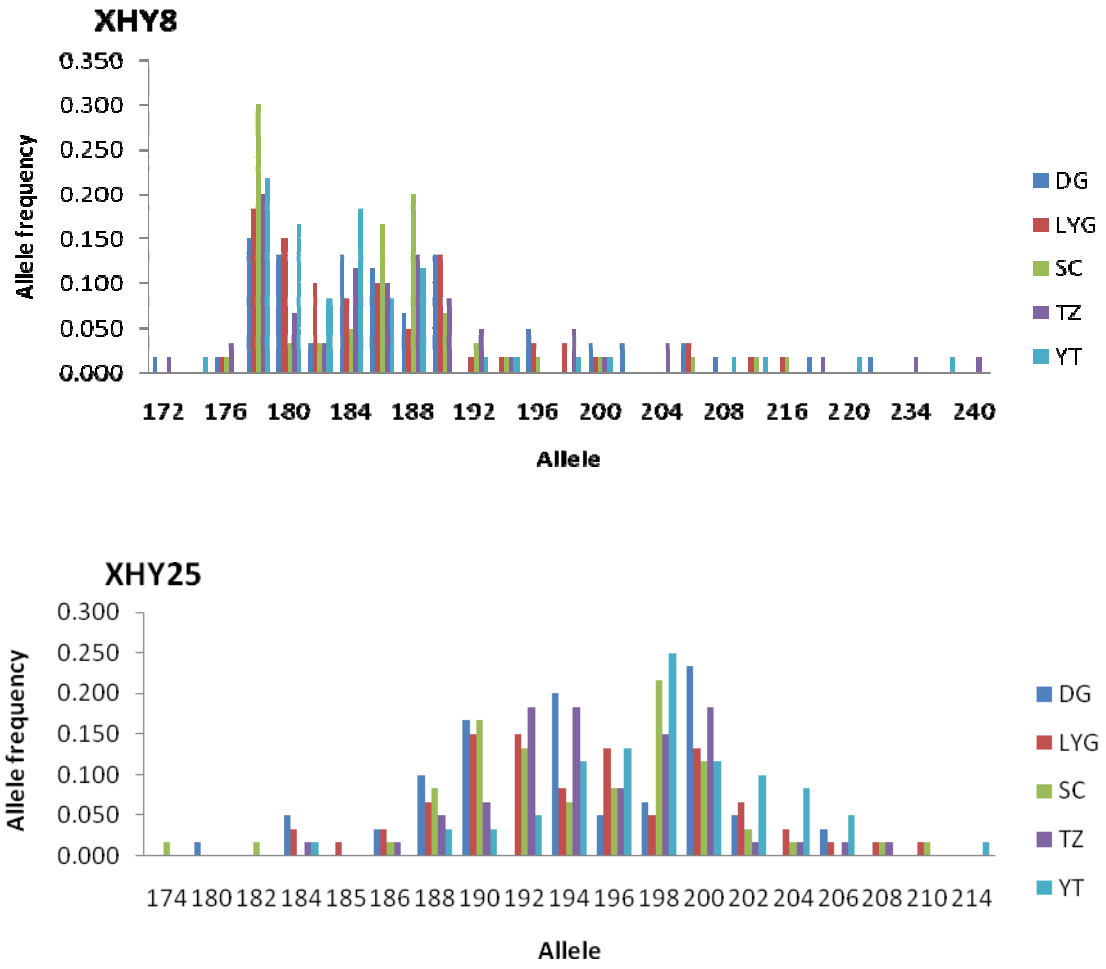
Figure Supplements Legends

Figure sup. 1 Allele frequencies at two selected microsatellite loci (XHY8 and XHY25) for the five populations: DG, LYG, SC, TZ, YT. The X axis shows allele sizes, while frequencies are indicated on the Y axis.

Figure sup. 2 Unweighted Pair-group Method with Arithmetic Means tree (UPGMA) among 5 populations of *Larimichthys polyactis* constructed with the Nei's genetic distances.



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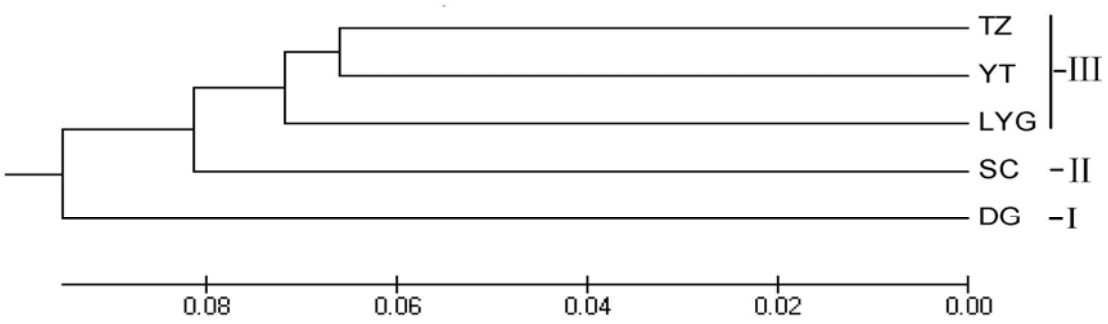

Figure sup. 2 Unweighted Pair-group Method with Arithmetic Means tree (UPGMA) among 5 populations of *Larimichthys polyactis* constructed with the Nei's genetic distances.

Table sup. 1 Statistics for genetic variation at 20 microsatellite loci in five populations of *Larimichthys polyactis* collected from the Yellow Sea and East China Sea

Locus	Pop.	Parameters					
		N_a	N_e	PIC	H_o	H_e	F_{IS}
XHY2	DG	19	14.286	0.926	0.833	0.930	0.121
	LYG*	24	17.822	0.941	0.767	0.944	0.204
	SC*	25	18.182	0.942	0.700	0.945	0.275
	TZ*	29	21.429	0.952	0.733	0.953	0.247
	YT	27	22.222	0.953	0.767	0.955	0.213
XHY4	DG	9	3.455	0.683	0.667	0.711	0.079
	LYG	7	2.098	0.494	0.533	0.523	-0.002
	SC	6	2.832	0.598	0.621	0.647	0.058
	TZ	8	3.454	0.682	0.724	0.710	-0.002
	YT	9	2.980	0.634	0.600	0.664	0.114
XHY8	DG	16	9.783	0.889	0.967	0.898	-0.060
	LYG	16	9.231	0.882	0.867	0.892	0.045
	SC	15	5.882	0.812	0.700	0.830	0.173
	TZ	17	9.730	0.889	0.867	0.897	0.051
	YT	15	7.229	0.848	0.800	0.862	0.088
XHY9	DG	17	10.843	0.902	0.700	0.908	0.245
	LYG	23	13.740	0.923	0.867	0.927	0.082
	SC	13	8.191	0.866	0.667	0.878	0.258
	TZ	22	13.953	0.924	0.867	0.928	0.083
	YT	19	14.754	0.928	0.700	0.932	0.265
XHY11	DG	15	7.377	0.853	0.867	0.864	0.014
	LYG	16	9.524	0.886	0.767	0.895	0.160
	SC	13	5.881	0.810	0.793	0.830	0.062
	TZ	17	7.692	0.858	0.933	0.870	-0.056
	YT	13	5.538	0.803	0.767	0.819	0.081
XHY12	DG	20	14.173	0.925	0.833	0.929	0.120
	LYG	24	17.822	0.941	0.833	0.944	0.134
	SC	23	15.431	0.931	0.897	0.935	0.059
	TZ	25	16.822	0.938	0.900	0.941	0.060
	YT	24	16.822	0.938	0.867	0.941	0.099
XHY14	DG	6	2.722	0.571	0.621	0.633	0.036
	LYG	5	2.550	0.552	0.533	0.608	0.139
	SC	6	2.581	0.548	0.519	0.612	0.172
	TZ	7	2.965	0.617	0.700	0.663	-0.039
	YT	5	2.846	0.601	0.586	0.649	0.114
XHY15	DG	22	16.071	0.934	0.800	0.938	0.163
	LYG	23	14.286	0.926	0.900	0.930	0.049
	SC	24	17.476	0.940	0.833	0.943	0.133
	TZ	23	14.876	0.929	0.967	0.933	-0.019

	YT	25	16.820	0.937	0.931	0.941	0.028
XHY16	DG	19	11.392	0.906	0.800	0.912	0.140
	LYG	23	15.254	0.931	0.867	0.934	0.089
	SC	17	11.845	0.909	0.724	0.916	0.226
	TZ	20	11.688	0.909	0.767	0.914	0.178
	YT*	23	16.981	0.938	0.733	0.941	0.237
XHY17	DG	14	8.654	0.874	0.933	0.884	-0.038
	LYG	11	7.377	0.851	0.967	0.864	-0.102
	SC	11	7.004	0.842	0.933	0.857	-0.072
	TZ	15	8.257	0.868	0.967	0.879	-0.083
	YT	14	9.278	0.883	0.833	0.892	0.083
XHY19	DG	9	2.985	0.635	0.633	0.665	0.065
	LYG	8	3.536	0.693	0.700	0.717	0.041
	SC	7	4.335	0.737	0.759	0.769	0.031
	TZ	9	4.206	0.731	0.700	0.762	0.098
	YT	10	3.543	0.694	0.667	0.718	0.088
XHY21	DG	22	16.981	0.938	0.967	0.941	-0.010
	LYG	17	12.162	0.912	0.800	0.918	0.145
	SC	21	14.286	0.926	0.900	0.930	0.049
	TZ	19	13.235	0.919	0.900	0.924	0.043
	YT	19	13.787	0.923	0.862	0.927	0.088
XHY22	DG	23	17.647	0.941	1.000	0.943	-0.043
	LYG*	23	12.245	0.913	0.800	0.918	0.145
	SC	25	18.689	0.944	1.000	0.946	-0.039
	TZ*	23	15.789	0.933	0.600	0.937	0.374
	YT*	25	16.514	0.937	0.833	0.939	0.130
XHY23	DG	10	6.360	0.825	0.900	0.843	-0.051
	LYG	14	5.217	0.794	0.733	0.808	0.110
	SC	13	6.300	0.825	0.862	0.841	-0.007
	TZ	13	4.147	0.742	0.767	0.759	0.007
	YT	13	6.186	0.821	0.933	0.838	-0.097
XHY24	DG	22	14.063	0.925	0.733	0.929	0.227
	LYG*	22	14.376	0.926	0.586	0.930	0.385
	SC*	22	16.071	0.934	0.800	0.938	0.163
	TZ*	18	13.244	0.919	0.552	0.924	0.418
	YT*	25	17.143	0.939	0.567	0.942	0.412
XHY25	DG	11	6.818	0.837	0.833	0.853	0.040
	LYG	15	9.677	0.888	0.833	0.897	0.087
	SC	14	7.860	0.860	0.833	0.873	0.062
	TZ	13	7.200	0.847	0.833	0.861	0.049
	YT	12	7.563	0.855	0.800	0.868	0.095
XHY28	DG	13	8.333	0.869	0.933	0.880	-0.044
	LYG	14	9.278	0.883	0.867	0.892	0.046
	SC	13	6.228	0.821	0.733	0.839	0.143

	TZ	13	6.294	0.824	0.733	0.841	0.145
	YT	9	7.469	0.851	0.767	0.866	0.132
XHY30	DG	3	1.779	0.367	0.233	0.438	0.480
	LYG	7	3.455	0.677	0.833	0.711	-0.156
	SC	6	3.247	0.639	0.724	0.692	-0.029
	TZ	6	2.941	0.601	0.600	0.660	0.108
	YT	6	2.552	0.562	0.655	0.608	-0.060
XHY32	DG	14	9.278	0.883	0.800	0.892	0.120
	LYG	13	6.870	0.842	0.833	0.854	0.042
	SC	11	6.316	0.824	0.667	0.842	0.224
	TZ	12	7.004	0.843	0.767	0.857	0.122
	YT*	9	6.228	0.821	0.633	0.839	0.261
XHY34	DG	17	12.162	0.912	0.933	0.918	0.000
	LYG	25	15.254	0.931	1.000	0.934	-0.053
	SC	20	14.400	0.926	0.900	0.931	0.050
	TZ	25	16.667	0.937	0.967	0.940	-0.011
	YT	23	18.947	0.945	0.933	0.947	0.032
All locus	DG	15.050	9.758	0.831	0.799	0.845	0.071
	LYG	16.500	10.089	0.843	0.794	0.852	0.085
	SC	15.250	9.652	0.835	0.778	0.850	0.101
	TZ	16.700	10.080	0.845	0.792	0.858	0.093
	YT	16.300	10.820	0.843	0.762	0.855	0.126

N_a = the number of alleles per locus, N_e = the number of effective alleles per locus, PIC = polymorphism information content, H_o = observed heterozygosity, H_e = expected heterozygosity, F_{IS} = the inbreeding coefficient (*, significantly value of HWE greater than zero after sequential Bonferroni corrections)

Table sup. 2 P-values of bottleneck tests for detecting the recent population declines of *Larimichthys polyactis* using two phased mutation model (TPM), stepwise mutation model (SMM) and mode shift indicator

Population	Heterozygosity excess (P value)				Mode-shift
	TPM (90%)	TPM (95%)	SMM (90%)	SMM (95%)	
DG	0.24900	0.55084	0.77381	0.79545	normal
LYG	0.90533	0.99141	0.99721	0.99721	normal
SC	0.67617	0.83501	0.95515	0.95872	normal
TZ	0.99466	0.99789	0.99928	0.99916	normal
YT	0.52184	0.63575	0.71470	0.71470	normal