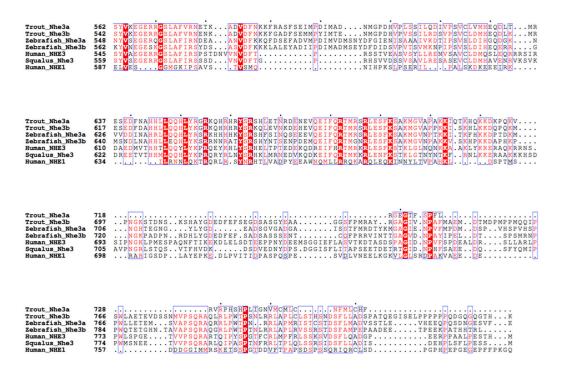
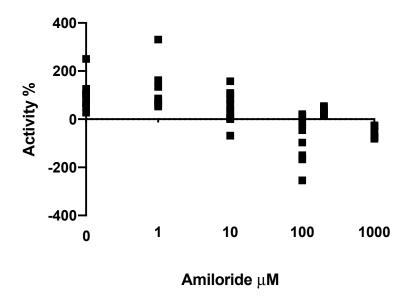
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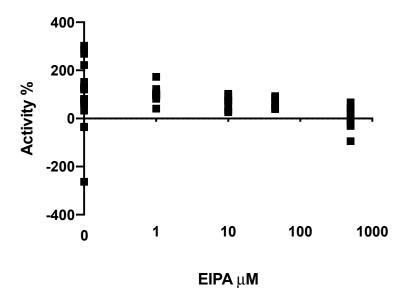




Supplemental Figure 1. Alignment of NHE proteins. Alignment of trout, zebrafish, human NHE1, and NHE1 and Squalus NHE3 protein. Conserved amino acids are colored red and conserved regions are boxed. White amino acids boxed in red represent regions of identity. Representatives included are; *Oncorhynchus mykiss*, Nhe3a, NM_001130995; Nhe3b, FJ376630.1; *Danio rerio*, Nhe3a, EF591984.1; Nhe3B, EF591980.1; *Homo sapiens*, NHE3, NG_046804.1; *Squalus suckleyi*, Nhe3, KR297236.1; *Homo sapiens*, NHE1, NM_003047. Amino acid alignment was using the MAFFT program [75].



Supplemental Figure 2. Raw data points associated with Figure 5 (Effect of varying concentrations of amiloride on activity of tNhe3a). Each individual data point is relative to the mean of the control (DMSO) which was normalized to 100% activity.



Supplemental Figure 3. Raw data points associated with Figure 6 (Effect of varying concentrations of amiloride on activity of tNhe3a). Each individual data point is relative to the mean of the control (DMSO) which was normalized to 100% activity.

Supplemental Tables

Supplemental Table S1. Sequences of primers and gene accession numbers used for cloning *nhe3a* and *nhe3b* from rainbow trout, *Oncorhynchus mykiss*. Restriction enzyme sites used in cloning are underlined.

Gene	Primer Set	Accession Number	Primer	Primer Sequence (5'-3')		
nhe3a	1st set	NM_001130995.1	Forward	TA <u>CCCGGG</u> ATGGCATGCAGAACTTGC		
			Reverse	CGC <u>GTCGAC</u> AAAATGACATAACATGAAATTACAC		
nhe3a	2 nd set	NM_001130995.1	Forward	AA <u>GAATTC</u> GCTAGCGCCACCATGGCATGCAGAACTTGCCTCTG		
			Reverse	CCG <u>GAATTC</u> ACCGGTCCAAAATGACATAACATGAAATTACA		
nhe3b	1st set	NM_001160482.1	Forward	CCAAGATTGATCAAAGCTCAAG		
			Reverse	AAAGAGGTCAGTTTGTGGA		
nhe3b	2 nd set	NM_001160482.1	Forward	TA <u>CCCGGG</u> ATGCCAGCTCTG		
			Reverse	CGT <u>GTCGAC</u> CTTGTGGGTTCC		
nhe3b	3 rd set	NM_001160482.1	Forward	AA <u>GAATTC</u> GCTAGCGCCACCATGCCAGCTCTGTGGCGCTCCACTTTCG		
			Reverse	CCG <u>GAATTC</u> GACCGGTCCCTTGTGGGTTCCCTGACCCTGTCCGTC		

Supplemental Table S2. Percent identity of trout amino acid sequences Nhe3a and trout Nhe3b with other NHEs.

	Trou	Trou	Zebrafis	Zebrafis	Huma	Squalu	Huma
	t_Nh	t_Nh	h_Nhe3	h_Nhe3	n_NH	s_Nhe	n_NH
	e3a	e3b	a	b	E3	3	E1
Trout_Nhe3a	100.0	78.77	66.44	61.80	57.66	55.48	35.19
Trout_Nhe3b		100.0	64.37	63.95	55.67	53.62	35.05
Zebrafish_Nh e3a			100.00	65.41	53.46	52.62	33.60
Zebrafish_Nh e3b				100.00	48.75	48.52	33.85
Human_NHE 3					100.00	73.35	38.40
Squalus_Nhe3						100.00	38.52
Human_NHE 1							100.00