

Identification and characterization of a novel immune-type receptor (NITR) gene cluster in the European sea bass, *Dicentrarchus labrax*, reveals recurrent gene expansion and diversification by positive selection

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Table S1. Tests for positive selection at NITR genes. Analysis using the F3x4 or F61 models of codon frequencies yielded virtually identical results; the results presented here refer to the F3x4 model. LRTs were performed between nested models that allow variation in dN/dS among codons “sites” models.

Data set	Model compared (^a)	χ^2 (^b)	df (^c)	P-Value	ω_{sel} (^d)	p _s (^e)
DI V-only	M1 VS M2	18.48	2	<0.0001	3.61	0.23
	M7 VS M8	22.06	2	<0.0001	3.44	0.26
	M8a VS M8	18.12	1	<0.0001	3.44	0.26
DI “intronless”	M1 VS M2	24.62	2	<0.0001	3.78	0.05
	M7 VS M8	26.52	2	<0.0001	3.04	0.08
	M8a VS M8	21.32	1	<0.0001	3.04	0.08
OI “intronless”	M1 VS M2	23.87	2	<0.0001	3.05	0.05
	M7 VS M8	22.19	2	<0.0001	2.4	0.07
	M8a VS M8	16.91	1	<0.0001	2.4	0.07
Sn “intronless”	M1 VS M2	36	2	<0.0001	3.14	0.18
	M7 VS M8	41.15	2	<0.0001	2.98	0.20
	M8a VS M8	36.19	1	<0.0001	2.98	0.20

^a Three comparisons were carried out, each involving a null model (M1, M7, and M8a) and a positive selection model (M2, M8). Specifically, models M1 (two classes of sites with rates, $\omega_0 < 1$, $\omega_1 = 1$) versus M2 (three rates $\omega_0 < 1$, $\omega_1 = 1$, and $\omega_{\text{sel}} > 1$), and M7 (fit to a beta distribution, 10 rates) versus M8 (fit to a beta distribution with an extra rate that allows $\omega_{\text{sel}} > 1$) (Nielsen and Yang, 1998; Yang et al., 2000). Additionally, the M8a model proposed by Swanson et colleagues (2003) was compared with M8.

^b $-2\ln\Delta L$ (where ΔL is the difference in likelihoods between the nested models) is distributed approximately as χ^2 .

^c df = Degrees of freedom, equal to the difference in the number of parameters between the models.

^d Estimated dN/dS of the sites under selection.

^e Percentage of sites under positive selection.