Enhancing the Credibility of Taxonomic Data: The National Wadeable Streams Assessment

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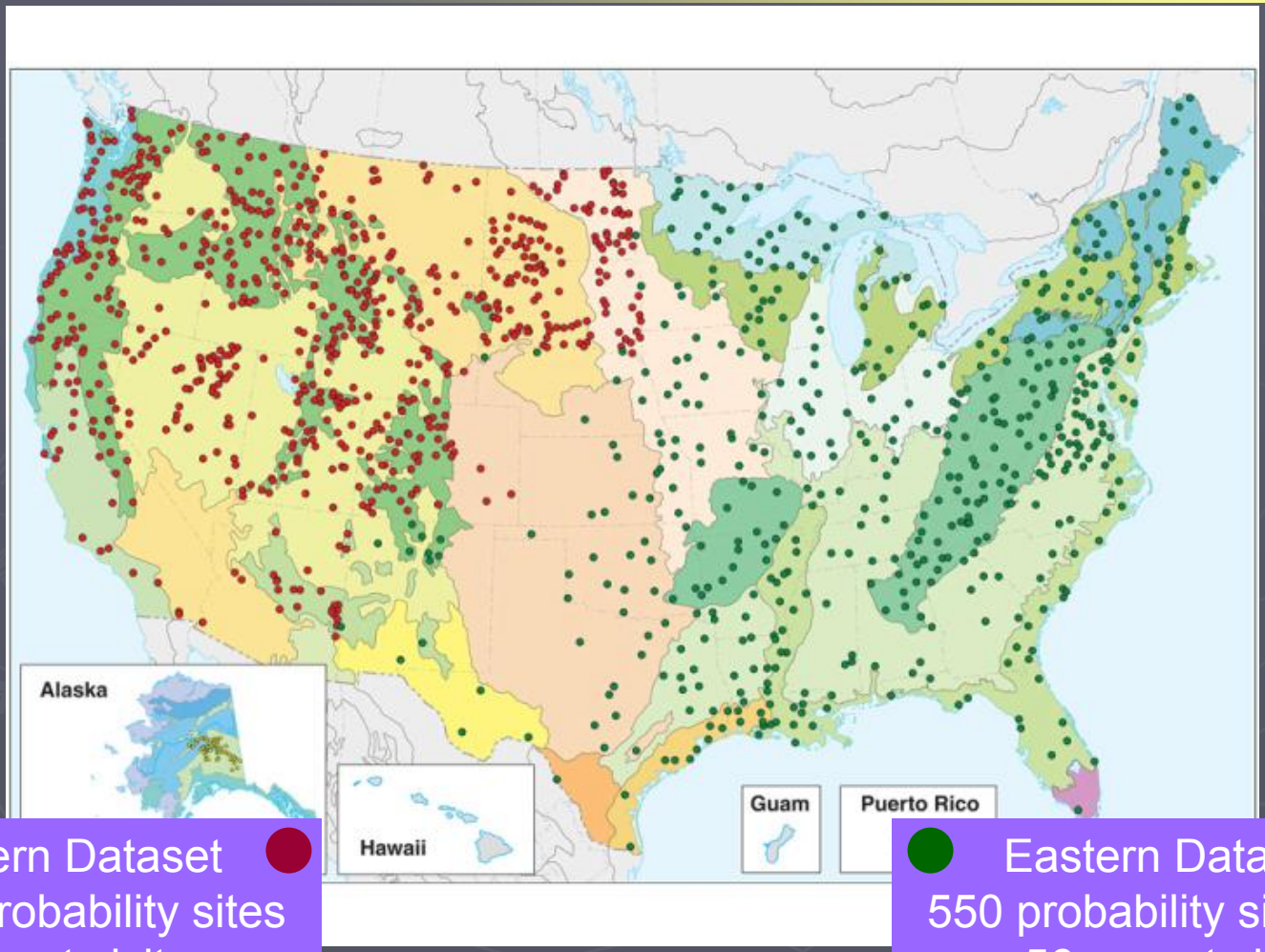
Purpose of presentation

- Scale and scope of the WSA
- Importance of taxonomic data quality in biological assessments
- Procedure for quantifying consistency, repeatability (i.e., precision) and completeness
- Results
  - Comparisons
  - Effectiveness of corrective actions
- Lessons learned

National Wadeable Streams Assessment (WSA)



Western Dataset
750 probability sites
50 repeat visits
50 reference sites

Eastern Dataset
550 probability sites
56 repeat visits
142 reference sites

Taxonomic data

- The identities of organisms contained within a sample
- Foundation of biological assessments
  - Multimetric indexes
  - O/E models
- For multimetric indexes, we are interested in 2 questions
  - What are their names? ***AND***
  - How many are there?

Two types of quality control

- Taxon-based
  - How well identification matches with “truth”
  - Accuracy
  - Traditional approach
- Sample-based
  - How well sample characterization matches between two taxonomists
  - Precision (consistency)
  - Because sample is focus of assessment

Three performance measures

- % taxonomic disagreement (precision)
  - Proportion of specimens in sample non-matching
  - Low values, greater precision
  - MQO=15%
- % difference in enumeration (precision)
  - Proportional difference in sample counts
  - Low values, greater precision
  - MQO=5%
- % taxonomic completeness (completeness)
  - Proportion of specimens in sample id'd to target level
  - High values, greater completeness
  - No specified MQO, but large majority of samples >90%

Process

T1 identifies all samples

▼

Intermediary (EPA) randomly selects 10% of all samples, per lab

▼

T1 sends selected samples to T2

▼

T2 *re-identifies* selected whole samples

▼

Results directly compared

▼

Taxonomic performance characteristics calculated

Purpose of process

- Determine inconsistencies
  - Where are they?
  - What are the causes?
- Develop steps to minimize inconsistencies
- Purpose is ***NOT*** to say one of the taxonomists is right and one is wrong

Most common causes of differences

- Damaged specimens
- Early instar/juvenile specimens
- Poor mounts (midges & worms)
- “Morphotyping” midges and worms
- Incomplete samples
- Incorrect data entry
- Less experience with certain taxa

Example corrective actions

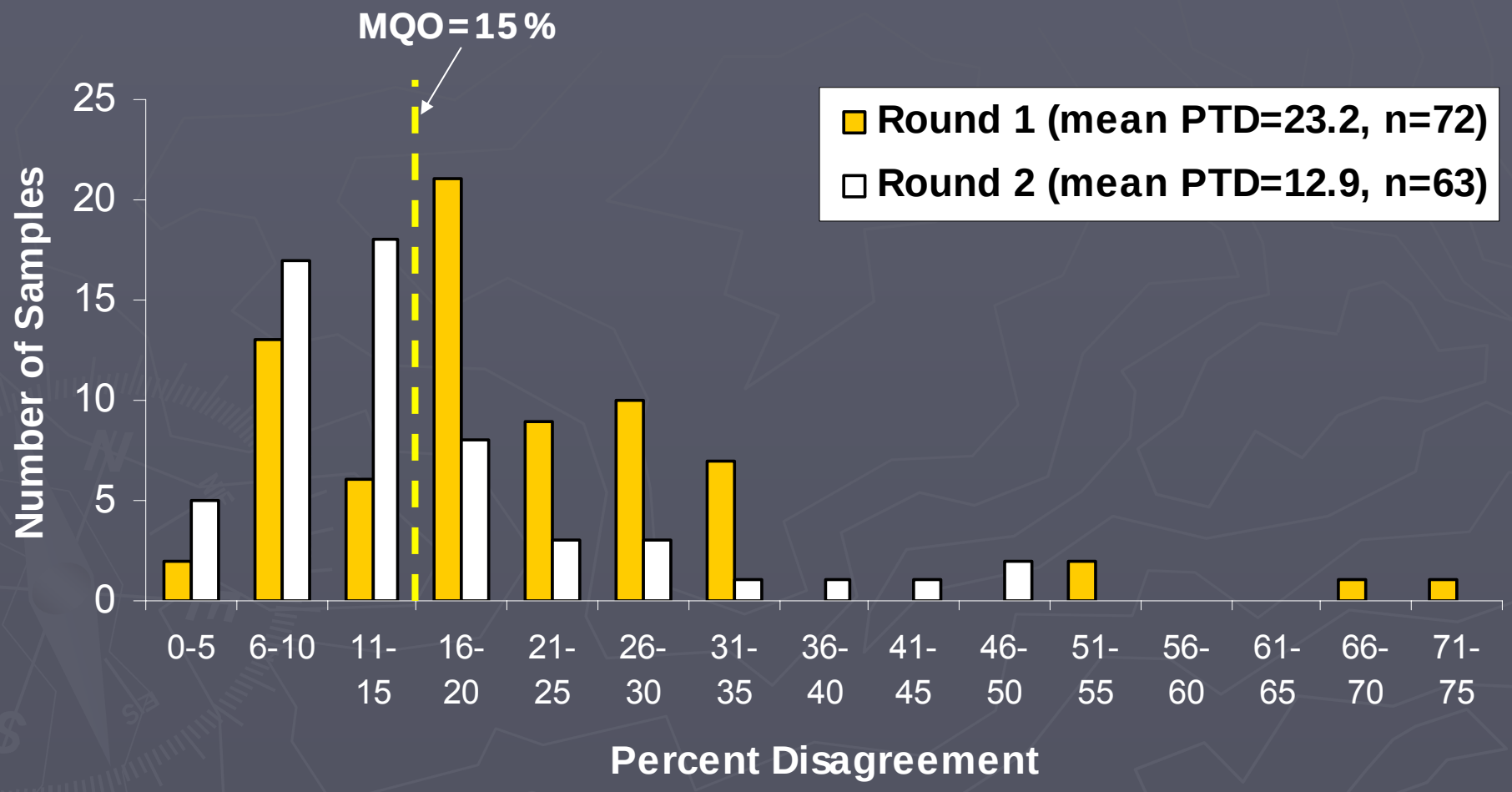
- Mount and re-identify all midges and worms (Chironomidae and Oligochaeta)
- Reexamine Baetidae and Acari
- Reexamine mollusk shells - ID only when “someone’s home”
- Ensure transferred samples are complete
- Carefully proofread all data entry
- Then, go to Round 2

Sample distribution

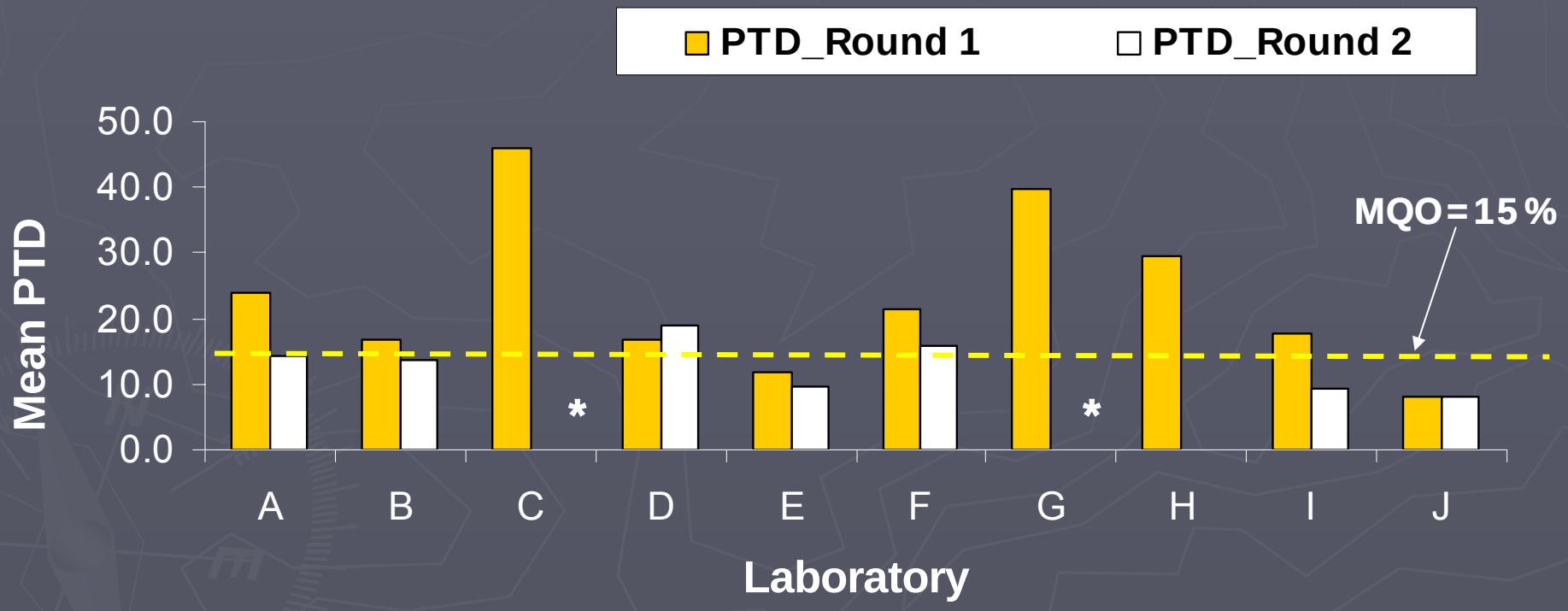
Laboratory	Number of Samples	
	Round 1	Round 2
A	11	14
B	20	26
C	3	*
D	12	12
E	3	3
F	3	3
G	3	*
H	10	13
I	3	2
J	4	na

* Samples absorbed by other labs

PTD (Round 1 vs. 2)



PTD – partitioned, by lab



*samples absorbed by other labs for R2

Effectiveness of corrective actions

Lab	Number of Samples		PTD change
	Round 1	Round 2	
A	11	14	-9.4
B	20	25	-3.3
C	3	*	na
D	12	12	+2.4
E	3	3	-2.2
F	3	3	-5.5
G	3	*	na
H	10	13	INC
I	3	2	-8.2
J	4	4**	0.0

*samples absorbed by other labs; **results carried over from Round 1

Other issues/lessons learned

- Problematic taxa may require collapsing to higher level
- Morphotyping of midges and worms
  - About 10% improvement in consistency WITH slide-mounting
  - Wide variability among taxonomists in morphotyping results
- Excessive damage to specimens
  - May need to modify sample/specimen handling procedures to minimize (both field and lab)
- Straight disagreements and hierarchical differences <u>roughly</u> equivalent

Other issues/lessons learned

- Must have <u>outside</u> laboratory or independent taxonomist for whole sample re-identifications
- Taxonomists (both T1 and T2) need to be well-trained AND experienced
  - Confirm through NABS certification (in part)
- Majority of labs/taxonomists viewed process as constructive for strengthening programs
- Can and should be applied to smaller programs