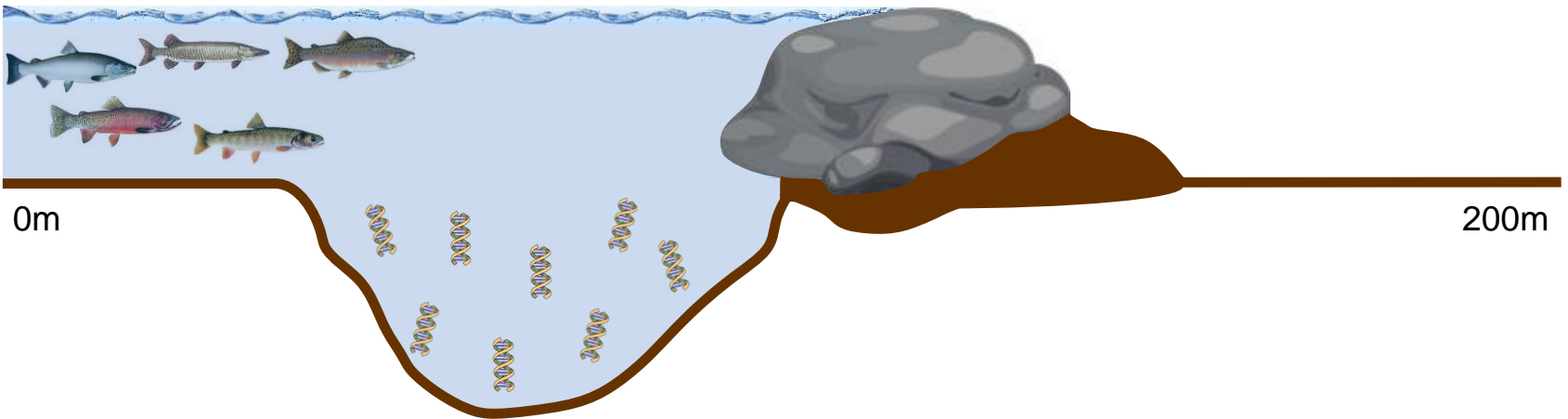
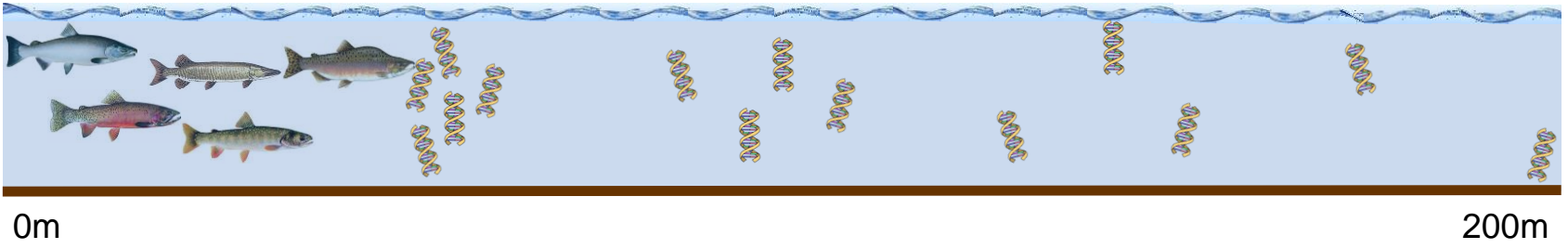
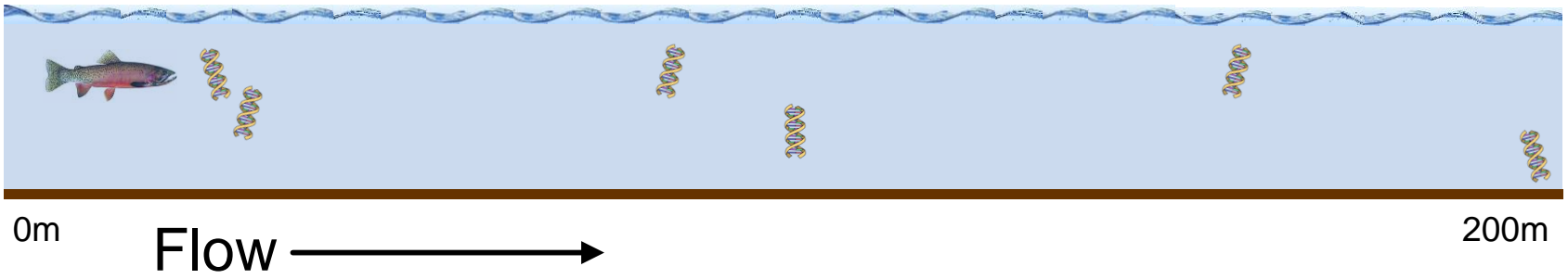


ENVIRONMENTAL DNA DETECTION OF CRYPTIC, RARE OR PROTECTED AQUATIC SPECIES



WHAT IS EDNA?

eDNA comes from biological material shed into the environment in the form of tissues, cells, feces, and naked DNA.





eDNA APPLICATIONS ARE VAST & DIVERSE

- Desert / terrestrial
- Wetland interface / semi – aquatic
- Estuary / Delta
- Riverine
- Lacustrine
- Alpine
- Coastal forest

OUR PHILOSOPHY

01

Where are
they?

02

How many
are there?

03

How are they
doing?



PRESENTATION OVERVIEW

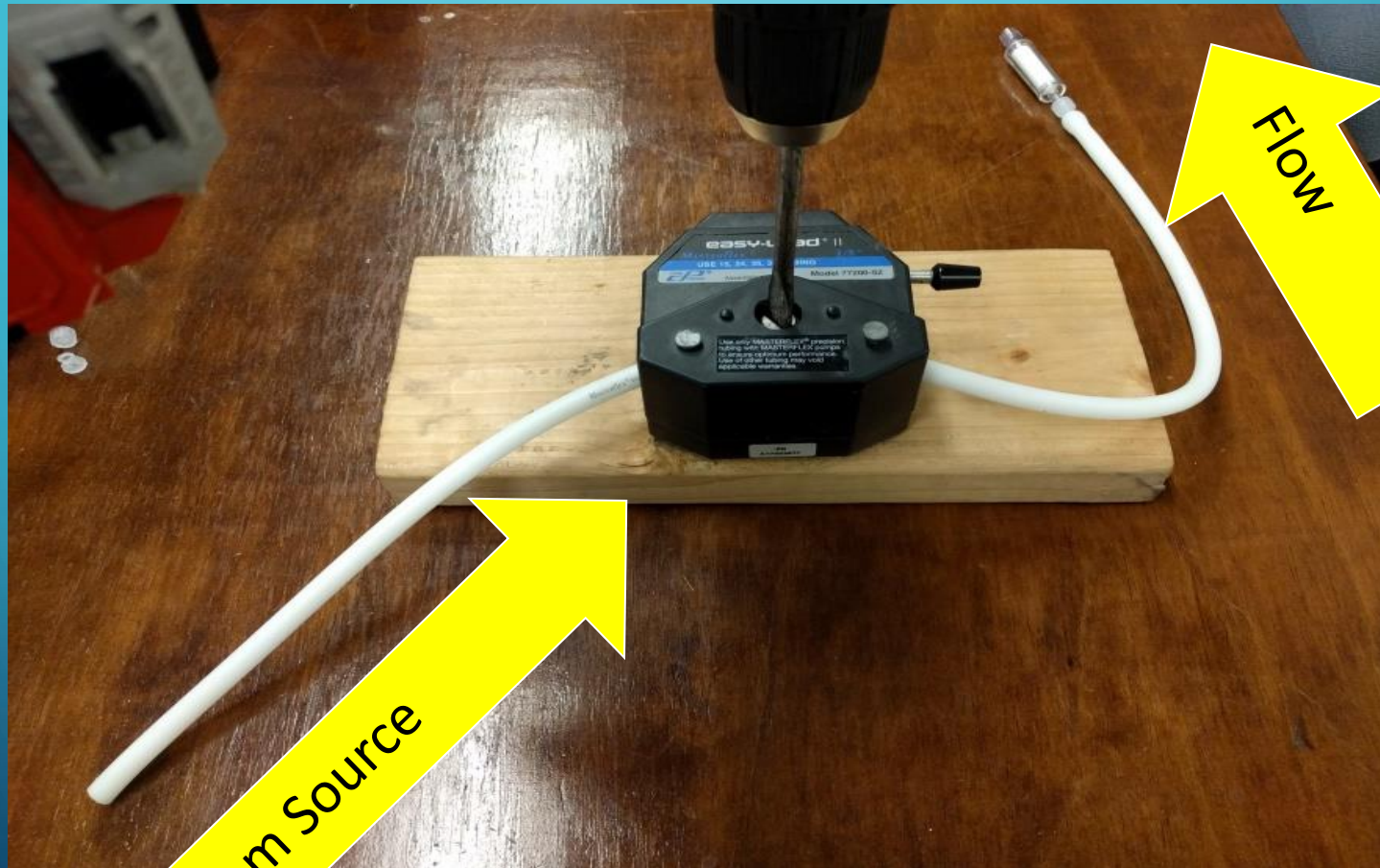
- Sample/Survey design
 - **Probability of Detection (PoD)?**
 - Life history
- Sampling methodology
 - Water filtration
 - Pore size
 - Volume
 - Replicates
- Sample storage/preservation/transport
- DNA extraction
- DNA analysis (**qPCR assay validation, MIQE**)
- **Data interpretation**

**Critical considerations for the application of
environmental DNA methods to detect aquatic species**

Caren Goldberg, et al.

May 2016

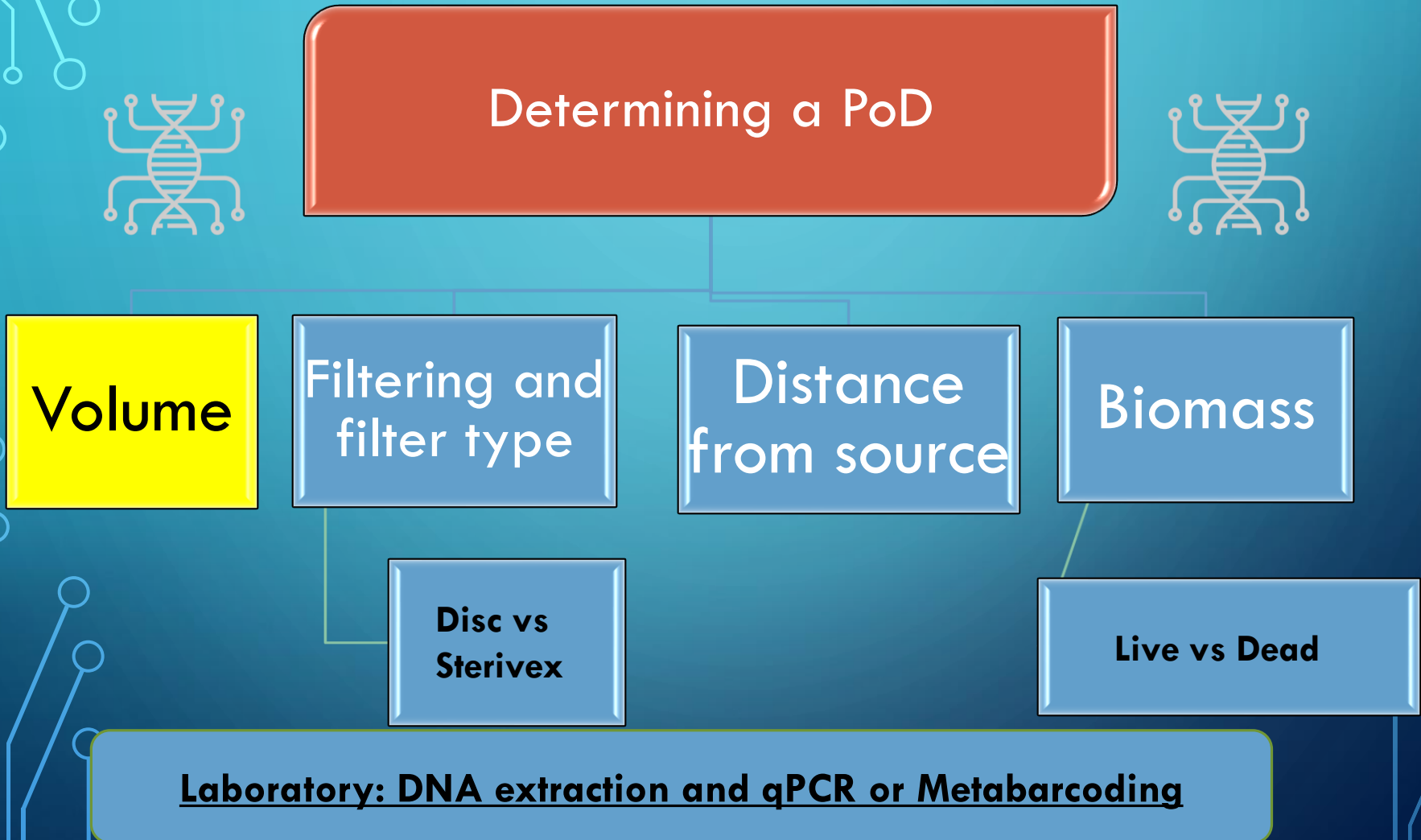
COMPLETE APPARATUS



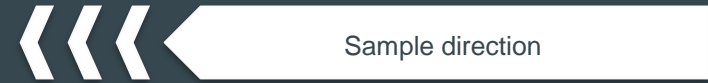
SAMPLING/SURVEY DESIGN

- Sampling apparatus
- Probability of Detection (PoD)
 - Habitat
 - Filter type
 - Volume
 - Replication
 - Frequency
 - Interval
 - Life History
- Budget
- Expectations?

Probability of detecting (PoD) eDNA



Determining PoD of Delta Smelt at CVP



N=20-100

Volume = 50ml - 300ml/ filter

Live

Live



Replicate = 2 filters/ point

Distance 10 20 30 40 50 200 300 400 500 600 700 800 900 1000

This distance configuration can be adjusted based on access/safety

What is Delta Smelt PoD at CVP?

PoD \approx 0.6

Volume

\approx 300 ml

Filter pore Size

= 0.45 μ m

Distance from source

\approx 200 m

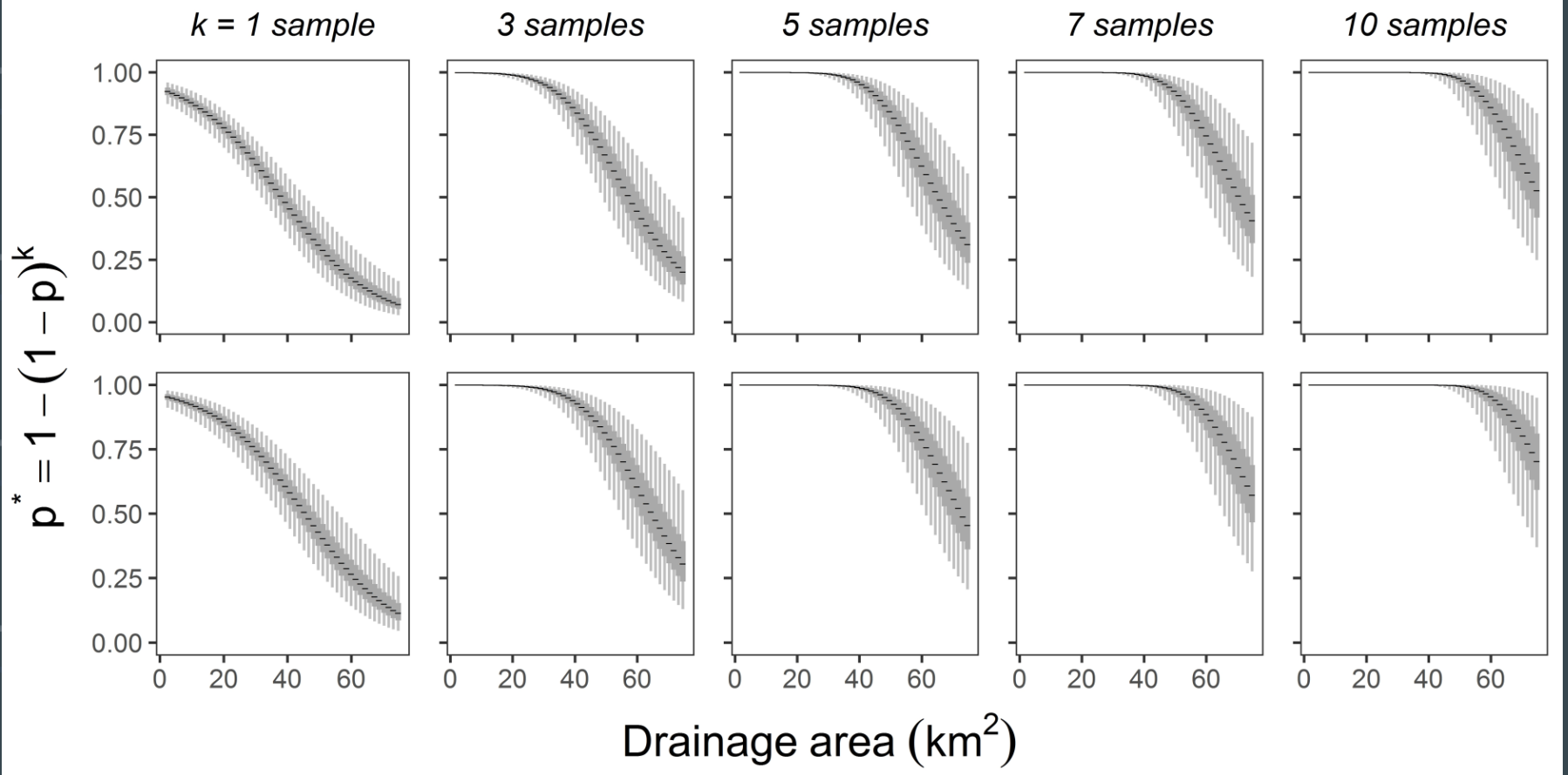
Biomass

=100 fish


Filters

N = 1

N = 5
PoD = 99%



* Eric Waits and Roy Martin
US EPA



ASSAY VALIDATION QUANTITATIVE POLYMERASE CHAIN REACTION (QPCR)

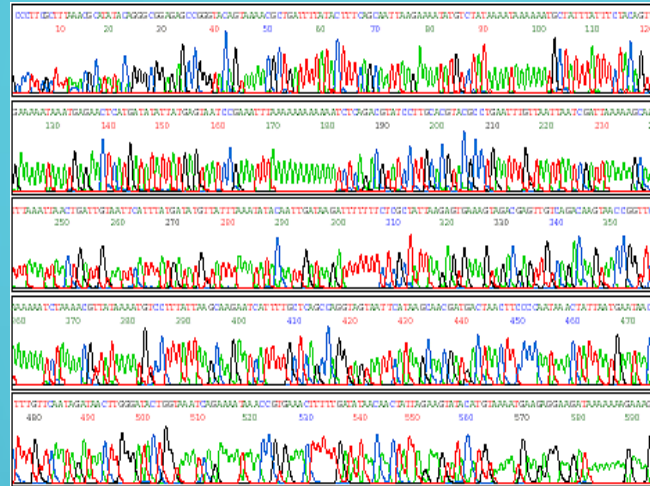
ASSAY DOCUMENTATION

The MIQE guidelines: minimum information for publication of quantitative real-time PCR experiments.

Bustin et al. 2009 Clinical Chemistry 55(4)

DNA Sequencing

DNA Extraction



Barcoding DNA Data Analysis

1. Find Conserved DNA Sequence

TTAATTCAACTACAAGAACCC
TAATGGCCAACCTTCGGAAAT
TAATTCAACTACAAGAACCC
TAATGGCCAACCTTCGGAAA



qPCR

Assay Development 16s, CytB

2. "In Silico" Validation:
Nucleotide BLAST
<http://blast.ncbi.nlm.nih.gov/Blast.cgi>



3. Assay Design

TTAATTC**AACTACAAGAACCC**
TAATGGCCAACCTTCGG**AAA**
Primer Express Software v2.0™
Applied Biosystems

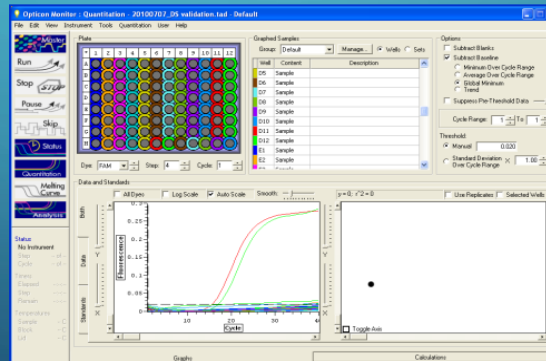


Assay Optimization/Validation (Sensitivity, Specificity)



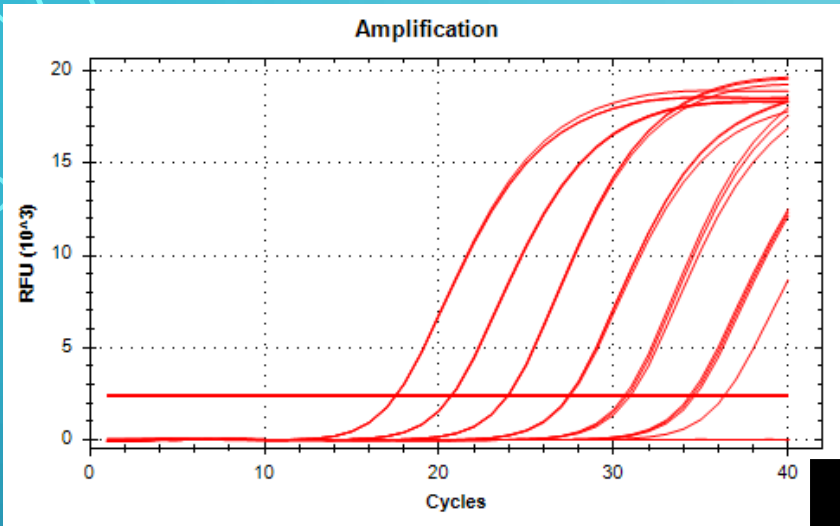
Vouchered Specimen

Unknowns?
Test on Field Samples

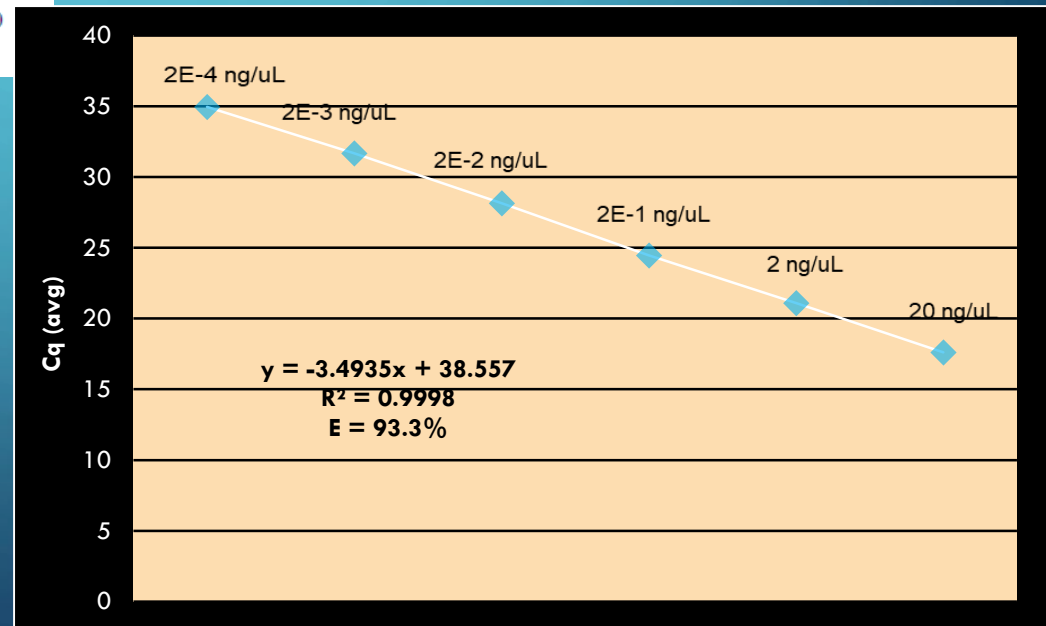


ASSAY VALIDATION

- Assay sensitivity and limit of detection



- PCR Efficiency (E) = 93.3% (slope - 3.4935)
- Y-intercept = 38.557
- $R^2 = 0.9998$
- 40% amplification of $2.0 \times 10^{-4} \text{ ng } \mu\text{L}^{-1}$



DATA

eDNA is a presence absence dataset

- eDNA is either there or not there?
 - C(q): strength of detection
 - Strength of detection in relation to other sites
- Where are they?
 - When are they there?



- Occupancy Model (ESA)
- Eradication or containment

Where
are
they?

How many
are there?
N=?

How are
they
doing?



Our ability to generate data has out paced our ability to confidently analyze, interpret, and compare across labs.

- Bioinformatics
- Publically available DNA reference databases
- Publically available qPCR assay database



Interpretation

Scaling



With caution, cooperation, and continued effort toward a greater understanding of methodology and an adherence to minimum reporting requirements the potential for eDNA will be realized.

