

**Microbial communities in different regions of the gastrointestinal tract in East Asian finless porpoises (*Neophocaena asiaeorientalis sunameri*)**

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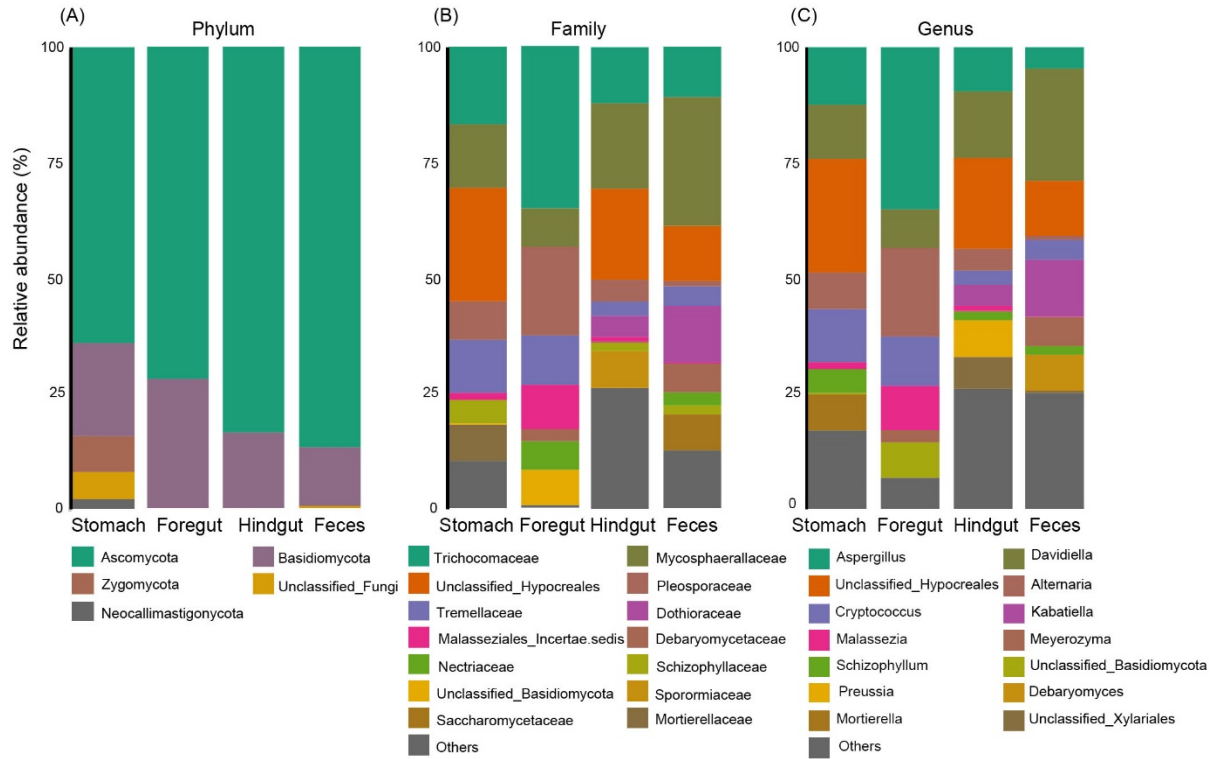
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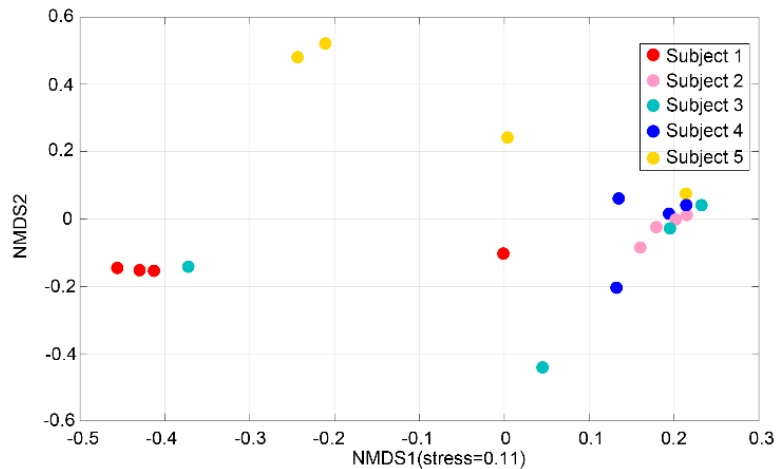
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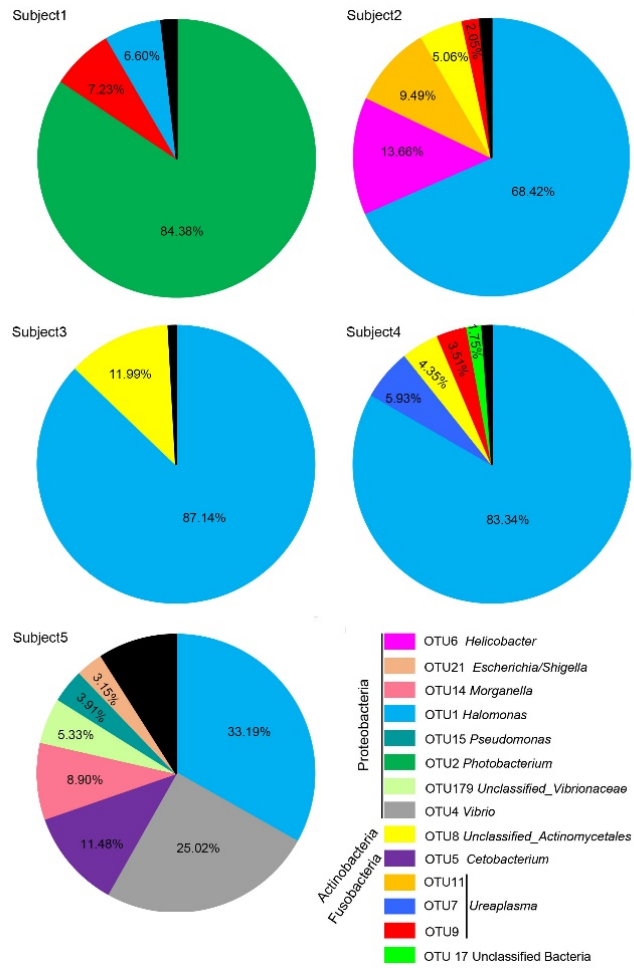
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**Figure S1.** Fungal composition along the GI tract of East Asian finless porpoises at the Phylum (A), Family (B) and Genus (C) levels.



**Figure S2.** NMDS analysis of all bacterial samples in five East Asian finless porpoises.



**Figure S3.** Shared microbiota within different GI regions. Others: taxa abundance <1%.

**Table S1.** Non-parametric multivariate dissimilarity tests of bacterial and fungal community composition along the GI tract. **Anosim**, analysis of similarity; MRPP, multi-response permutation procedures; **Adonis**, permutational multivariate analysis of variance using distance matrices. Results presented are based on distance matrices calculated with Bray-Curtis index. *P* values <0.1 are in bold.

	Group1	Group2	Anosim		MRPP		Adonis	
			<i>R</i>	<i>P</i>	$\delta$	<i>P</i>	<i>F</i>	<i>P</i>
Bacteria	<b>Stomach</b>	<b>Foregut</b>	0.134	<b>0.078</b>	0.639	<b>0.027</b>	2.216	<b>0.029</b>
	Stomach	Hindgut	-0.062	0.720	0.804	0.346	0.974	0.489
	Stomach	Feces	0.070	0.293	0.843	0.349	1.151	0.412
	Foregut	Hindgut	-0.068	0.680	0.600	0.538	0.476	0.514
	Foregut	Feces	0.080	0.226	0.640	0.178	1.560	0.183
	Hindgut	Feces	-0.140	0.800	0.810	0.586	0.474	0.649
Fungi	Stomach	Foregut	-0.186	0.99	0.975	0.975	0.576	0.983
	Stomach	Hindgut	-0.150	0.931	0.953	0.990	0.483	0.993
	Stomach	Feces	-0.026	0.555	0.911	0.694	0.838	0.65
	Foregut	Hindgut	-0.022	0.560	0.962	0.728	0.880	0.736
	Foregut	Feces	0.084	0.198	0.920	0.295	1.112	0.279
	Hindgut	Feces	-0.062	0.592	0.900	0.816	0.671	0.800

**Table S2.** Non-parametric multivariate dissimilarity tests of bacterial and fungal community composition among five East Asian finless porpoises. **Anosim**, analysis of similarity; MRPP, multi-response permutation procedures; **Adonis**, permutational multivariate analysis of variance using distance matrices. Results presented are based on distance matrices calculated with Bray-Curtis index. *P* values <0.1 are in bold.

	Group1	Group2	Anosim		MRPP		Adonis	
			<i>R</i>	<i>P</i>	$\delta$	<i>P</i>	<i>F</i>	<i>P</i>
Bacteria	<b>Subject1</b>	<b>Subject2</b>	0.875	<b>0.027</b>	0.418	<b>0.037</b>	0.418	<b>0.037</b>
	<b>Subject1</b>	<b>Subject3</b>	0.427	<b>0.048</b>	0.673	0.180	0.673	0.180
	<b>Subject1</b>	<b>Subject4</b>	0.750	<b>0.026</b>	0.529	<b>0.071</b>	0.529	<b>0.071</b>
	<b>Subject1</b>	<b>Subject5</b>	0.885	<b>0.024</b>	0.616	<b>0.027</b>	0.616	<b>0.027</b>
	Subject2	Subject3	-0.031	0.524	0.607	0.277	0.607	0.277
	Subject2	Subject4	-0.042	0.657	0.463	0.441	0.463	0.441
	<b>Subject2</b>	<b>Subject5</b>	0.552	<b>0.058</b>	0.550	<b>0.052</b>	0.550	<b>0.052</b>
	Subject3	Subject4	-0.083	0.759	0.719	0.695	0.719	0.695
	<b>Subject3</b>	<b>Subject5</b>	0.490	<b>0.063</b>	0.806	0.208	0.806	0.208
	<b>Subject4</b>	<b>Subject5</b>	0.438	<b>0.078</b>	0.662	0.128	0.662	0.128
Fungi	Subject1	Subject2	0.084	0.198	0.920	0.295	1.112	0.279
	Subject1	Subject3	-0.062	0.592	0.900	0.816	0.671	0.800
	Subject1	Subject4	-0.021	0.574	0.900	0.529	0.738	0.671
	<b>Subject1</b>	<b>Subject5</b>	0.229	<b>0.089</b>	0.803	0.106	1.713	0.101
	Subject2	Subject3	0.026	0.441	0.914	0.200	1.481	0.175
	Subject2	Subject4	0.083	0.192	0.910	0.202	1.261	0.200
	Subject2	Subject5	-0.016	0.435	0.817	0.303	1.097	0.332
	<b>Subject3</b>	<b>Subject4</b>	0.229	0.128	0.928	<b>0.064</b>	1.344	<b>0.055</b>
	Subject3	Subject5	-0.094	0.892	0.924	0.689	0.798	0.723
	<b>Subject4</b>	<b>Subject5</b>	0.401	<b>0.028</b>	0.831	<b>0.028</b>	2.207	<b>0.029</b>