

Title:

Microsatellite standardization and genotyping error in a large multi-partner research programme for conservation of Atlantic salmon (*Salmo salar* L.)

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Authors:

Ellis JS¹, Gilbey J², Armstrong A², Balstad T¹⁰, Cauwelier C², Cherbonnel C³,
Consuegra S⁴, Coughlan J⁵, Cross TF⁵, Crozier W⁶, Dillane E⁵, Ensing D⁶,
García de Leániz C⁷, García- Vázquez E⁸, Griffiths AM⁹, Hindar K¹⁰, Hjorleifsdottir S¹¹, Knox D²,
Machado-Schiaffino G⁸, McGinnity P⁵, Meldrup D¹², Nielsen EE¹², Olafsson K¹¹,
Primmer CR¹³, Prodohl P¹⁶, Stradmeyer L², Vähä J-P¹³, Verspoor E², Wennevik V¹⁵ and Stevens J R¹

¹School of Biosciences, Hatherly Laboratories, University of Exeter, Prince of Wales Rd, Exeter, EX4 4PS, UK.

²Marine Scotland, Freshwater Laboratory, Faskally, Pitlochry, Scotland, PH16 4LB, UK.

³GENINDEXE, 6 rue des Sports, 17000 La Rochelle, France

⁴Institute of Biological, Environmental & Rural Sciences Aberystwyth University, Edward Llwyd Building Penglais Campus, Ceredigion, SY23 3DA, UK

⁵Department of Zoology, Ecology & Plant Science/Aquaculture & Fisheries Development Centre, University College, Cork, Ireland

⁶Agri-Food and Biosciences Institute Northern Ireland, Fisheries and Aquatic Ecosystems Branch, Newforge Lane, Belfast, Northern Ireland, BT9 5PX

⁷School of the Environment and Society, Swansea University, Swansea, Wales.

⁸Departament of Functional Biology, Genetics, Universidad of Oviedo, C/ Julian Claveria s/n, 33006 Oviedo, Spain

⁹Marine Biological Association of the UK, The Laboratory, Citadel Hill, Plymouth PL1 2PB, UK

¹⁰Norwegian Institute for Nature Research (NINA), N-7485 Trondheim, Norway

¹¹Matis ohf., Vinlandsleid 12, 113 Reykjavik, Iceland.

¹²DTU Aqua, National Institute of Aquatic Resources, Technical University of Denmark, Vejlsøve 39, 8600 Silkeborg

¹³DTU Aqua, National Institute of Aquatic Resources, Technical University of Denmark, Vejlsøve 39, 8600 Silkeborg

¹⁴Department of Biology, University of Turku, FIN-20014, Finland

¹⁵Institute of Marine Research, Nordnesgaten 50, 5005 Bergen, Norway

Corresponding author: J. R. Stevens, email: J.R.Stevens@exeter.ac.uk, tel: 01392 263775

Supplementary data Allelic error rates for each locus and laboratory, including number of alleles at each locus

(observed by baseline laboratory for control plate samples), locus size range and repeat type. A: before calibration, B: after calibration

Allelic error																
	Ssa14	Ssa171	Ssa197	Ssa202	Ssa289	SsaD144	SsaD157	SsaD486	SsaF43	SSsp1605	SSsp2201	SSsp2210	SSsp2216	SSsp3016	SSspG7	Ssol85
Size range	24	84	160	184	42	188	204	64	54	102	180	84	124	96	132	64
No. of alleles	5	30	28	23	6	36	32	12	10	10	35	14	21	18	28	20
Repeat type	di	di	tetra	tetra	di	tetra	tetra	tetra	di	tetra	tetra	tetra	tetra	tetra	tetra	di
A																
A		0.0000	0.0100	0.0000		0.0000	0.0035	0.0068		0.0000	0.0000	0.0000	0.0000	0.0000		0.0000
B	0.0029	0.0115	0.0000	0.0000	0.0029	0.0029	0.0199	0.0000	0.1552	0.0261	0.0208	0.0000	0.0057	0.0145	0.0259	
C	0.0056	0.0028	0.0141	0.0063	0.0000		0.0032	0.0057	0.0552	0.0158	0.0131	0.0090	0.0061	0.0114	0.0150	0.0056
D	0.0000	0.0029	0.0174	0.0000	0.0029	0.0086	0.0000	0.0000	0.0257	0.0219	0.0000	0.0029	0.0172	0.0058	0.0000	
E			0.0058	0.0114						0.0368		0.0143			0.7184	
F		0.0000			0.0030	0.0099	0.0097				0.0066					0.0065
G	0.0057	0.0029	0.0028	0.0000	0.0029	0.0000	0.0029	0.0000	0.0058	0.0000	0.0057	0.0028	0.0000	0.0000	0.0057	
H	0.0000	0.0028	0.0000	0.0116	0.0000	0.0118	0.0234	0.0000	0.0056	0.0037	0.0208	0.0227	0.0000	0.0028	0.0144	0.0057
I	0.0062	0.0194	0.0034	0.0149	0.0111	0.3294	0.0361		0.0559	0.0150	0.0663	0.0087	0.0093	0.0243	0.6441	0.1169
J	0.0540	0.0824	0.0763	0.0000	0.1051	0.0085	0.0116		0.0819	0.0000	0.0086	0.0028	0.0621	0.0795	0.0114	0.0876
K	0.0142	0.0143	0.0959	0.0115	0.0114	0.4109	0.5057	0.0057	0.0175	0.0481	0.1444	0.4080	0.1424		0.7632	0.0374
L	0.0057	0.0200	0.0320	0.0029	0.0000	0.1358	0.0118		0.0171	0.0036	0.0089	0.4118	0.0000	0.0057	0.6571	0.0374
B																
A		0.0000	0.0100	0.0000		0.0000	0.0035	0.0068		0.0000	0.0000	0.0000	0.0000	0.0000		0.0000
B	0.0029	0.0115	0.0000	0.0000	0.0029	0.0029	0.0199	0.0000	0.0316	0.0261	0.0208	0.0000	0.0057	0.0145	0.0259	
C	0.0056	0.0028	0.0141	0.0063	0.0000		0.0032	0.0057	0.0552	0.0158	0.0131	0.0090	0.0061	0.0114	0.0150	0.0056
D	0.0000	0.0029	0.0174	0.0000	0.0029	0.0086	0.0000	0.0000	0.0257	0.0219	0.0000	0.0029	0.0000	0.0058	0.0000	
E			0.0058	0.0114						0.0368		0.0143			0.0086	
F		0.0000			0.0030	0.0099	0.0097				0.0066					0.0065
G	0.0057	0.0029	0.0028	0.0000	0.0029	0.0000	0.0029	0.0000	0.0058	0.0000	0.0057	0.0028	0.0000	0.0000	0.0057	
H	0.0000	0.0028	0.0000	0.0116	0.0000	0.0118	0.0234	0.0000	0.0056	0.0037	0.0208	0.0227	0.0000	0.0028	0.0144	0.0057
I	0.0000	0.0191	0.0034	0.0375	0.0000	0.0320	0.0361		0.0510	0.0000	0.0259	0.0000	0.0094	0.0000	0.0172	0.0974
J	0.0540	0.0625	0.0763	0.0000	0.1051	0.0085	0.0116		0.0819	0.0000	0.0086	0.0028	0.0621	0.0795	0.0114	0.0621
K	0.0057	0.0086	0.0145	0.0115	0.0113	0.0471	0.0114	0.0029	0.0205	0.0410	0.0706	0.0000	0.0203		0.0116	0.1337
L	0.0057	0.0171	0.0320	0.0029	0.0000	0.0086	0.0118		0.0171	0.0036	0.0089	0.0029	0.0000	0.0057	0.0171	0.0029