Helbing/Langlois Lab
eDNA Inventory

Helbing/Langlois Laboratory eDNA Technical Bulletin

All eDNA tools are validated through a rigorous multi-step evaluation protocol that includes tests of DNA target specificity and amplification sensitivity[1-3].

General eDNA Assay Information

Target Species: Atlantic salmon (*Salmo salar*)
Species Code: te-SASA
eDNA qPCR Tool: te-SASA2
eDNA qPCR Format: TaqMan
Gene Target: MT-ND2
Published in:

eDNA Assay Sensitivity Test Summary using gBlocks™ Synthetic DNA

LOD 0.4 95% CI 0.3-0.6 Copies/Rxn LOQ 1.3 95% CI 1-2.2 Copies/Rxn LOB 0 hits/8
$LOQ_{continuous}$ 4 Copies/Rxn

Binomial-Poisson model for 8 technical replicates determined using eLowQuant R code[4]. When the LOQ < LOD, use the LOD for the LOQ. Enzyme: Immolase

eDNA Assay Specificity Test Information

Each qPCR reaction in the specificity assay contained 10 picograms of voucher target gDNA (n=25 technical replicates)

Species	Common Name (*Species*)	Detection	# Voucher Specimens	Sample Sources/Locations
te-SASA	Atlantic salmon (*Salmo salar*)	Yes	6	Canada: Quebec: Fleuve St-Laurent, riviere Metabetchouane Canada: Quebec: Fleuve St-Laurent, riviere Ouasiemsca Malbaie
te-SATR	Brown trout (*Salmo trutta*)	No	1	Canada: New Brunswick: Mc Quarrie Brook
te-ONGO	Pink salmon (*Oncorhynchus gorbuscha*)	No	1	Canada: British Columbia: Indian River
te-SAFO	Brook trout (*Salvelinus fontinalis*)	No	1	Canada: Quebec: Fleuve St-Laurent, riviere Trinite
te-LAAP	Lethenteron appendix (*Lampetra appendix*)	No	1	Canada: Quebec: Fleuve St-Laurent, riviere du Sud
te-PEMA	Sea lamprey (*Petromyzon marinus*)	No	1	Canada: Quebec: Fleuve St-Laurent, riviere Ste-Marguerite
te-COCL	Lake white fish (*Coregonus clupeaformis*)	No	1	Canada: Quebec: Fleuve St-Laurent, riviere St-Nicolas
te-ONMY	Rainbow trout (*Oncorhynchus mykiss*)	No	1	Québec, Canada
ma-CALUfa	Canine (*Canis lupus familiaris*)	No	1	Québec, Canada
ma-FECA	Cat (*Felis catus*)	No	1	Québec, Canada
ma-HOSA	Human (*Homo sapiens*)	No	1	Québec, Canada

References

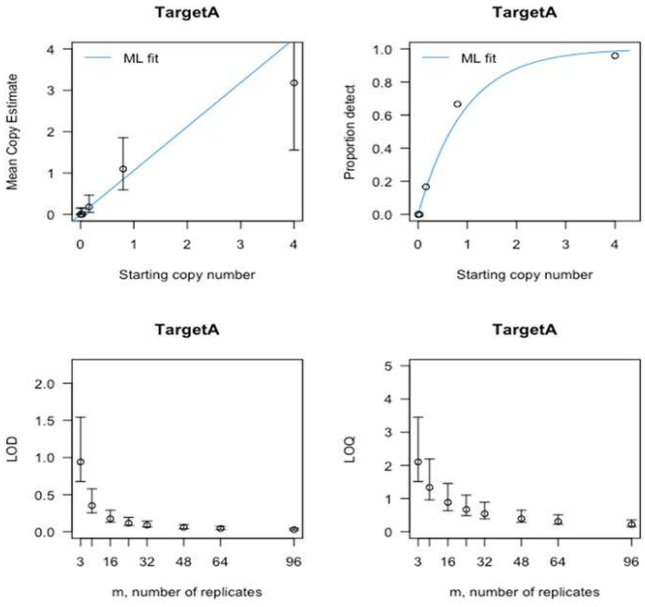
1. Hobbs, J, Adams, IT, Round, JM, Goldberg, CS, Allison, MJ, Bergman, LC, Mirabzadeh, A, Allen, H, Helbing, CC (2020) Revising the range of Rocky Mountain tailed frog, *Ascaphus montanus* , in British Columbia, Canada, using environmental DNA methods. Environmental DNA, 2: 350-361. https://doi.org/10.1002/edn3.82

2. Hobbs, J, Round, JM, Allison, MJ, Helbing, CC (2019) Expansion of the known distribution of the coastal tailed frog, *Ascaphus truei* , in British Columbia, Canada, using robust eDNA detection methods. PLOS ONE 14(3): e0213849. https://doi.org/10.1371/journal.pone.0213849

3. Langlois, VS, Allison, MJ, Bergman, LC, To, TA, and Helbing, CC (2020) The need for robust qPCR-based eDNA detection assays in environmental monitoring and risk assessments. Environmental DNA, 3: 519-527. doi: 10.1002/edn3.164

4. Lesperance, M, Allison, MJ, Bergman, LC, Hocking, MD, and Helbing, CC (2021) A statistical model for calibration and computation of detection and quantification limits for low copy number environmental DNA samples. Environmental DNA, 3: 970-981. doi: 10.1002/edn3.220

eDNA Assay Sensitivity Test Details using gBlocks™ synthetic DNA



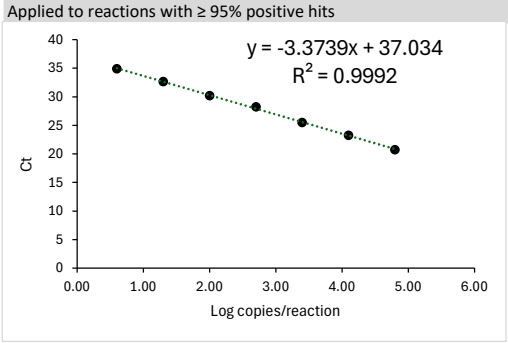
To generate tables for different numbers of replicates, use raw csv data files.

From 8 Technical Replicates

# Detects	# Copies	SE
0	0	0
1	0.078	0.127
2	0.277	0.21
3	0.515	0.313
4	0.739	0.396
5	1.071	0.533
6	1.569	0.76
7	2.445	1.232

Determined using eLowQuant R code[4].

Applied to reactions with ≥ 95% positive hits



Binomial-Poisson model: No intercept
Determined using eLowQuant R code[4].
Based on a 2 µL DNA input in a total 15 µL reaction

Efficiency 98%

Field Sample Validation

Sample Type	Known Presence	# Samples	Detected	Location
Water	Y	48	Y	Rivière Jacques-Cartier, Québec, Canada

Abbreviations

95% CI	95% Confidence interval	LOQ	Limit of quantification
eDNA	Environmental DNA	MT-ND2	Mitochondrial NADH dehydrogenase subunit 2
gDNA	Total genomic DNA extracted from voucher specimen	NTC	qPCR no template control
LOB	Limit of blank	qPCR	Quantitative real-time polymerase chain reaction
LOD	Limit of detection	SE	Standard error