarity between fish and humans (Lamason et al., 2005)

Translational medicine

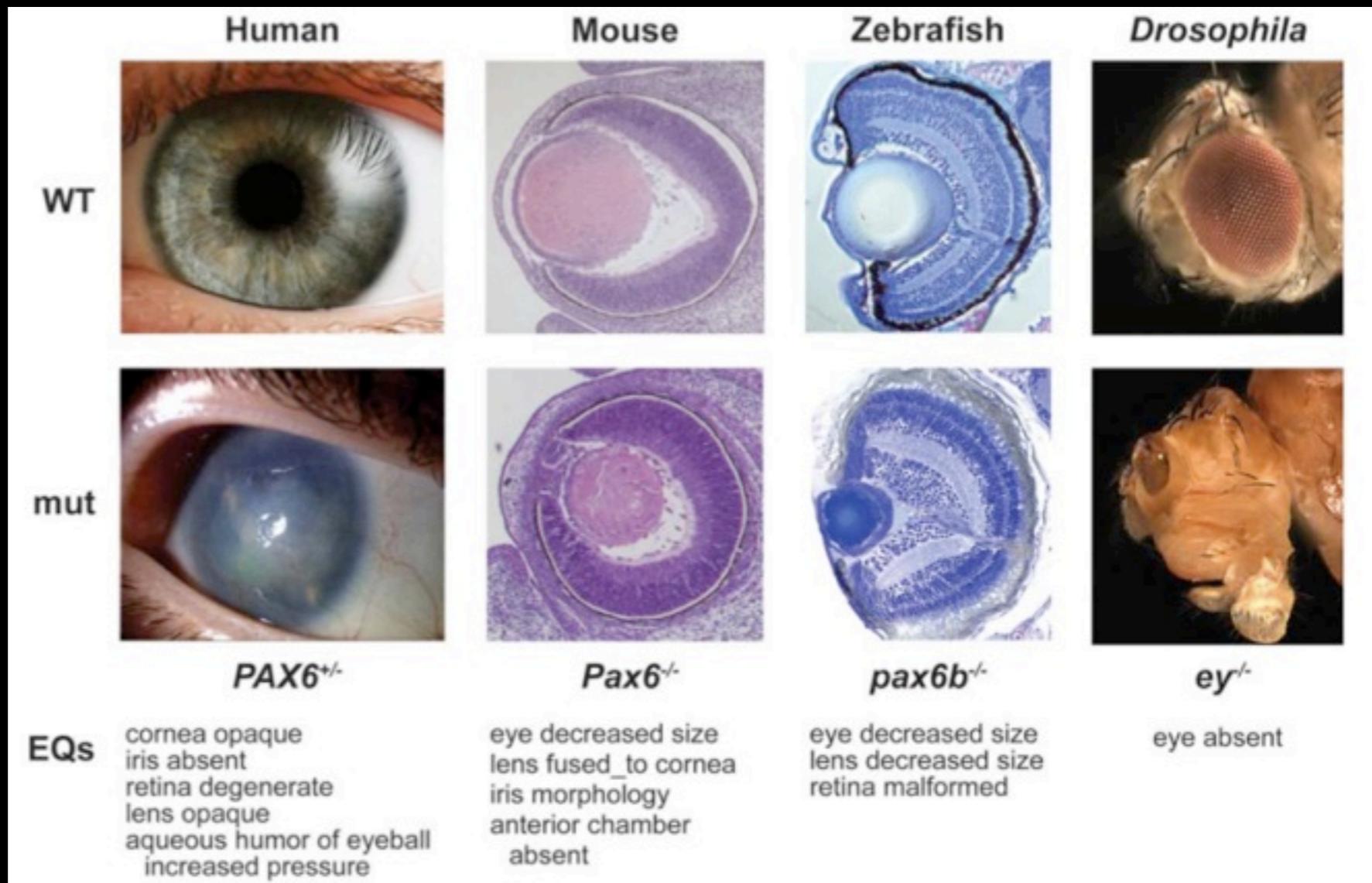


Fig. 1, Washington et al., 2010

Translation from model organisms to humans

'Translational biodiversity'

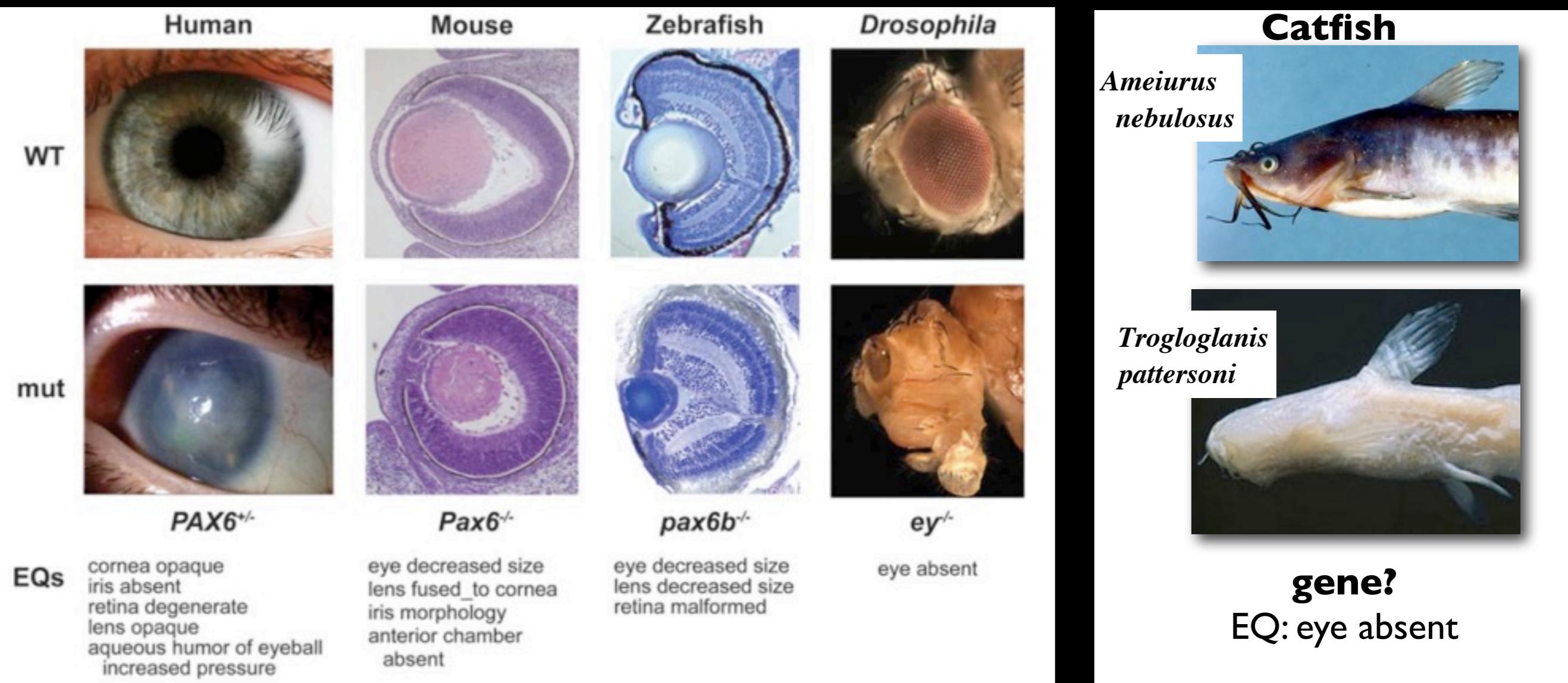


Fig. 1, Washington et al., 2010

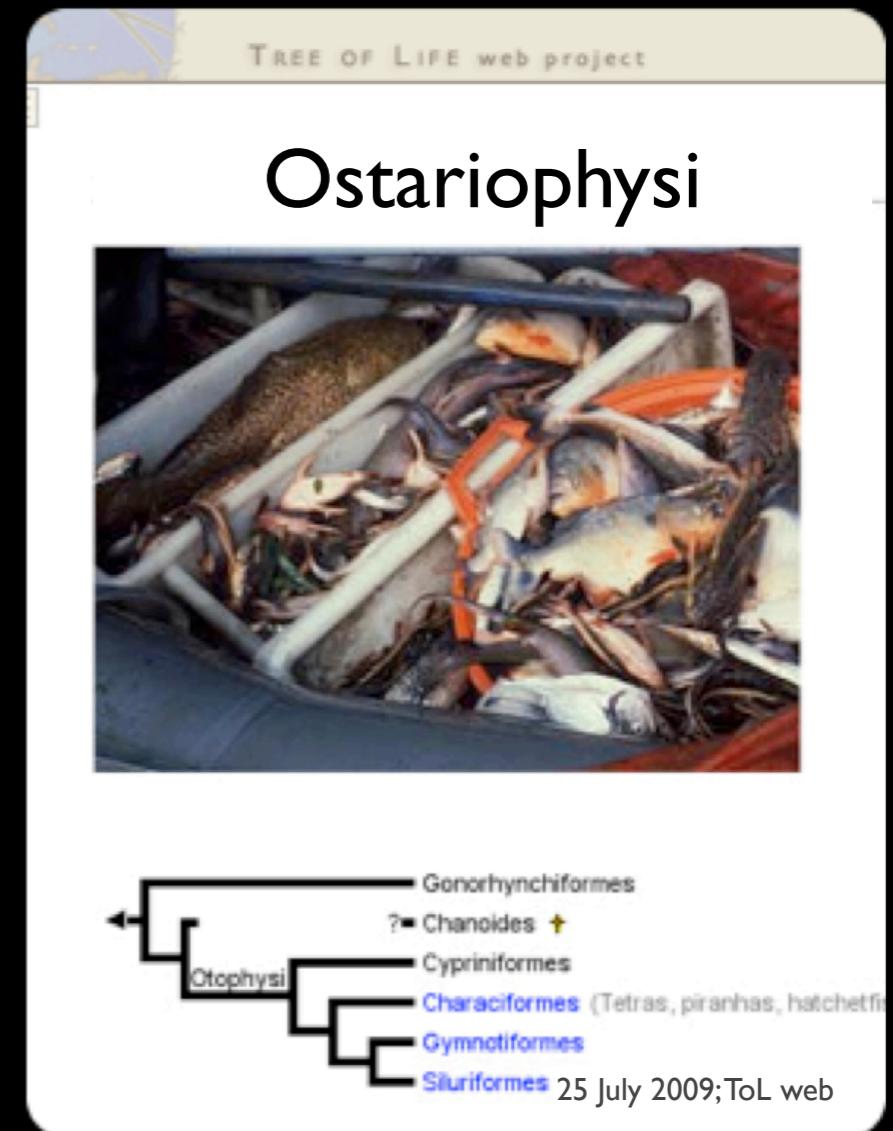
Translation from model organisms to evolutionary species



Phenoscape



- Teleost fishes + zebrafish
- Aim: Map evolutionary phenotype data to genetic databases
- Foster ‘devo-evo’ synthesis; candidate gene discovery; data aggregation
- Create resource to enable data-mining and discovery for broad scale evolutionary patterns





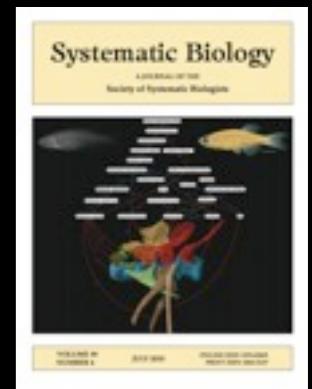
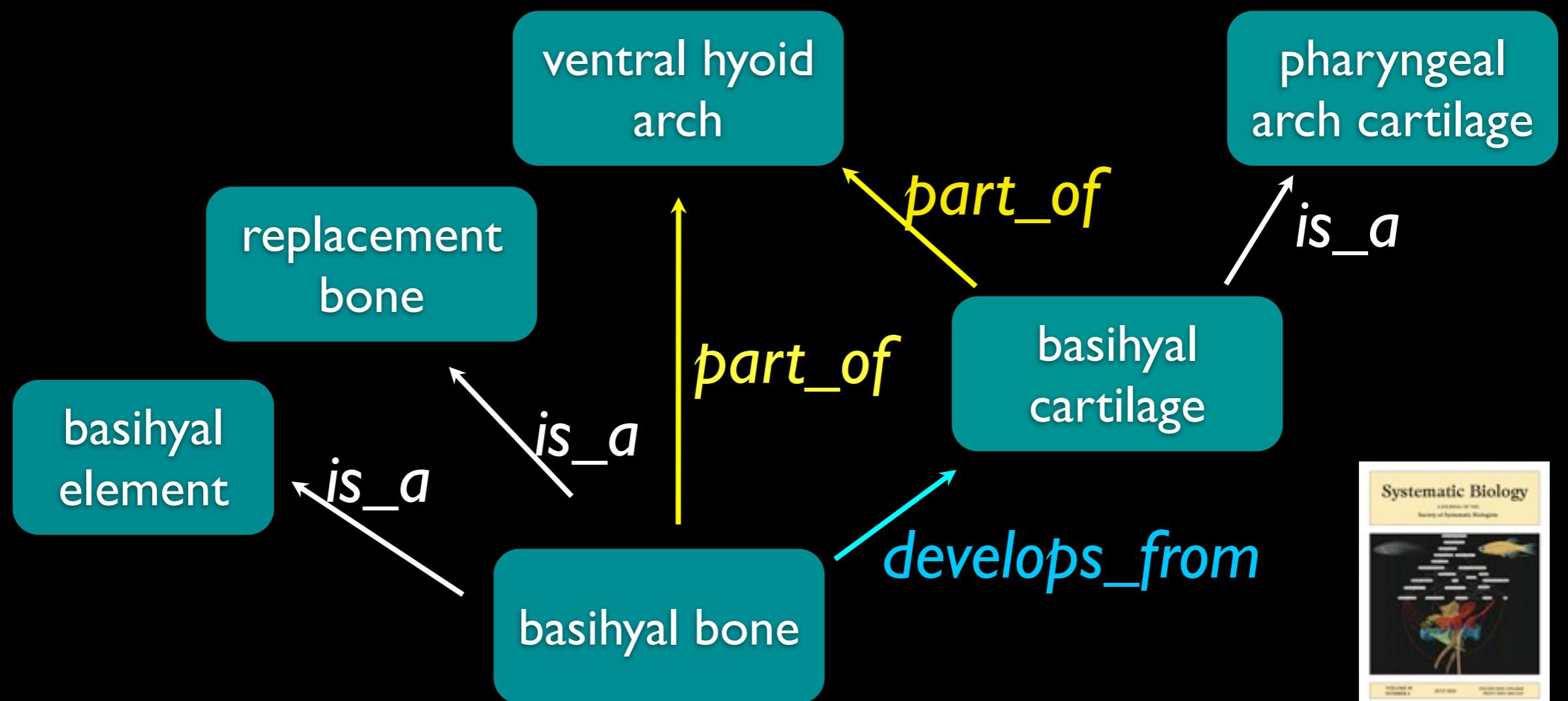
Phenoscape



- Teleost fishes + zebrafish
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Multispecies anatomy ontology: Teleost Anatomy Ontology



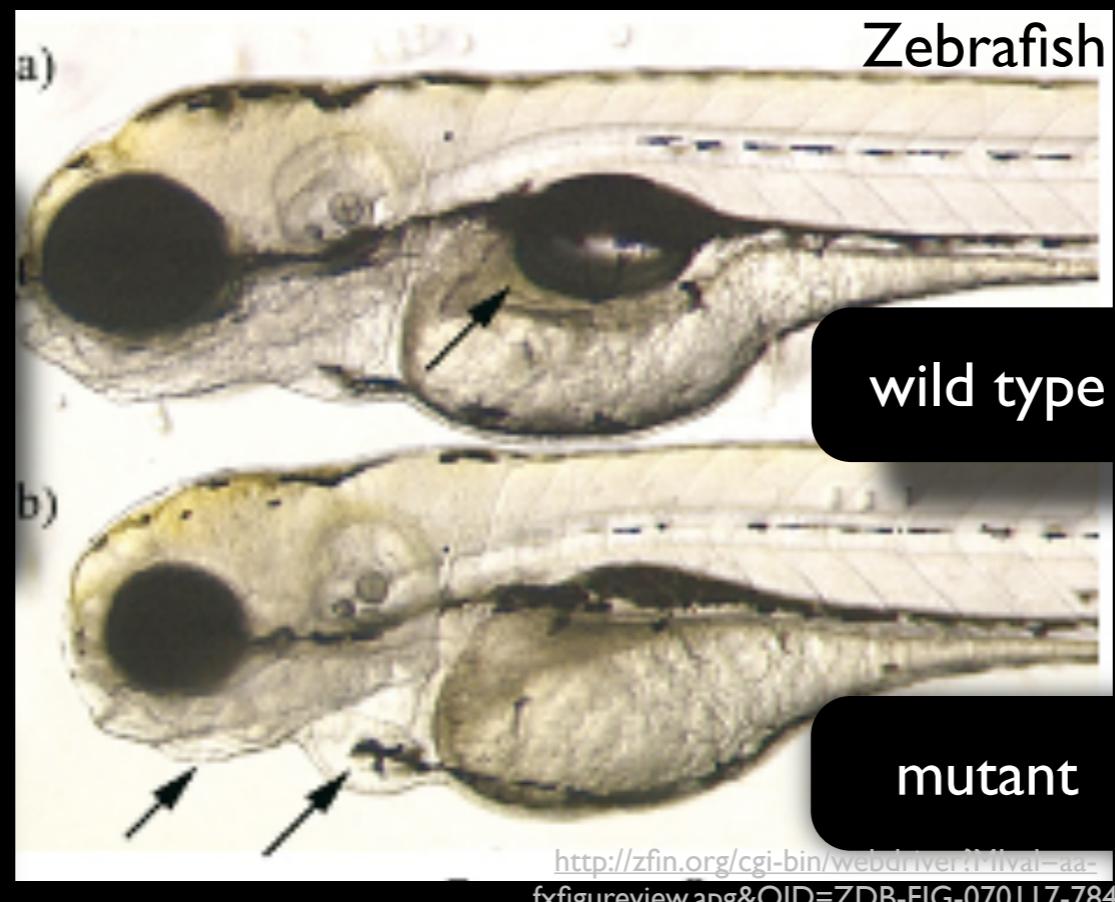
Dahdul et al., 2010,
Systematic Biology

Phenotype annotation of gene

Gene Ontology
(>76,000 terms)

Zebrafish Anatomy
Ontology
(2196 terms; 310 skeletal)

Quality
Ontology
(1,323 terms)



Gene	Entity	Quality
<i>fam32al</i>	Head	Small size
	Eye	Small size
	Ventral mandible	Thick
	Heart	Edematous

Phenotype annotation of taxon

Teleost Taxonomy
Ontology
(38,590 terms;
59,664 synonyms)

Teleost Anatomy
Ontology
(3,039 terms; 618 skeletal)

Quality
Ontology
(1,323 terms)



Taxon	Entity	Quality
species 1	Head	cylindrical
	Adipose fin	absent
species 2	Head	flat
	Adipose fin	present

The screenshot shows the Phenex software interface with several windows:

- Characters**: A list of 20 character descriptions, including "Ethmopalatine ossification in the floor of nasal" and "Especially deep posterior myodome with eye n".
- States**: A list of symbols and state descriptions, such as "present" and "absent".
- Term Info: mesethmoid bone**: Provides basic info (Term: mesethmoid bone, ID: TAO:0000323, Ontology: teleost_anatomy), definition (Median unpaired cartilage bone that ossifies as a perichondrial lamellae ensheathing the nasal septum anterodorsally and laterally (Harrington, 1955). In adult *D. rerio*, the center of the mesethmoid remains cartilaginous (Cubbage & Mabee, 1996). The mesethmoid meets the supraethmoid dorsally, the lateral ethmoids posterolaterally, and the vomer and parasphenoid ventrally in synostoses. Anterolaterally the mesethmoid meets the preethmoids in synchondroses.), and synonyms (EXACT: ethmoid).
- Phenotypes**: Shows a single entry for the mesethmoid bone.
- Graph View**: A hierarchical graph showing the ancestry of the mesethmoid bone, with nodes for various anatomical and tissue types.

Phenex



Balhoff et al., 2010 PLoS ONE

- Desktop phenotype annotation software
- Familiar ‘character matrix’ interface
- Experts focus on translation of character states to EQ

Download: <http://sourceforge.net/projects/phenex/>

Taxon phenotype annotations

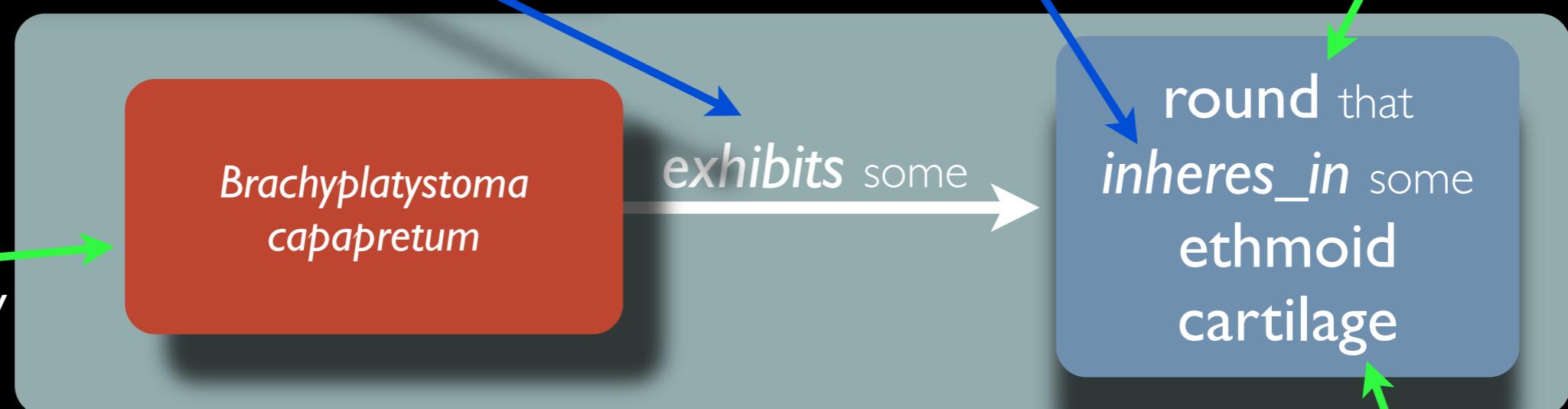
TABLE 1. CHARACTER STATE MATRIX USED FOR PHYLOGENETIC ANALYSIS OF THE PLACEMENT OF *B. capapretum* WITHIN PIMELODIDAE AND *Brachyplatystoma*. Character states described in Appendix 1 and text.

	12345	1	11111	11112	22222	22223	33333
	12345	67890	12345	67890	12345	67890	12345
<i>Steindachneridion</i>	11110	00000	00000	21000	00000	00000	00011
<i>Phractocephalus</i> - <i>Lebiasinus</i> group	11110	00000	00000	00000	00000	00000	00001
<i>Pimelodus</i> group	11111	11111	00000	00000	00000	00000	00000
<i>Calophysus</i> group	11111	11111	00000	00000	01110	00000	01201
<i>Zungaro</i>	11111	10000	00000	01001	20000	00000	00010
<i>Sorubim</i> group	11111	10000	00000	20001	20000	00000	00011
<i>Platynemichthys</i>	11111	10000	11000	00000	00000	00000	00000
<i>Brachyplatystoma vaillantii</i>	11111	10000	11111	11000	00000	00000	00000
<i>B. tigrinum</i>	11111	10000	11121	00111	11000	00000	10010
<i>B. platynemum</i>	11111	10000	11120	11111	11110	00000	11100
<i>B. filamentosum</i>	11111	10000	11111	11111	21101	11111	01101
<i>B. capapretum</i>	11111	10010	11111	11111	21101	11111	01101
<i>B. rousseauxii</i>	11111	10000	11111	11111	21101	11100	01101
Heptapteridae	00000	00000	00000	00001	00000	00000	00001
Pseudopimelodidae	00000	00000	00000	00000	01000	00000	10010
Bagridae	00100	00000	00000	01000	00000	00000	00000
Ictaluridae	00000	00000	00000	00001	00000	00000	00000

Links a quality to entity

Quality ontology term

Taxon ontology term



Anatomy ontology term

Gene phenotype annotations

ZFIN

Home Genes / Markers / Clones Research BLAST GBrowse General Information Expression Antibodies Mutants / Morphants / Tg ZIRC Anatomy Publications Maps

ZFIN ID: ZDB-GENO-980202-957

Genotype: *tfap2a*^{ts213/}_{ts213}

Background: Unspecified

Affected Gene: *tfap2a*

Current Source: Nüsslein-Volhard Lab (alive)

Note:

GENOTYPE COMPOSITION

Feature	Zygosity	Parental Genotype	Lab of Origin	Construct
ts213 (in 2 genotypes)	homozygous	ts213 ♀+/- ♂+/-	Nüsslein-Volhard Lab	

GENE EXPRESSION (current status)

Gene expression in *tfap2a*^{ts213/}_{ts213}

Expressed Gene	Structure	Figures
crestin	unspecified	1 figure from Knight et al., 2003
csf1ra	unspecified	1 figure from Knight et al., 2004
dct	unspecified	1 figure from Knight et al., 2003
dlx2a	brain, mandibular arch skeleton, (not) neural crest (all 5) ▶	4 figures from 4 publications
dlx3b	unspecified	1 figure from Knight et al., 2004

Show all [25 genes, 8 figures](#)

PHENOTYPE (current status)

Phenotype in *tfap2a*^{ts213/}_{ts213}

Conditions	Observed in
Standard or control	ceratobranchial cartilage
Standard or control	ceratohyal cartilage

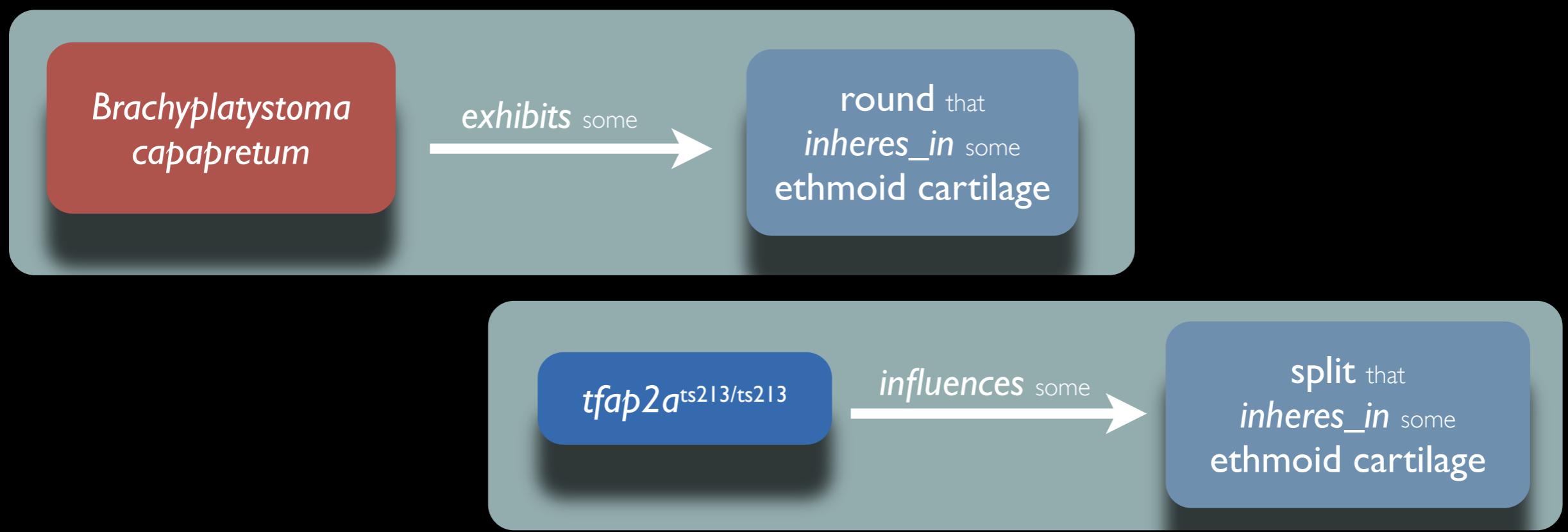
tfap2a^{ts213/}_{ts213}

Import from ZFIN; data
in EQ format

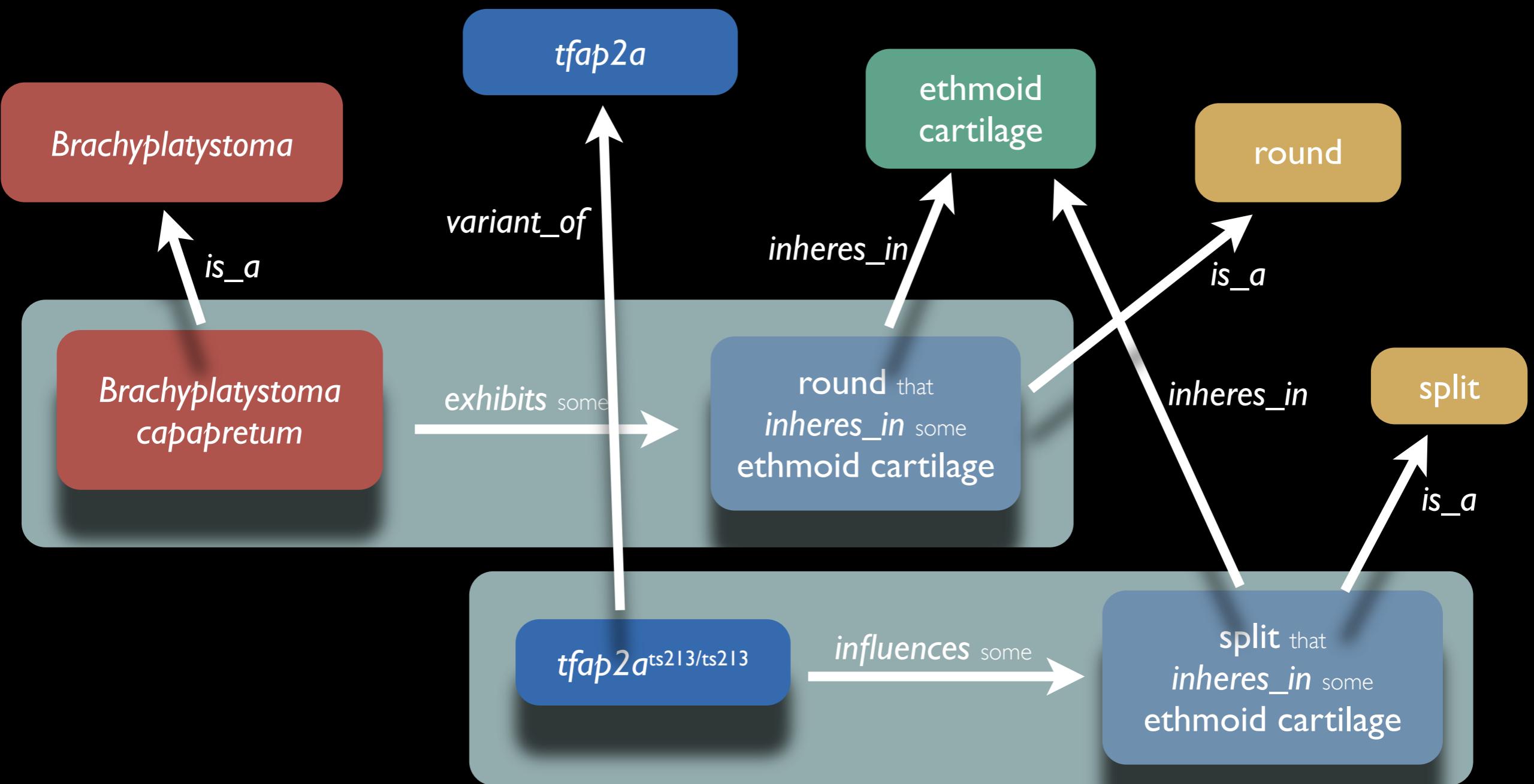
influences some →

split that
inheres_in some
ethmoid cartilage

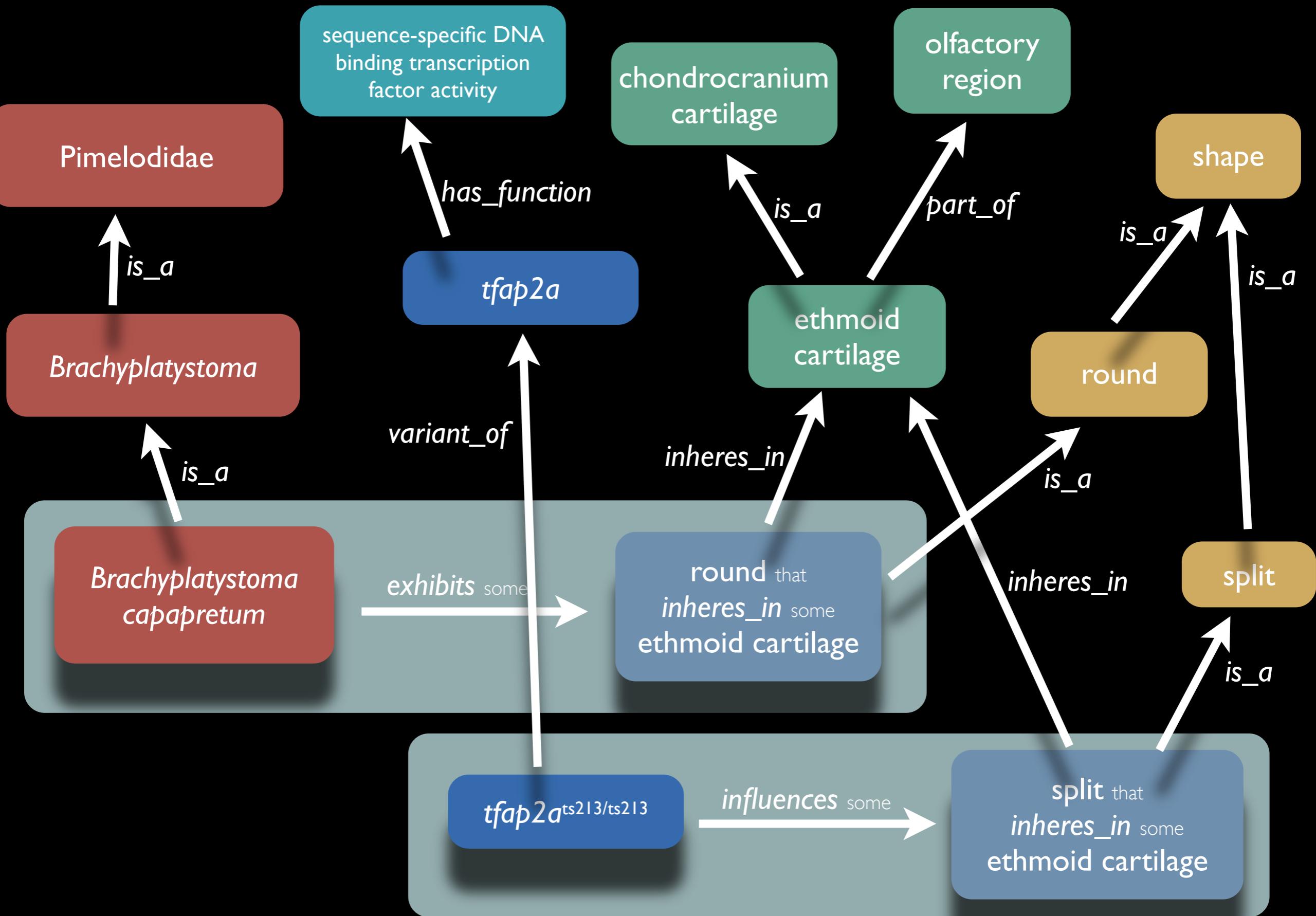
Reasoning across logical relationships



Reasoning across logical relationships



Reasoning across logical relationships



Phenoscape Knowledgebase

509,211 taxon phenotypes for 38,667 taxa 23,471 gene phenotypes for 4,007 genes

The screenshot shows the Phenoscape Knowledgebase homepage. At the top left is the Phenoscape logo with three green wavy lines above the word "PHENOSCAPE". A message box at the top right provides statistics: "The Knowledgebase currently contains 560,462 phenotype statements about 2,487 taxa, sourced from 54 publications, as well as 23,471 phenotype statements about 4,007 genes, retrieved from ZFIN. The data were last loaded into the Knowledgebase on 2011-10-07." Below this is a "Feedback" button. The main navigation bar includes "Workspace", "About", and "Acknowledgments".

Find a specific term: A search input field with a "Search" button. Below it is a note: "Type at least 3 characters to select from matching ontology terms. If there are many matches, the autocomplete menu may take a few seconds to respond. Search entity terms (e.g. basihyal bone), phenotypic qualities (e.g. shape, size), taxonomic names (e.g. Ictaluridae), gene names or symbols (e.g. cacherin 6, cdh6), or publications."

Browse data (faceted view): Includes links to "Phenotypes", "Browse ontologies (tree view)", "Taxa", "Anatomical entities", and "Phenotypic qualities".

Query data: Includes links to "Phenotypes", "Phenotype annotations to taxa", "Phenotype annotations to genes", "Taxa", "Genes", and "Comparative publications".

Visualize data: Includes links to "Phenotypic profile tree" and "Phenotype variation tree".

Phenoscape News: A list of recent news items:

- Notes from ISWC 2011 by tvision - Nov 03, 2011
- Phenoscape visits Xenbase for Anatomy Ontology Update by wdahdul - Sep 23, 2011
- ICBO 2011 by wdahdul - Aug 12, 2011
- Postdoctoral Opportunity: Semantic Reasoning for Biological Phenotypes by tvision - Jul 29, 2011
- CSHALS 2011 by Jim - Mar 09, 2011

Interactive user testing of interface

kb.phenoscape.org

Global view of skeletal data

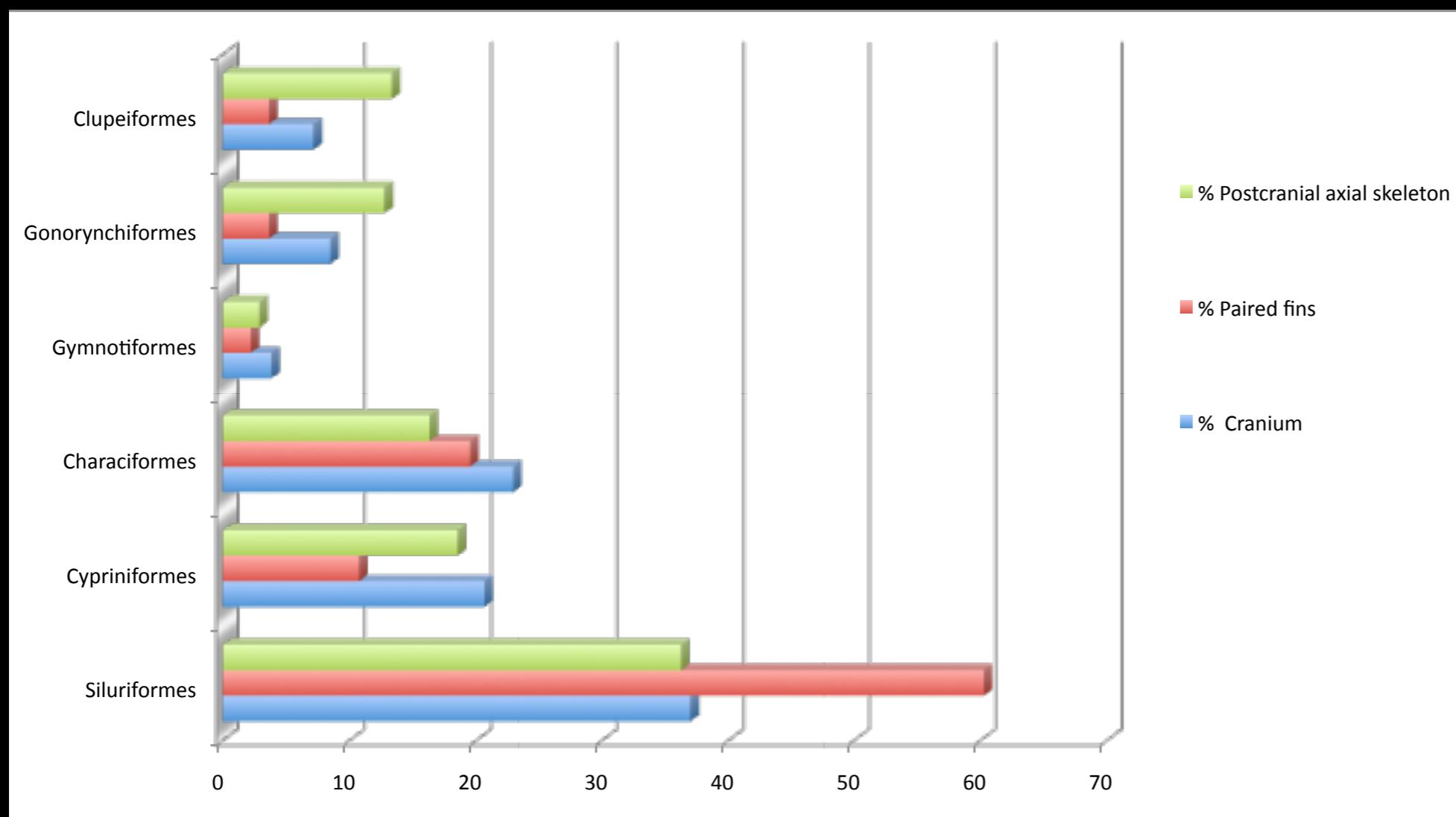


Image from Sabaj-Perez

Skeletal variation across taxa and regions



image:<http://www.ustacrosport.com/buried-treasure>

500,000+ testable hypotheses...

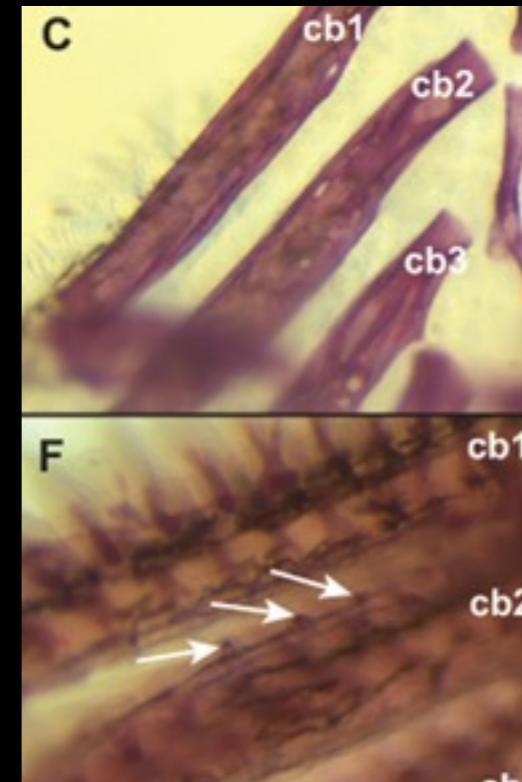


image:<http://www.ustacrosport.com/buried-treasure>

500,000+ testable hypotheses...

kb.phenoscape.org

Gill rakers, absent



Harris et al., 2008

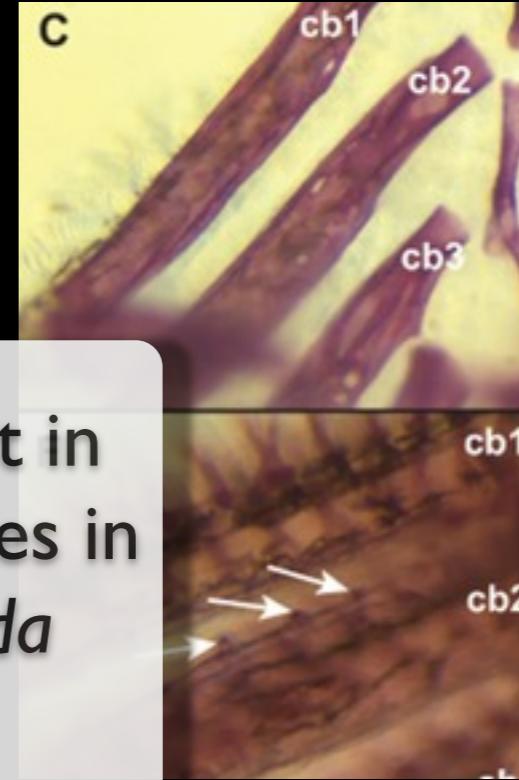
taxa: **Anguilliforms**,
(195)
some catfish, e.g.,
Sisor rabdophorus,
Chaca chaca

genes: **eda**,
(2) **edar**,

Gill rakers, absent



Are gill rakers absent in eels because of changes in regulation of the *eda* pathway?

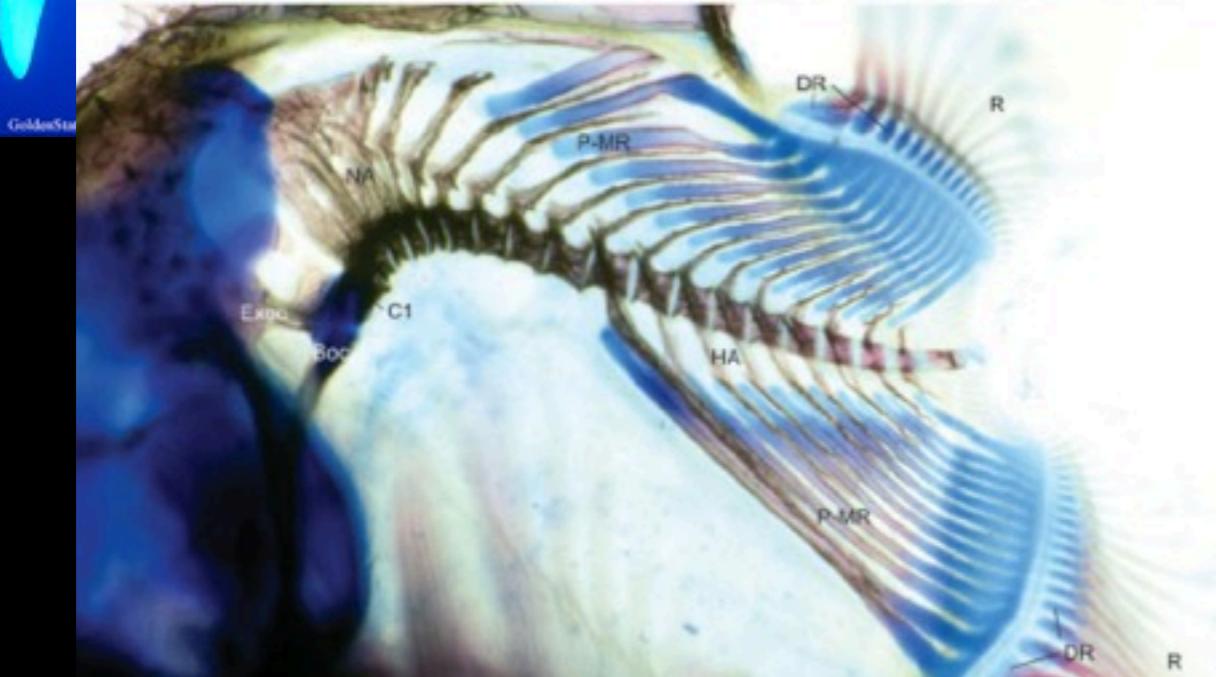


Harris et al., 2008

taxa: **Anguilliforms**,
(195)
some catfish, e.g.,
Sisor rabdophorus,
Chaca chaca

genes: ***eda***,
(2) ***edar***,

Caudal fin, absent



Britz & Johnson, 2005

taxa: **Mola**,
(25) Gymnotiformes



genes: **smc3**,
(3) **tll1**,
yap1

Caudal fin, absent



GoldenStar



Britz & Johnson, 2005

Did *Mola* lose its caudal fin
because of changes in
regulation of *yap1*?

taxa: *Mola*,
(25) Gymnotiformes



Jiang et al., 2009
yap-MO

genes: *smc3*,
(3) *tll1*,
yap1

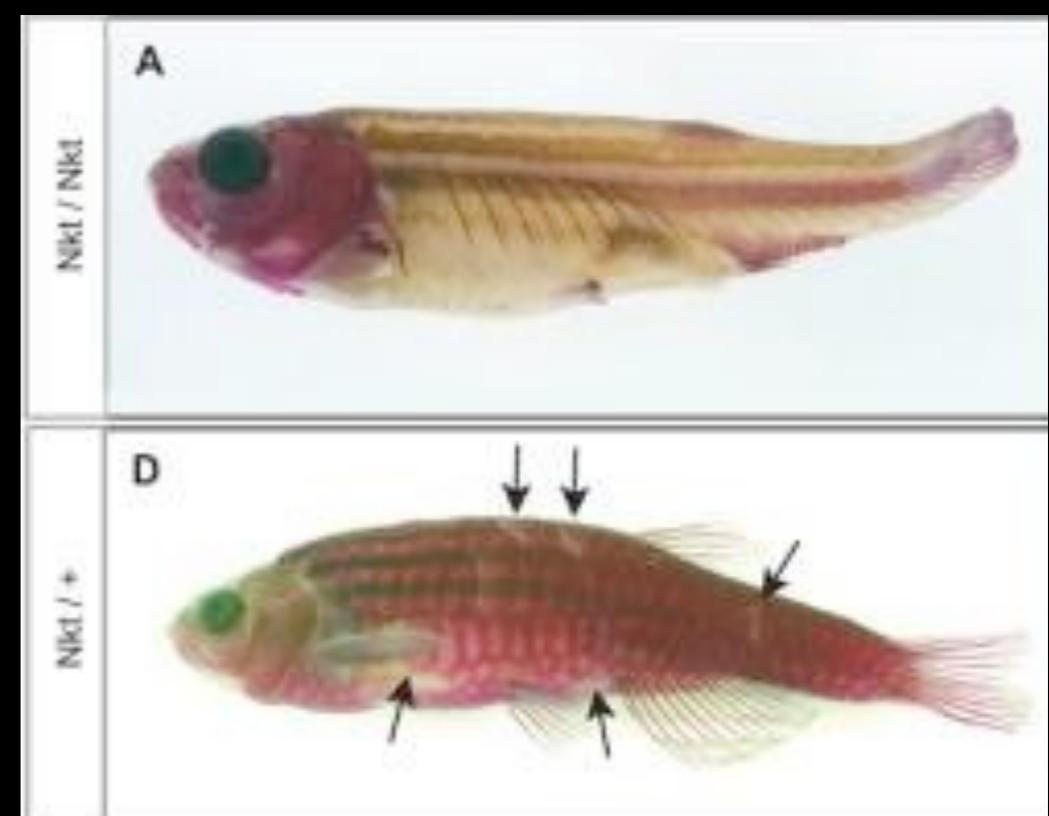
Scales, absent



Copyright © Jean Ricardo Simões Vitule, All Rights Reserved
Ictalurus punctatus

taxa:
(316)

Siluriformes
many other taxa, many places

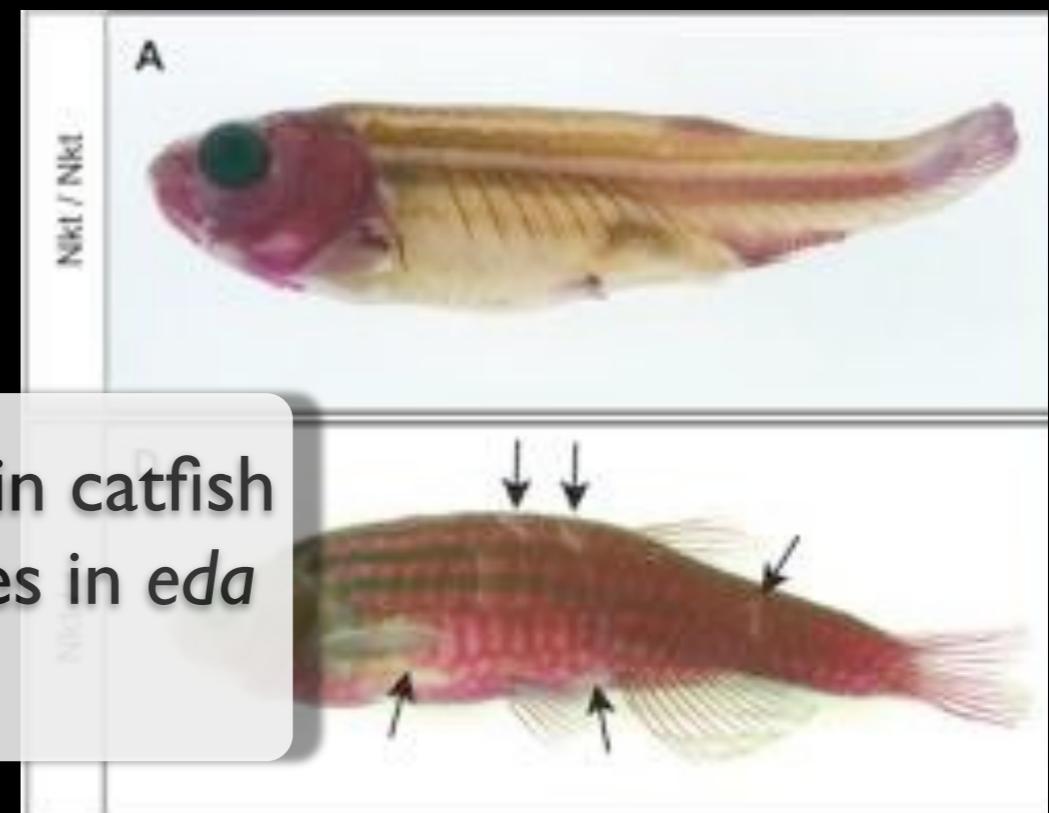


genes: *eda*
edar
(3) *unm_t31273*

Scales, absent



Are scales absent in catfish
because of changes in *eda*
& *edar*?



Harris et al., 2007

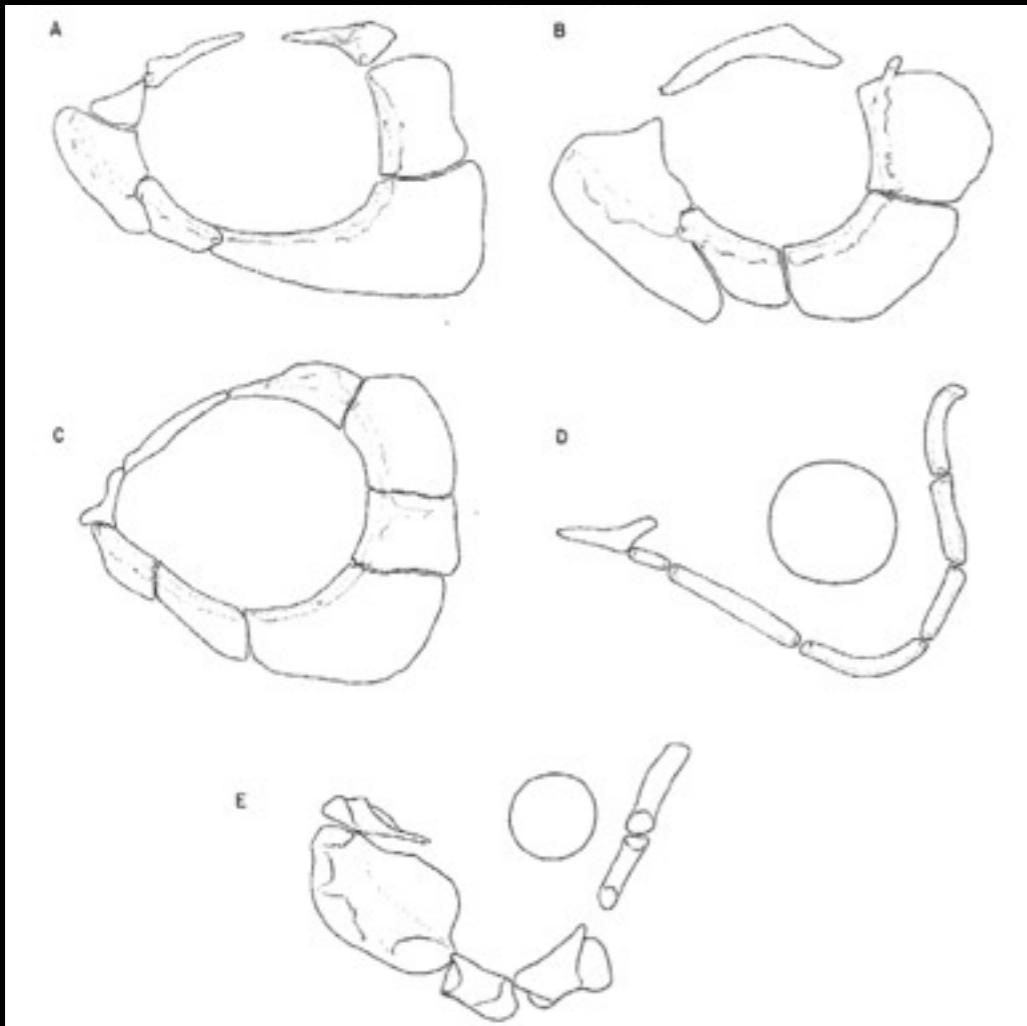
Copyright © Jean Ricardo Simões Vitule, All Rights Reserved
Ictalurus punctatus

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Siluriformes
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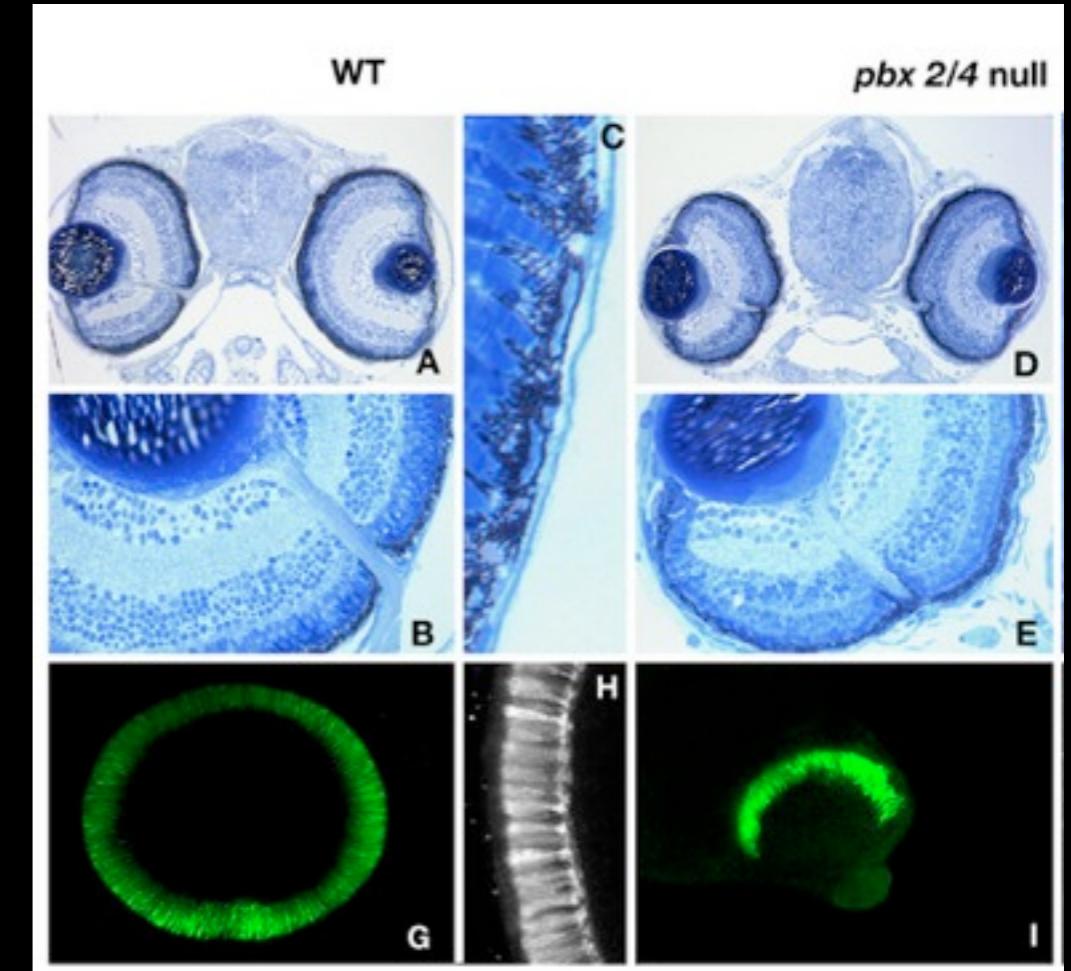
genes: *eda*
edar
(3) *unm_t31273*

Eye, decreased in size



Fink & Fink, 1981; Fig. 7

taxa: Gymnotiformes
Siluriformes

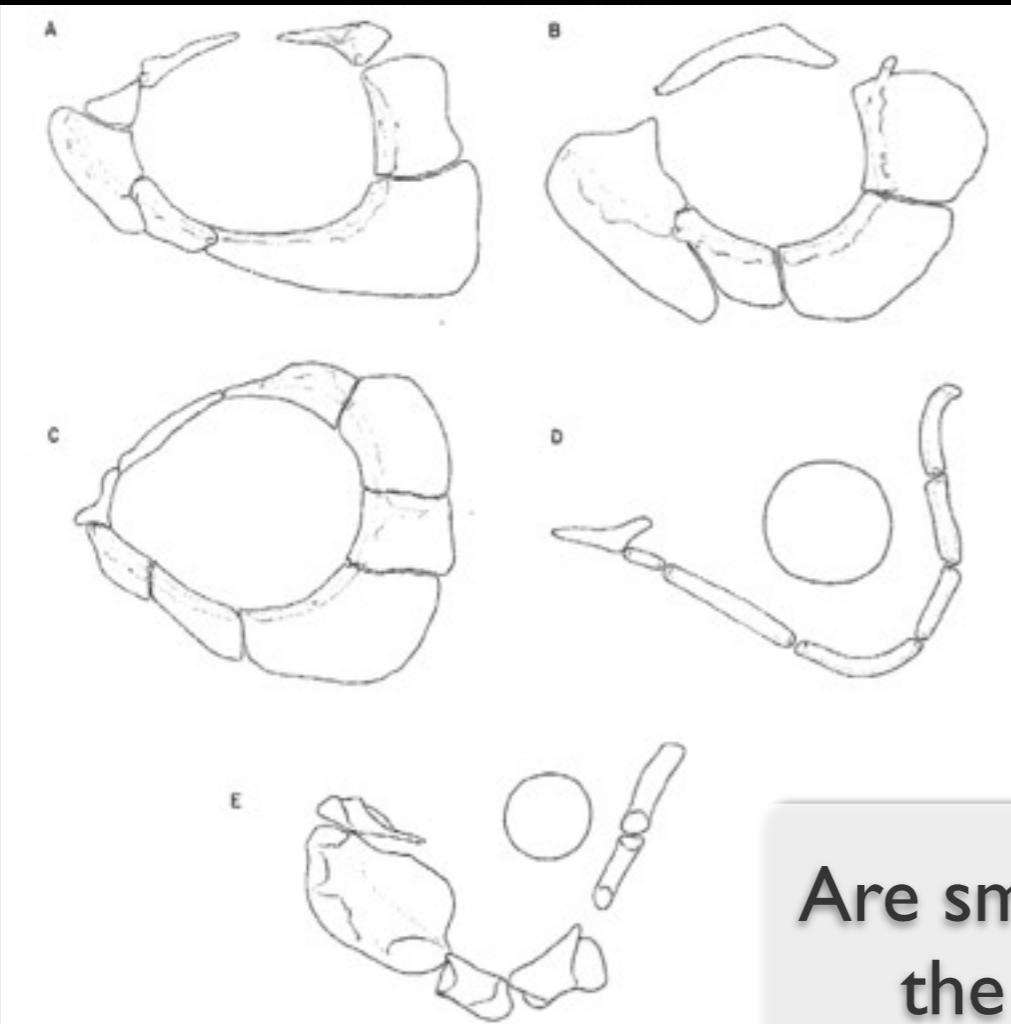


French et al., 2007

genes:
(497)

appb, arf1, arnt2, atat1, atp1a1, atp5o, atp6ap1, atp6ap2, atp6v0ca, atp6v0d1, atp6v1b, atp6v1f, atp6v1h, bas, bch, bil, birc5a, bly, bot, bysl, c1orf109, c2orf71, cactin, cad, camk2n2, capzb, cnna2, cco, cct2, cct3, cct5, cct7, cdc16, cdc26, cdc37, cdh23, cdh4, cdh6, cdip1, cdk1, cempl, cenpn, cep290, cfl1, cfs, cfy, chaf1b, chd, chm, chmp6b, chrdl2, chy, cle, clint1, cmyb, cnc, cnot1, cob, col4a3bpa, coo, cox5aa, cox5ab, cps3, crfb5, csrnp1b, cst3, ctcf, ctidp1, cwc25, cwf192, cyp26a1, cyp26b1, dcaf7, dctn1a, dctn2, ddx18, ddx27, ddx46, ddx51, ddx54, ddx56, ddf, dharma, dhdds, disc1, dkk1b, dist, dmap1, dnr, doy, dri, dry, dsl, dul, dyncl1h1, dyncl2h1, dyncl2i1, dynrl1b, ebna1bp2, ef1a, eif3d, eif3ea, eif3g, eif4a1a, ele, esc02, exosc4, exosc8, fac, fam123b, fam32al, fbl, fbxo5, fen1, flc, foig, foxe1a, foxc1b, foxd3, foxl1, gart, gdf6a, gdr, ghrl, gins3, gja3, gle1, gn13, gt3aa, hai, hdac1, heatr1, hec, hinfp, hmx1, hsf1, hspa8, hspa9, ht, it57, itf88, insrb, insrb, irx1a, irx4a, itf, kars, kas, kes, kgg, kiaa0947l, klf11, krl1, lama1, lamb1a, lamlc1, lee, lgsn, lman2la, lop, lox, ltv1, mars, mcm2, mcm3, mcm3ap, mcm5, mcm7, mcr, meis1, melk, mfn2, mga, mgf, mia, mil, mic, mil, mxka, mlk, mntr, mur, mybbp1a, nar, nba, nbd, nbl1, ncapd2, ncapg, ncaph, ncbp2, ncl, ndrg4, nduf5, nfyc, nkpl, nmd3, nme2b1, noc2l, noc3l, noc10, nolc1, nolp10, nolp10, nolp58, nup205, obscnl, obscnl, odc1, ogt1, ogt2, olfm1, olfm2, otbp, ott, ouj, p4htm, pabpc1a, paf1, pafah1b1a, pafah1b1b, paics, pak1, pax2a, pax6b, **pbx4**, pes, pgu, pho, pi4kaa, pi4kb, pink1, pio, plt, pleg1, plk1, pno, poc1b, pod, pola1, polr1a, polr1c, polr1d, polr2gl, polr3, ppo, ppp1r10, prkci, prkp3, psmbl, psmc6, ptenb, ptbra, pufa, pua, pyr, qars, rab11a, rab11ip4a, rab5c, rae1, ralrb, rbm42, rbp4l, rcl1, rdy, rerea, rfc4, ric8b, rnf113a, rngtt, roh, rgprra, rpl11, rpl12, rpl14, rpl21, rpl28, rpl6, rpl71, rpl9, rplp1, rprd1b, rps11, rps19, rps3a, rps5, rpsa, rrm1, rrm2, rrp12, rys, sars, sars3, sh1, sdad1, sec13, sec61al1, seph, ser, sf1, sf3b1, sf3b4, sf3b5, sff, sfpq, shank3a, shank3b, shha, sich211-114c12.2, sim1a, skiv2l, skp1, slc17a7, slc25a24l, slc25a5, slc4a4a, slit1a, smarca4, smarca5, smc4, smo, smooc1, snrp, sox3, spg11, spy, srp68, srrt, stl, stmn2b, stxbp3, suds3, sumo3a, supth6, surfl, surf6, tafl1, tafl2, tafl7, tal1, tdo, tdp2b, terfa, tew, tlap2a, thc, thi, thoc2, tictr, timm23, tmie, tmx3, tp53, tp73, tpm4, traf3ip1, trdm11, tre, trnt1, trpm7, tsr2, ttc27, ttk, tub, tubg1, twistnb, tyms, ubc21, ufd1l, uhrfr1, unc45b, unm_m210, unm_m220, unm_m283, unm_m287, unm_m394, unm_m489, unm_m621, unm_m668, unm_m708, unm_m756, unm_m771, unm_s111, unm_s168, unm_s181, unm_s332, unm_s507, unm_s509, unm_s545, unm_s547, unm_t30762, unm_ta42, unm_ta85d, unm_tc234d, unm_tc234e, unm_tc280d, unm_tc294a, unm_tc31, unm_tc311x, unm_te322, unm_te374b, unm_ts262a, unm_ts276f, unm_ts40, unm_ts227c, unm_ts279c, unm_tu202, unm_ts235b, unm_ts274b, unm_ts262a, unm_ts276f, unm_ts40, unm_ts227c, unm_ts279c, unm_tu202, unm_ts235b, unm_ts274b, unm_ty60c, unm_tw4, unm_tx238f, unm_ty103a, unm_ty105g, unm_ty17b, unm_ty224, unm_ty5, unm_ty7c, unm_tx284, usp18, usp19, usp20, usp21, usp33, usp111, vars, vis, vps39, vsx2, wdr12, wdr33, wdr36, wdr43, wdr55, wdr75, wdr82, web, wib, wls, wnt10b, woo, wrb, yhd, zug, zc4h2, zcchc7, zea, zem, zif9, zmat2, znf503, znf513, zny

Eye, decreased in size



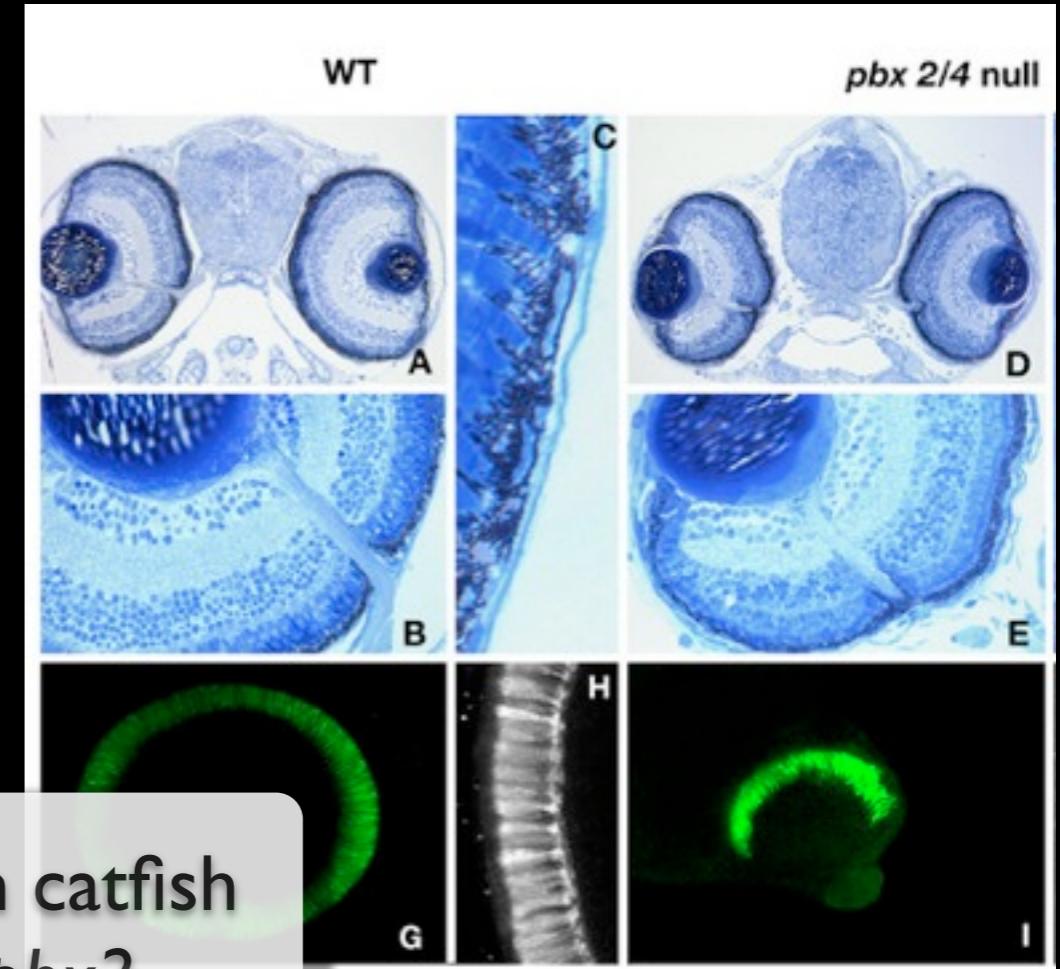
Fink & Fink, 1981; Fig. 7

Are small eyes in catfish
the result of *pbx2*
mutation?

French et al., 2007

taxa: Gymnotiformes
Siluriformes

genes:
(497)



appb, arf1, arnt2, atat1, atp1a1, atp5o, atp6ap1, atp6ap2, atp6v0ca, atp6v0d1, atp6v1e1b, atp6v1f, atp6v1h, bas, bch, bil, birc5a, bly, bot, bysl, c1orf109, c2orf71, cactin, cad, camk2n2, capzb, cnna2, cco, cct6, cct7, cct16, cdc26, cdc37, cdh23, cdh4, cdh6, cdip1, cdk1, cempl, cenp, cep290, cfl1, cfs, cfy, chaf1b, chd, chm, chmp6b, chrdl2, chy, cle, clin1, cmby, cnc, cnot1, cob, col4a3bpa, coo, cox5a, cox5ab, cps3, crfb5, csrc1, cst3, ctcf, ctidp1, cwc25, cwf192, cyp26a1, dcaf7, dctn1a, dctn2, ddx18, ddx27, ddx46, ddx51, ddx54, ddx56, ddf, dharma, dhdds, disc1, dkk1b, dist, dmap1, dnr, doy, dri, dry, dsl, dul, dyncl1h1, dyncl2h1, dyncl2i1, dyrk1b, ebna1bp2, ef1a, eif3d, eif3ea, eif3g, eif4a1a, ele, esc02, exosc4, exosc8, fac, fam123b, fam32a1, fbl, fbxo5, fen1, flc, foig, fox1a, foxc1b, foxd3, foxl1, gart, gdf6a, gdr, ghrl, gins3, gja3, gle1, gn13, gt3aa, hai, hdac1, heatr1, hec, hinfp, hmx1, hsf1, hsp8, hspa9, htt, itf7, itf88, insra, insrb, irx1a, irx4a, itf, kars, kas, kex, kgg, kiaa0947l, klf1, krl1, lama1, lamb1a, lamlc1, lee, lgsn, lman2la, lop, lox, ltv1, mars, mcm2, mcm3, mcm3ap, mcm5, mcm7, mcr, meis1, melk, mfn2, mga, mgf, mia, mil, mic, mil, mur, mybbp1a, nar, nba, nbd, nbl1, ncad2, ncagp, ncaph, ncgp2, ncl, ndrg4, nduf5, nfyc, nkpl, nmd3, nme2b1, noc2l, noc3l, noc10, nolc1, nolp10, nolp56, nolp58, nup205, obscnl, obscnl, odc1, ogt1, ogt2, olfm1a, olfm2, otbp, ott, oui, p4htm, pabpc1a, paf1, pafah1b1a, pafah1b1b, paics, pak1, pax2a, pax6b, pbx4, pes, pgv, pho, pi4kaa, pi4kb, pink1, pio, plt, pleg1, plk1, pno, poc1b, pod, pola1, polr1a, polr1c, polr1d, polr2gl, polr3, ppo, ppp1r10, prkci, prp13, psmbl1, psmc6, ptenb, ptbra, pufa, pua, pyr, qars, rab11a, rab11ip4a, rab5c, rae1, ralrb, rbm42, rbp4l, rcl1, rdy, rerea, rfc4, ric8b, rnf113a, rngt, roh, rgprg, rpl11, rpl12, rpl14, rpl21, rpl26, rpl6, rpl71, rpl9, rplp1, rprd1b, rps11, rps19, rps3a, rps5, rpsa, rrm1, rrm2, rrp12, rys, sars, sar3, sh1, sdad1, sec13, sec61a1, seph, ser, sf1, sf3b1, sf3b4, sf3b5, sff, sfpq, shank3a, shank3b, shha, sich211-114c12.2, sim1a, skiv2l, skp1, slc17a7, slc25a24l, slc25a5, slc4a4a, slit1a, smarca4, smarca5, smc4, smo, smo1, smrp, sox3, spg11, spy, srp68, srrt, stl, stmn2b, stxbp3, suds3, sumo3a, supth6, surfl, surf6, tafl1, tafl2, tafl7, tal1, tdo, tdp2b, terfa, tew, tlap2a, thc, thi, thoc2, tictr, timm23, tmie, tmx3, tp53, tp73, tpm4, traf3ip1, trdm1t, tre, trnt1, trpm7, tsr2, ttc27, ttk, tub, tubg1, twistnb, tyms, ubc21, ufd1, uhrfr1, unc45b, unm_m210, unm_m220, unm_m283, unm_m287, unm_m394, unm_m489, unm_m621, unm_m668, unm_m708, unm_m756, unm_m771, unm_s111, unm_s168, unm_s181, unm_s332, unm_s507, unm_s509, unm_s545, unm_s547, unm_t30762, unm_ta42, unm_ta85d, unm_tc234d, unm_tc234e, unm_tc280d, unm_tc294a, unm_tc31, unm_tc311x, unm_te322, unm_te374b, unm_tg26, unm_tg266, unm_tg279, unm_th9, unm_tj20c, unm_tj229g, unm_tk254b, unm_tl17a, unm_tm102e, unm_tm130g, unm_tm28, unm_tm308, unm_tm42d, unm_tm46b, unm_tm83c, unm_tm88e, unm_tm9d, unm_tm14, unm_tm15, unm_tm20c, unm_tp230, unm_tp46, unm_tq235b, unm_to262a, unm_ts276f, unm_ts40, unm_tt227c, unm_tt279c, unm_tu202, unm_tu235b, unm_tu274b, unm_ty60c, unm_tw4, unm_tx238f, unm_ty103a, unm_ty105g, unm_ty17b, unm_ty224, unm_ty5, unm_ty7c, unm_ty284, usp18, usp19, usp20, usp21, usp33, upf111, vars, vis, vps39, vsx2, wdr1, wdr12, wdr33, wdr36, wdr43, wdr55, wdr75, wdr82, web, wib, wls, wnt10b, woo, wrb, yhd, yug, zc4h2, zcchc7, zea, zem, zif9, zmat2, znf503, znf513, zny

Quantify phenotypic similarity

Similarity (IC)	Taxon	Taxon phenotype	Candidate gene	Gene phenotype	Subsuming phenotype
13.43	Eels	<i>gill rakers, absent</i>	<i>eda</i>	<i>gill rakers, absent</i>	<i>gill rakers count</i>
12.85	<i>Minytrema</i>	<i>lateral line, absent</i>	<i>pcsk5a</i>	<i>lateral line, reduced</i>	<i>lateral line, size</i>
12.44	Siluriformes	<i>basihyal, absent</i>	<i>brpf1</i>	<i>basihyal, absent</i>	<i>basihyal, count</i>
11.32	<i>Gyrinocheilus</i>	<i>ceratobranchial 5 teeth, absent</i>	<i>eda</i>	<i>ceratobranchial teeth, absent</i>	<i>tooth, count</i>
11.11	Siluriformes	<i>scales, absent</i>	<i>eda</i>	<i>scales, absent</i>	<i>scales, count</i>
9.91	Siluriformes	<i>opercle, shape</i>	<i>ednl</i>	<i>maxilla, shape</i>	<i>dermatocranum, shape</i>
9.19	<i>Mola</i>	<i>caudal fin, absent</i>	<i>yapl</i>	<i>median fin, absent</i>	<i>median fin, count</i>
9.19	Gonorynchiformes	<i>dorsal fin, absent</i>	<i>tflp2a</i>	<i>median fin, absent</i>	<i>median fin, count</i>
5.17	Siluriformes	<i>eye, reduced</i>	<i>pbx2</i>	<i>eye, small</i>	<i>eye, size</i>



Summary

- I. Genes mapped to taxa via phenotype
 - Candidate genes
 - Candidate taxa
2. Powerful approach for data synthesis and discovery
3. Makes data accessible for broad group of researchers and creates opportunities for new and synthetic research



Phenoscape



- Expand taxonomically: Map vertebrate evolutionary phenotype data to vertebrate model organism databases (zebrafish, *Xenopus*, mouse)
- Restricted annotation: Fin-limb transition genes and phenotypes
- Implement homology reasoning
- Develop ‘Phenoblast’ search

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