

Antimicrobial Peptides of Salmonid Fish: From Form to Function

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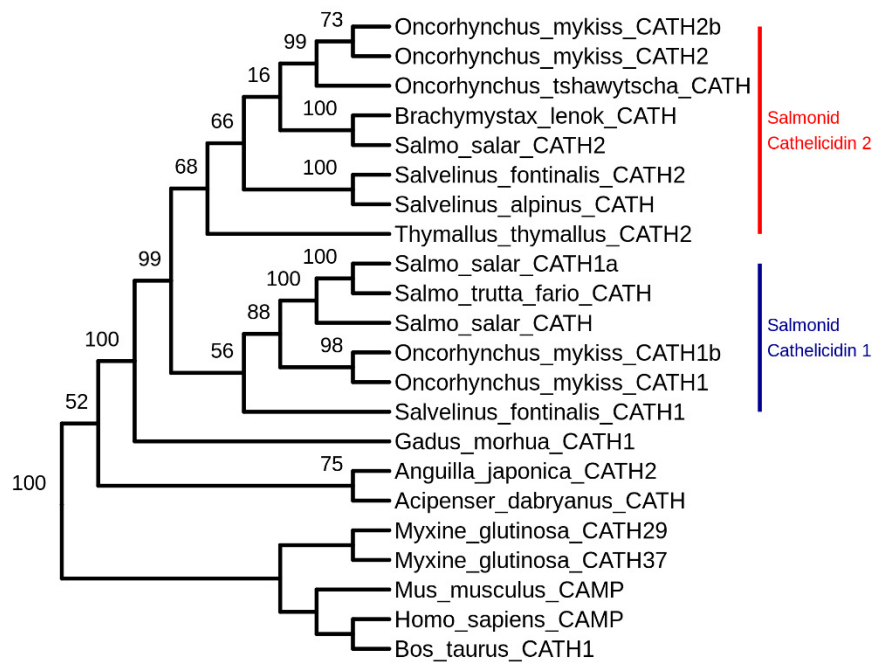


Figure S1. Phylogenetic tree of published salmonid cathelicidins. Cathelicidins form two well-supported clades within salmonids. The tree was constructed on exon 1-3 as exon 4 is highly variable. All analysis was done in R v3.6.1 (The R Core Team 2020). Amino acid sequences were retrieved from GenBank and aligned using ClustalW. A pairwise distance matrix was constructed with the pairwise deletion option selected. The tree was constructed with the improved neighbour-joining method BIONJ [1]. The tree is rooted with 3 mammalian and 2 agnatha sequences. Root nodes indicate bootstrap values (1000 replicates) in percent.

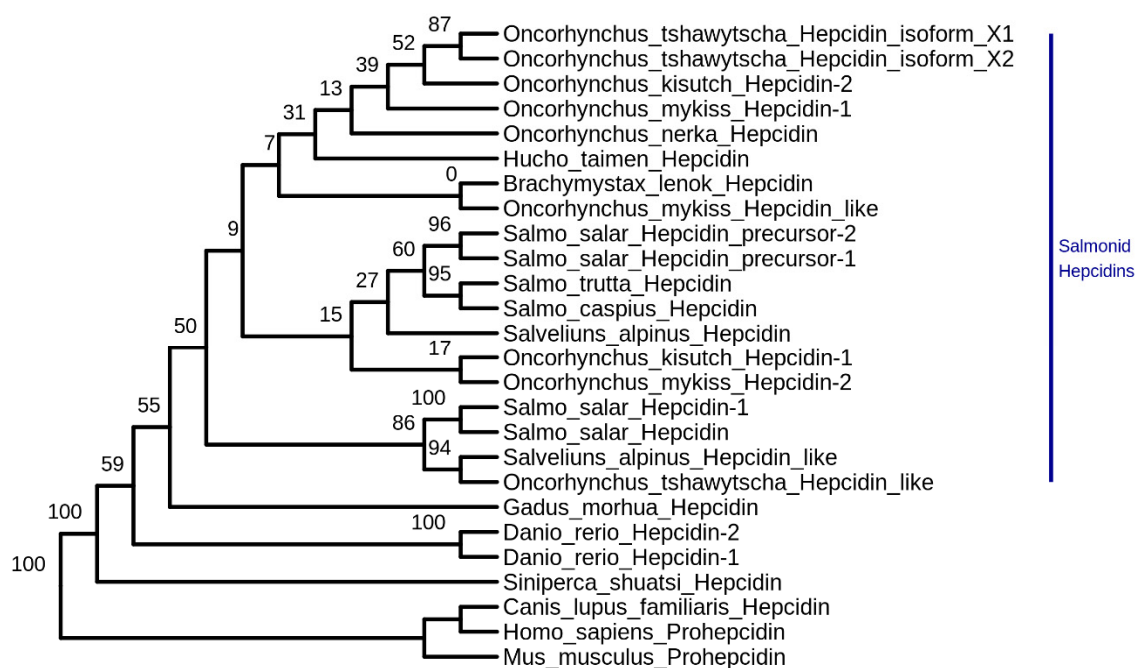


Figure S2. Phylogenetic tree of published and predicted salmonid hepcidins. Hepcidins form one clade within salmonids. For analysis details, see description of Figure S1. Amino acid sequences were retrieved from GenBank. The tree is rooted with 3 mammalian sequences. Root nodes indicate bootstrap values (1000 replicates) in percent.

Table S1. Salmonid Antimicrobial Peptides from Databases.

ID	Name	Source	Sequence
DRAMP02344	40S ribosomal protein S30	<i>O. mykiss</i>	KVHGSLARAGK
AP03058	CK11	<i>O. mykiss</i>	AIPKCCVGTSRNIPLSILMRVERYDVQHNHGACEIDAVVLHANGRKYCADPRVKKVLGVAMQIRKAQL MREKLNSIMRR
AP01326	Oncorhyncin I	<i>O. mykiss</i>	SKGKKANKDVELARG
AP0041	Oncorhyncin II	<i>O. mykiss</i>	KAVAAKSPKKAKKPATPKKAAKSPKKVKKPAAAAKKAASPKKATKAAKPKAAKPKAAKAKKAAP KKK
AP00410	Oncorhyncin III	<i>O. mykiss</i>	PKRKSATKGDEPARRSARLSARPVPKPAAPKPKAAAPKKAVKGKKAENGDAKAEAKVQAAGDGAG NAK
DRAMP02334	Hepcidin	<i>O. mykiss</i>	XSHLSLCRWCCNCCHNKGXGFCCKF
DRAMP02338	Beta-defensin 1	<i>O. mykiss</i>	MVTLVLLVFLLLNVVEDEAASFPFSCPTLSGVCRKLCLPTMFFGPLGCGKGFLCCVSHF
DRAMP02339	Histone H6-like protein	<i>O. mykiss</i>	PKRKSATKGDEPA
DRAMP18698	Histone H2A	<i>O. mykiss</i>	AERVGAGAPVYL
DRAMP02340	Salmocidin-1	<i>O. mykiss</i>	XXSVPAFGHYLPAXP
DRAMP02341	Salmocidin-2A	<i>O. mykiss</i>	SGFVLKGYTKTSQ
DRAMP02342	Salmocidin-IIb	<i>O. mykiss</i>	AGFVLKGYTKTSQ
DRAMP02343	Salmocidin-3	<i>O. mykiss</i>	XXPQQLGHVKAAXSDY
DRAMP02345	LEAP2A	<i>O. mykiss</i>	PEGQRALKRMARMTPLWRTMGTKPYGAYCLNNYECSTGICRGGHCFMSQPIKS
DRAMP02346	LEAP2B	<i>O. mykiss</i>	GVCLVALILMHQVCASPIGSHDSRLSLQQGTKLLERRTRMTPLWRFMGTKPTGAYCRDHFECSTQICRRG HCALSGA
AP02535	rtCATH-1a	<i>O. mykiss</i>	RRSKVRICSRGKNCVSRLGGGSIIGRPGGGSLIGRPGGGSVIGRPGGGSPPGGGSFNDEFIRDHSDGNRFA
AP02536	rtCATH-1b	<i>O. mykiss</i>	RRSKVRICSRGKNCVSRPGGGSGVIGRPGGGSPPGGGSFNDEFIRDHSDGNRFA
AP02537	rtCATH-1c	<i>O. mykiss</i>	RRSKVRICSRGKNCVSRPGGGSFNDEFIRDHSDGNRFA
AP02538	rtCATH-1d	<i>O. mykiss</i>	RRSKVRICSRGKNCVSFNDEFIRDHSDGNRFA
AP02539	rtCATH-2a	<i>O. mykiss</i>	RRGKDSGGPKMGRKDSKGCWRGRPGSGSRPFGSGIAGASGVNHVGTLPASNSTTHPLDNCKISPQ
AP02540	rtCATH-2b	<i>O. mykiss</i>	RRGKDSGGPKMGRKDSKGCWRGRPGSGSRPFGSGIAGASGVNHVGTLP
DRAMP04588	rtCATH-1	<i>O. mykiss</i>	RICSRDKNCVSRPGVGSIIIGRPGGGSLIGRPGGGSGVIGRPGGGSPPGGGSFNDEFIRDHSDGNRFA
AP03053	Bthepc	<i>S. trutta</i>	QSHLSLCRWCCNCCHNKGCGFCCKF
DRAMP02324	SAMP H1	<i>S. salar</i>	AEVAPAPAAAAPAKAPKKKAAAKPKKAGPS
DRAMP02313	Hepcidin-1	<i>S. salar</i>	QIHLSLCGLCCNCCHNIGCGFCCKF
AP02175	CATH_BRALE	<i>B. lenok</i>	RRSKARGSGRSGMGRKDSKGGSRGRPGSGSRPGGGSSIAGASRGDRGGTRNA

Information in this table was obtained from The Antimicrobial Peptide Database (APD): <http://aps.unmc.edu/AP/main.php> and the Data Repository of Antimicrobial Peptides (DRAMP): <http://dramp.cpu-bioinform.org/>.

References

1. Gascuel, O. BIONJ: An improved version of the NJ algorithm based on a simple model of sequence data. *Mol. Biol. Evol.* **1997**, *14*, 685–695, doi:10.1093/oxfordjournals.molbev.a025808.



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