

Supplementary Information 4 for:

Adaptive variation in opsin expression of sticklebacks from different photic habitats.

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Table S2 Model summary table of linear mixed-effects models for the effects of water clarity, generation, the interaction between water clarity and generation, reproductive state and sex on the proportional expression separated by single cones (SWS1, SWS2) and double cones (RH2, LWS) of the SWS1, SWS2, RH2 and LWS opsin genes. Study population served as random effect in all models. Significant results are highlighted in bold ($p < 0.05$). Numerator degrees of freedom were always 1. Denominator degrees of freedom are given as denDF

Dependent variable	Explanatory variables	<i>F</i>	<i>denDF</i>	<i>p</i>	Random factor
SWS1 (transformed)	water clarity	27.256	87	<0.001	population
	generation	26.683	87	<0.001	
	water clarity x generation	0.096	87	0.757	
	reproductive state	0.664	87	0.417	
	sex	2.373	87	0.757	
SWS2 (transformed)	water clarity	27.806	87	<0.001	population
	generation	24.587	87	<0.001	
	water clarity x generation	0.525	87	0.471	
	reproductive state	2.607	87	0.110	
	sex	1.263	87	0.264	
RH2	water clarity x generation	4.461	87	0.038	population
	reproductive state	6.949	87	<0.01	
	sex	0.342	87	0.560	
LWS	water clarity x generation	4.461	87	0.038	population
	reproductive state	6.949	87	<0.01	
	sex	0.342	87	0.560	

Table S3 Post-hoc pairwise comparisons of the proportional expression separated by single cones (SWS1, SWS2) and double cones (RH2, LWS) of the SWS1, SWS2, RH2 and LWS opsin genes shown in wild-caught and lab-bred fish from the two water clarity conditions (clear, tea-stained). Significant p-values are highlighted in bold ($p < 0.05$) and trends indicated in italics ($0.05 < p < 0.1$)

Dependent variable	Pairs		<i>t</i>	<i>df</i>	<i>p</i>
SWS1 (transformed)	<i>wild-caught</i> – clear	<i>wild-caught</i> – tea-stained	3.737	18.4	<0.01
	<i>lab-bred</i> – clear	<i>lab-bred</i> – tea-stained	3.046	7.04	<i>0.072</i>
	<i>wild-caught</i> – clear	<i>lab-bred</i> – clear	3.957	93.4	<0.01
	<i>wild-caught</i> – tea-stained	<i>lab-bred</i> – tea-stained	3.091	71.2	0.015
SWS2 (transformed)	<i>wild-caught</i> – clear	<i>wild-caught</i> – tea-stained	-3.703	18.4	<0.01
	<i>lab-bred</i> – clear	<i>lab-bred</i> – tea-stained	-3.232	7.04	<i>0.055</i>
	<i>wild-caught</i> – clear	<i>lab-bred</i> – clear	-3.599	93.4	<0.01
	<i>wild-caught</i> – tea-stained	<i>lab-bred</i> – tea-stained	-2.920	71.2	0.024
RH2	<i>wild-caught</i> – clear	<i>wild-caught</i> – tea-stained	1.912	23.4	0.251
	<i>lab-bred</i> – clear	<i>lab-bred</i> – tea-stained	-0.758	10.3	0.871
	<i>wild-caught</i> – clear	<i>lab-bred</i> – clear	2.184	93.1	0.135
	<i>wild-caught</i> – tea-stained	<i>lab-bred</i> – tea-stained	-0.551	81.8	0.946
LWS	<i>wild-caught</i> – clear	<i>wild-caught</i> – tea-stained	-1.912	23.4	0.251
	<i>lab-bred</i> – clear	<i>lab-bred</i> – tea-stained	0.758	10.3	0.871
	<i>wild-caught</i> – clear	<i>lab-bred</i> – clear	-2.184	93.1	0.135
	<i>wild-caught</i> – tea-stained	<i>lab-bred</i> – tea-stained	0.551	81.8	0.946

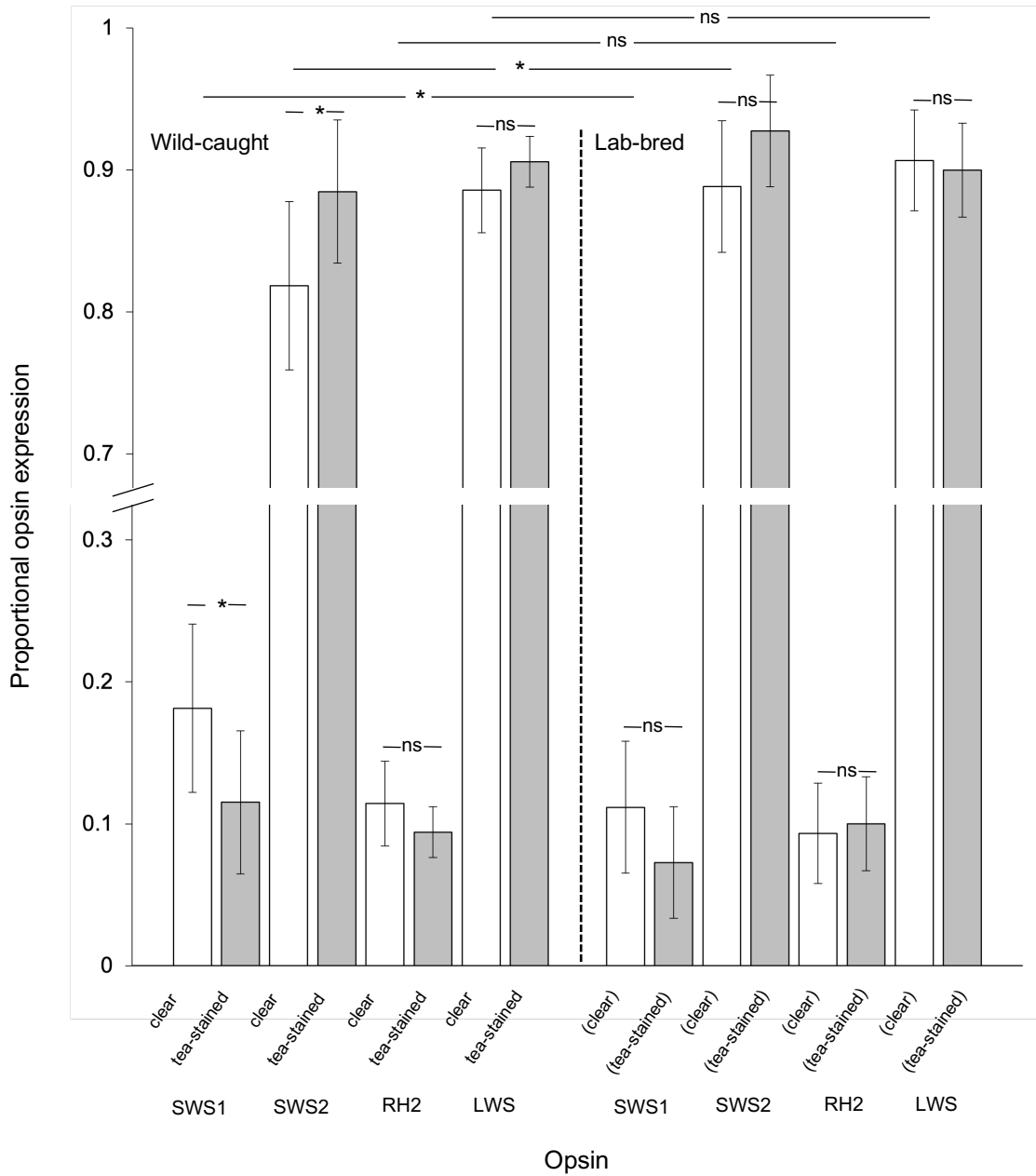


Fig. S2 Proportional opsin expression separated by single cones (SWS1, SWS2) and double cones (RH2, LWS) of the four opsin genes SWS1, SWS2, RH2 and LWS in wild-caught (left half) and lab-bred F1 (right half) fish from clear-water (white bars) and tea-stained lakes (grey bars) on North Uist. Indicated are mean values $\pm$ SD. * $p < 0.05$, ns $p > 0.05$