SUPPORTING FILES

Integrative view of α2,3-sialyltransferases (ST3Gal) molecular and functional evolution in deuterostomes: significance of lineage specific losses.

Daniel Petit, Elin Teppa, Anne-Marie Mir, Dorothée Vicogne, Christine Thisse, Bernard Thisse, Cyril Filloux and Anne Harduin-Lepers

1- Supplemental Tables: Nomenclature, name and accession number of *st3gal* gene sequences identified and used in this study

Table S1: Nomenclature, name and accession number in INSDC (GenBank/ENA/DDBJ) of *st3gal* gene sequences

Table S2: Nomenclature, name and contig/scaffold number of amphibian *st3gal* gene sequences in specialized databases (Xenbase and Sal-site)

Table S3. Tissue diversity of *st3gal* gene expression in several vertebrate models. For each species and gene, Shannon index was calculated from the log-transformed values of EST numbers recorded in each tissue (see material and method section). The dataset of selected tissues was the same as for the construction of figure S9. A null value corresponds to an expression limited to one tissue, and a dash a total absence of expression in any tissue. The background darkness is related to the value level.

Table S1: Nomenclature, name and accession number in GenBank/EMBL/DDBJ of *st3gal* gene sequences identified and used in this study. The name of the organism and length of the predicted protein are indicated.

subfamily	**organism**	**Acc Nber GenBank**	**length**
ST3Gal8 (GR1)			
ST3Gal8	*Proteropterus aethiopicus*	FL668363	265
ST3Gal8	*Anolis carolinensis*	XM_003220475	326
ST3Gal8	*Chrysemys picta bellii*	HG531973	329
ST3Gal8	*Danio rerio*	AJ783740	341
ST3Gal8	*Latimeria chalumnae*	HG531974	332
ST3Gal8	*Melopsittacus undulatus*	XM_005147589	319
ST3Gal8	*Silurana tropicalis*	AJ585763	332
ST3Gal8A	*Xenopus laevis*	AJ585762	332
ST3Gal8B	*Xenopus laevis*	HG531975	332
ST3Gal8	*Gallus gallus*	XM_417321	313
ST3Gal8	*Python bivittatus*	HG531976	328
ST3Gal8	*Lepisosteus oculatus*	HG531977	340
ST3Gal2 (GR1)			
ST3Gal2	*Anolis carolinensis*	GADO01065579	350
ST3Gal2	*Bos taurus*	AJ748841	350
ST3Gal2	*Chrysemys picta bellii*	HG531978	347
ST3Gal2	*Danio rerio*	AJ783741	374
ST3Gal2	*Gallus gallus*	AJ585761	349
ST3Gal2	*Homo sapiens*	X96667	350
ST3Gal2	*Latimeria chalumnae*	HG531979	349
ST3Gal2	*Loxodonta africana*	XM_003417075	350
ST3Gal2	*Monodelphis domestica*	XM_001362558	350
ST3Gal2	*Ornithorhynchus anatinus*	XM_003431271	350
ST3Gal2	*Petromyzon marinus*	HG531980	>309
ST3Gal2	*Python bivittatus*	HG531981	347
ST3Gal2	*Silurana tropicalis*	XM_002931660	351
ST3Gal2	*Taeniopygia guttata*	XM_002188528	348
ST3Gal2	*Takifugu rubripes*	AJ626817	376
ST3Gal1 (GR1)			
ST3Gal1	*Anolis carolinensis*	XM_003219376	342
ST3Gal1	*Bos taurus*	NM_001097983	339
ST3Gal1	*Chrysemys picta bellii*	HG531982	360
ST3Gal1	*Gallus gallus*	X80503	342
ST3Gal1	*Homo sapiens*	L29555	340
ST3Gal1A	*Latimeria chalumnae*	HG531983	342
ST3Gal1B	*Latimeria chalumnae*	HG531984	342
ST3Gal1	*Lepisosteus oculatus*	HG531985	329
ST3Gal1	*Loxodonta africana*	XM_003408191	340
ST3Gal1	*Monodelphis domestica*	XM_001381537	342
ST3Gal1	*Oryzias latipes*	AJ871407	334
ST3Gal1	*Python bivittatus*	HG531986	>335
ST3Gal1	*Silurana tropicalis*	FN550106	334

ST3Gal1	*Taeniopygia guttata*	XM_002188126	341
ST3Gal1	*Takifugu rubripes*	AJ626816	333
ST3Gal1	*Tetraodon nigroviridis*	AJ744802	334
ST3Gal5 (GR3)			
ST3Gal5	*Anolis carolinensis*	XM_003226613	370
ST3Gal5	*Callorhinchus milii*	HG532005	>301
ST3Gal5	*Lepisosteus oculatus*	HG531987	>316
ST3Gal5	*Danio rerio*	AJ619960	364
ST3Gal5	*Gallus gallus*	AY515255	363
ST3Gal5	*Homo sapiens*	AB018356	362
ST3Gal5	*Monodelphis domestica*	XM_001379503	362
ST3Gal5	*Mus musculus*	Y15003	358
ST3Gal5	*Ornithorhynchus anatinus*	HG531988	384
ST3Gal5	*Petromyzon marinus*	HG531989	>331
ST3Gal5	*Silurana tropicalis*	FN550108	372
ST3Gal5	*Takifugu rubripes*	AJ865087	316
ST3Gal5	*Taeniopygia guttata*	XM_002186654	368
ST3Gal7 (GR3)			
ST3Gal7	*Danio rerio*	AJ783742	383
ST3Gal7	*Oryzias latipes*	AJ871411	386
ST3Gal7	*Takifugu rubripes*	AJ865347	386
ST3Gal7	*Lepisosteus oculatus*	HG531990	365
ST3Gal3 and ST3Gal3-r (GR3)			
ST3Gal3	*Anolis carolinensis*	XM_003220202	390
ST3Gal3	*Danio rerio*	AJ626821	355
ST3Gal3-r	*Danio rerio*	AJ626820	372
ST3Gal3	*Gallus gallus*	AJ865086	374
ST3Gal3	*Gasterosteus aculeatus*	HG531992	370
ST3Gal 3-r	*Gasterosteus aculeatus*	HG531991	356
ST3Gal3	*Lepisosteus oculatus*	HG531993	333
ST3Gal3	*Latimeria chalumnae*	HG531994	375
ST3Gal3	*Homo sapiens*	L23768	444
ST3Gal3	*Xenopus laevis*	BC169739	360
ST3Gal3	*Meleagris gallopavo*	XM_003208778	390
ST3Gal3	*Mus musculus*	X84234	374
ST3Gal3	*Python bivittatus*	HG531995	369
ST3Gal3	*Oryzias latipes*	HG531996	371
ST3Gal3	*Silurana tropicalis*	AJ626823	374
ST3Gal3	*Taeniopygia guttata*	XM_002192118	374
ST3Gal3	*Takifugu rubripes*	AJ626818	356
ST3Gal6 (GR2)			
ST3Gal6	*Homo sapiens*	AF119391	331
ST3Gal6	*Mus musculus*	AF119390	331
ST3Gal6	*Gallus gallus*	AJ585767	329
ST3Gal6	*Anolis carolinensis*	GAFZ01198187	327
ST3Gal6	*Latimeria chalumnae*	HG531997	329
ST3Gal6	*Silurana tropicalis*	AJ626744	331

ST3Gal6	*Taeniopygia guttata*	XP_002194132	356
ST3Gal6	*Meleagris gallopavo*	XP_003202812	329
ST3Gal4 (GR2)			
ST3Gal4	*Anolis carolinensis*	XP_003225763	329
ST3Gal4	*Callorhinchus milii*	HG531998	>243
ST3Gal4	*Danio rerio*	AJ744809	332
ST3Gal4	*Gallus gallus*	AJ866777	328
ST3Gal4	*Homo sapiens*	L23767	333
ST3Gal4	*Latimeria chalumnae*	HG531999	>181
ST3Gal4	*Meleagris gallopavo*	XM_003212645	328
ST3Gal4	*Mus musculus*	X95809	333
ST3Gal4	*Silurana tropicalis*	AJ622908	330
ST3Gal4	*Takifugu rubripes*	AJ865346	272
ST3Gal4	*Python bivittatus*	HG532000	342
ST3Gal4	*Lepisosteus oculatus*	HG532001	381
ST3Gal9 (GR2)			
ST3Gal9	*Gallus gallus*	XM_004945803	394
ST3Gal9	*Meleagris gallopavo*	HG532002	312
ST3Gal9	*Ornithorhynchus anatinus*	XM_001508863	322
ST3Gal9	*Pelodiscus sinensis*	HG532003	365
ST3Gal1/2/8 (GR1)			
	Ciona intestinalis	AJ703817	379
	Ciona savignyi	AJ626814	374
	Branchiostoma lanceolatum	HG532006	312
	Branchiostoma floridae	XM_002604587	377
	Saccoglossus kowalevskii	XM_002741450	350
	Strongylocentrotus purpuratus	AM420340	357
	Oscarella carmela	HG532004	374
ST3Gal3/3-r/5/7 (GR3)			
	Strongylocentrotus purpuratus A	XM_001184759	398
	Strongylocentrotus purpuratus B	XM_003730192	472
	Strongylocentrotus purpuratus C	XM_776047	335
	Branchiostoma floridae	XM_002601289	480
ST3Gal3/3-r/5/7/4/6/9 (GRx)			
	Saccoglossus kowalevskii	HG532008	393
	Branchiostoma lanceolatum	HG532007	365
	Branchiostoma floridae	XM_002606112	371

Table S2 : Nomenclature, name and contig/scaffold number of amphibian *st3gal* gene sequences identified and used in this study. These *st3gal* sequences were identified in specialized EST/mRNA databases available at the URL http://www.ambystoma.org/genome-resources/21-blast for *Ambystoma mexicanum* (1) and http://xenbase.org/genomes/blast.do? for *Xenopus laevis* (2). The name of the organism and length of the predicted protein are indicated. These annotated α2,3-sialyltransferase sequences are available upon request.

subfamily	**organism**	**Contig/scaffold**	**Range**	**length**
ST3Gal8 (GR1)				
ST3Gal8	*Ambystoma mexicanum*	Contig 54315	1121-132	330
ST3Gal2 (GR1)				
ST3Gal2	*Ambystoma mexicanum*	Contig 108051	2-426	>280
ST3Gal1 (GR1)				
ST3Gal1	*Ambystoma mexicanum*	Contig 144365	2272-1245	330
ST3Gal1	*Xenopus laevis*	Scaffold 81582	672055-646912	336
ST3Gal5 (GR3)				
ST3Gal5	*Ambystoma mexicanum*	Contig 158505	3-1061	>352
ST3Gal6 (GR2)				
ST3Gal6	*Ambystoma mexicanum*	Contig 316123	405-1391	322
ST3Gal4 (GR2)				
ST3Gal4	*Ambystoma mexicanum*	Contig 337204	408-1328	>307

(1) Smith JJ, Putta S, Walker JA, Kump DK, Samuels AK, Monaghan JR, Weisrock, Staben C and Voss RS. (2005) Sal-Site: integrating new and existing ambystomatid salamander research and informational resources. BMC Genomics 6, 181. doi: 10.1186/1471-2164-6-181

(2) Bowes JB, Snyder KA, Segerdell E, Gibb R, Jarabek CJ, Pollet N, Vize PD. (2009) Xenbase: a Xenopus biology and genomics resource. Nucleic Acids Res., D761-7. doi:10.1093/nar/gkm826

Table S3. Tissue diversity of *st3gal* gene expression in several vertebrate models. For each species and gene, Shannon index was calculated from the log-transformed values of EST numbers recorded in each tissue (see material and method section). The dataset of selected tissues was the same as for the construction of figure S9. A null value corresponds to an expression limited to one tissue, and a dash a total absence of expression in any tissue. The background darkness is related to the value level.

	Gene	HSA	MMU	BTA	GAL	DRE	Mean	St. Err
GR1	*ST3Gal1*	2.694	2.537	1.549	0.661	1.720	1.832	0.368
	ST3Gal2	2.613	2.385	2.264	0.671	2.284	2.043	0.349
	ST3Gal8	-	-	-	0.693	1.810	1.251	0.353
GR2	*ST3Gal4*	2.714	2.383	2.153	0.000	1.714	1.793	0.477
	ST3Gal6	2.492	2.463	2.385	2.292	-	2.408	0.040
	ST3Gal9	-	-	-	1.377	-	1.377	-
GR3	*ST3Gal3*	2.236	2.380	2.043	1.383	2.276	2.064	0.179
	ST3Gal5	2.800	2.283	2.107	1.375	2.287	2.170	0.230
	ST3Gal7	-	-	-	-	1.764	1.764	-