



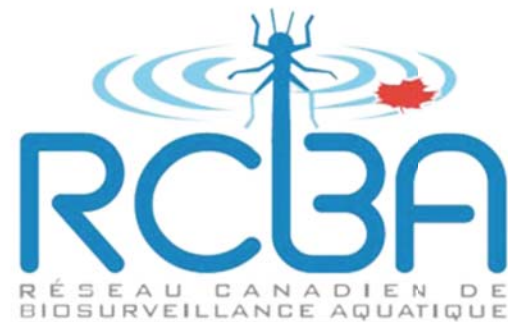
Biomonitoring 2.0: generating and harnessing data on an epic scale for ecosystem assessment

Donald J Baird
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Fredericton, NB

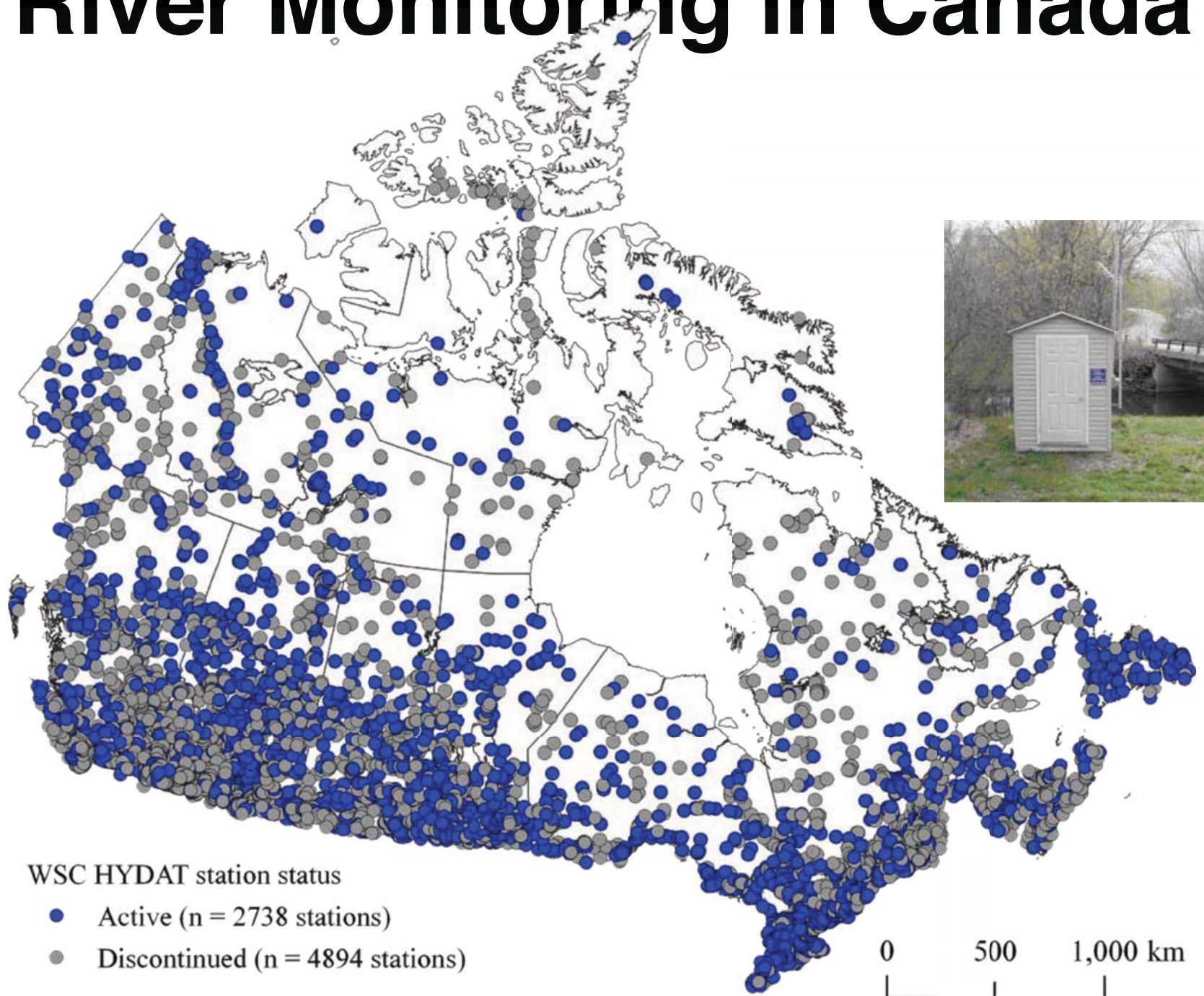


Roadmap

- The challenges of biological monitoring in a data-poor nation
- Technological fixes and their importance
- Biomonitoring 2.0



River Monitoring in Canada



WSC HYDAT station status

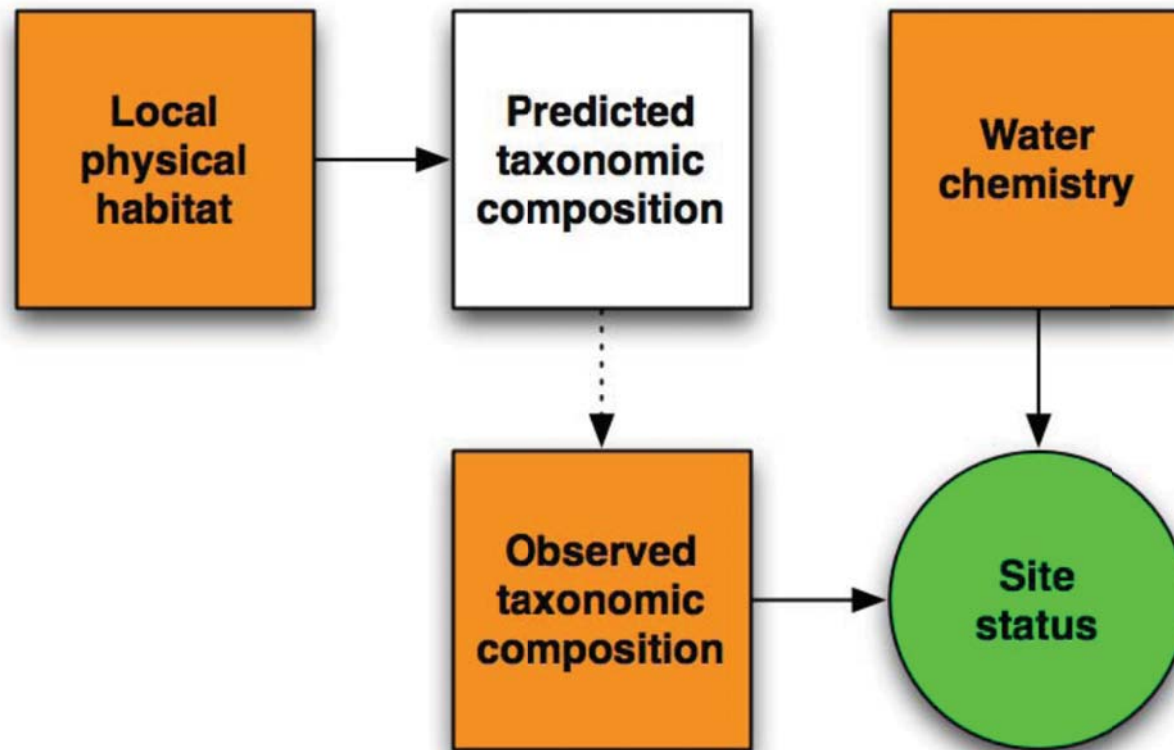
- Active (n = 2738 stations)
- Discontinued (n = 4894 stations)

0 500 1,000 km

Benthic macroinvertebrates

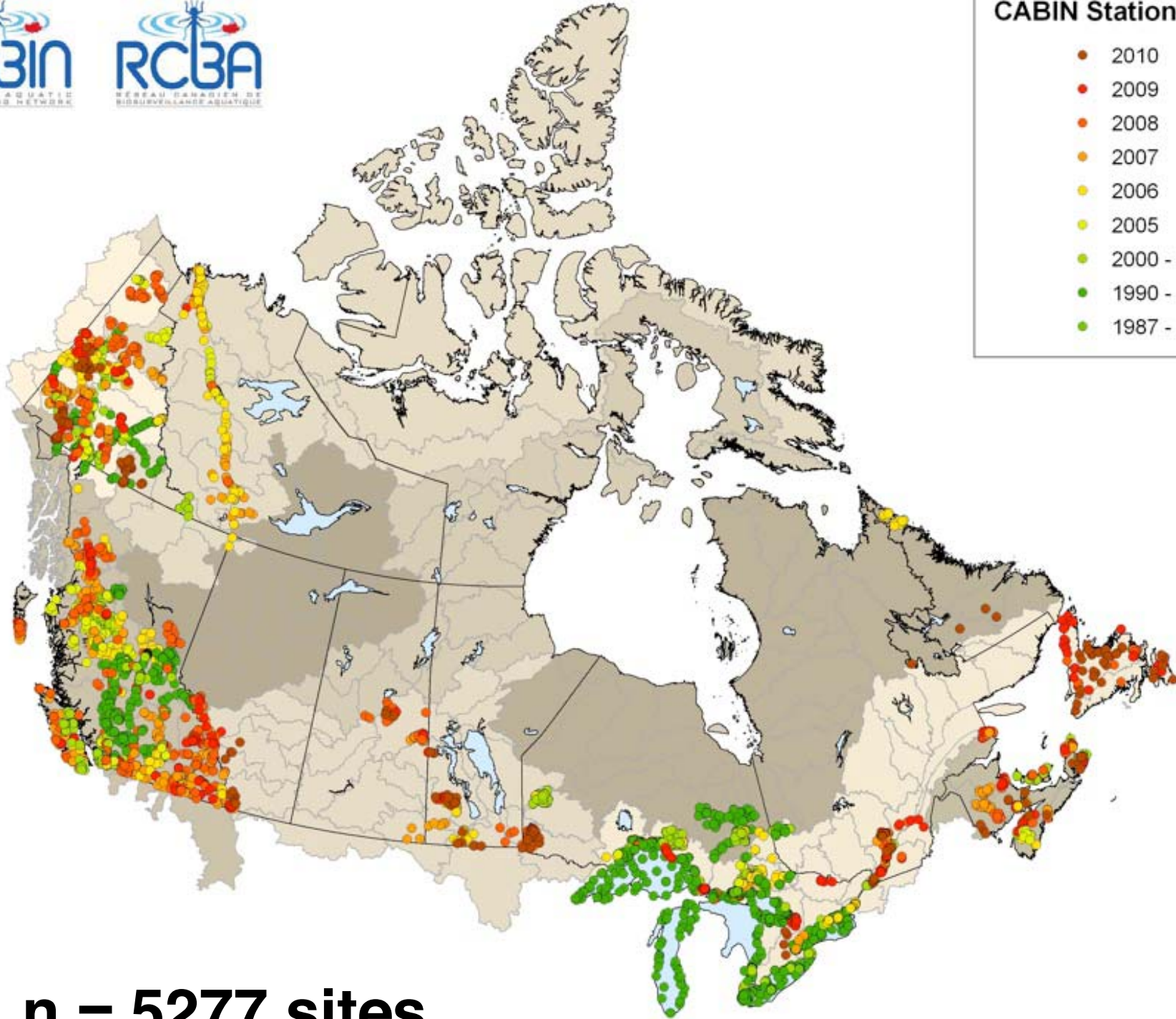


Biomonitoring 1.0: observing biodiversity in rivers



CABIN Stations by Year




- 2010
- 2009
- 2008
- 2007
- 2006
- 2005
- 2000 - 2004
- 1990 - 1999
- 1987 - 1989

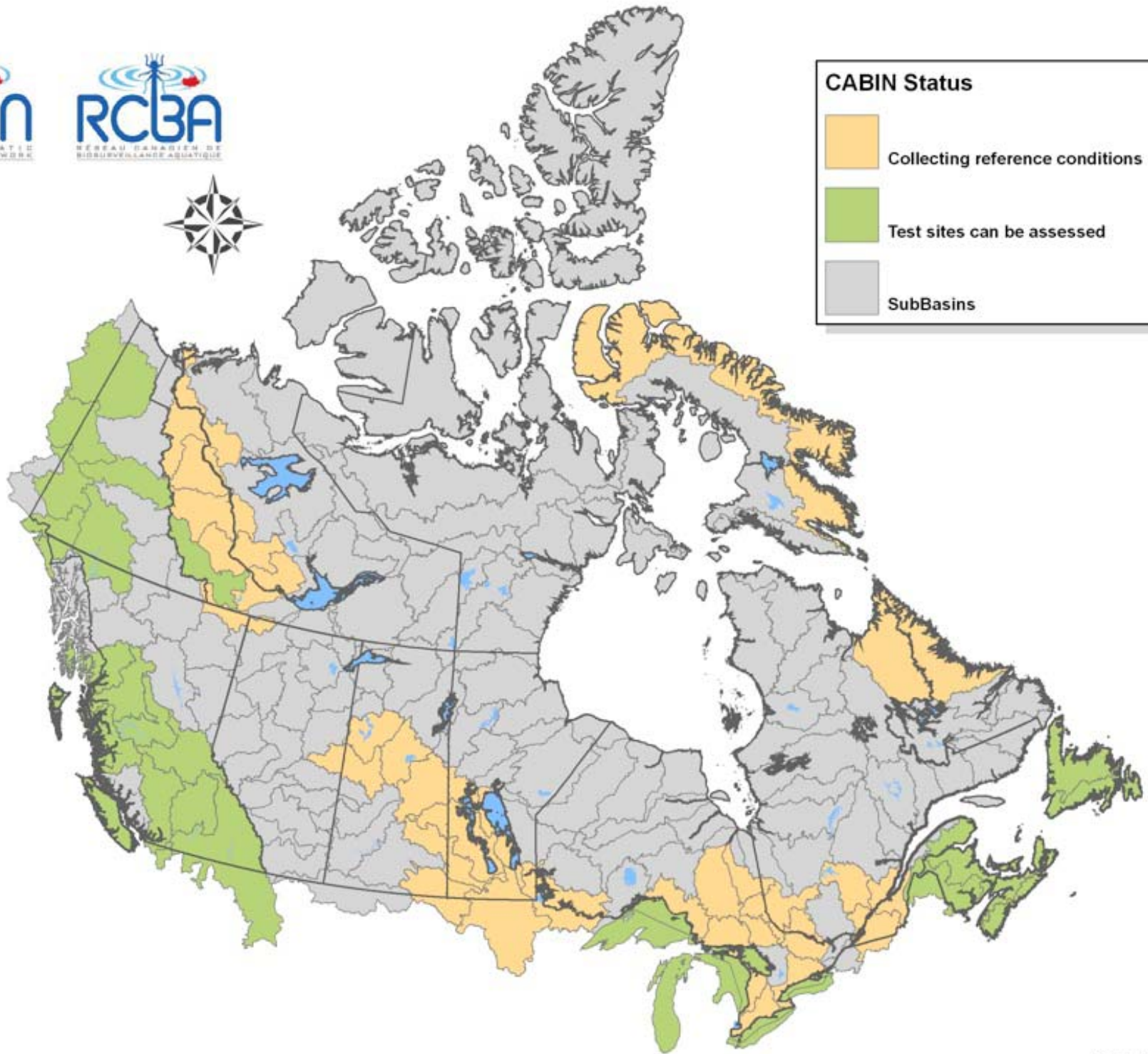


n = 5277 sites



CABIN Status

-  Collecting reference conditions samples
-  Test sites can be assessed
-  SubBasins

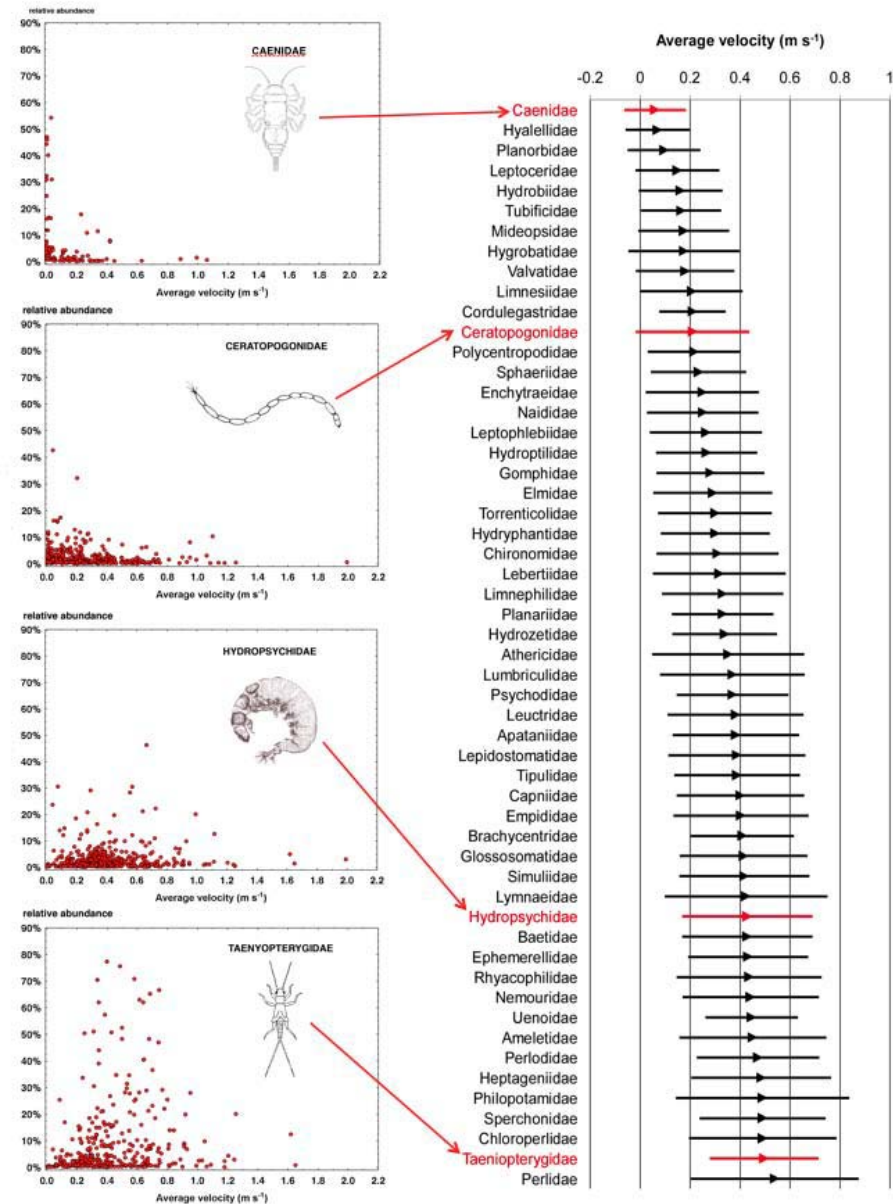


Do we have enough data?

- Data to build reference condition models?
Yes, but we know little or nothing about temporal variability.
- Data to develop new diagnostic tools?

New diagnostic tools

- Taxonomy-based indices
- Traits-based indices
- Genomics-based indices



e.g. Armanini et al., Riv.Res.App. (2011)

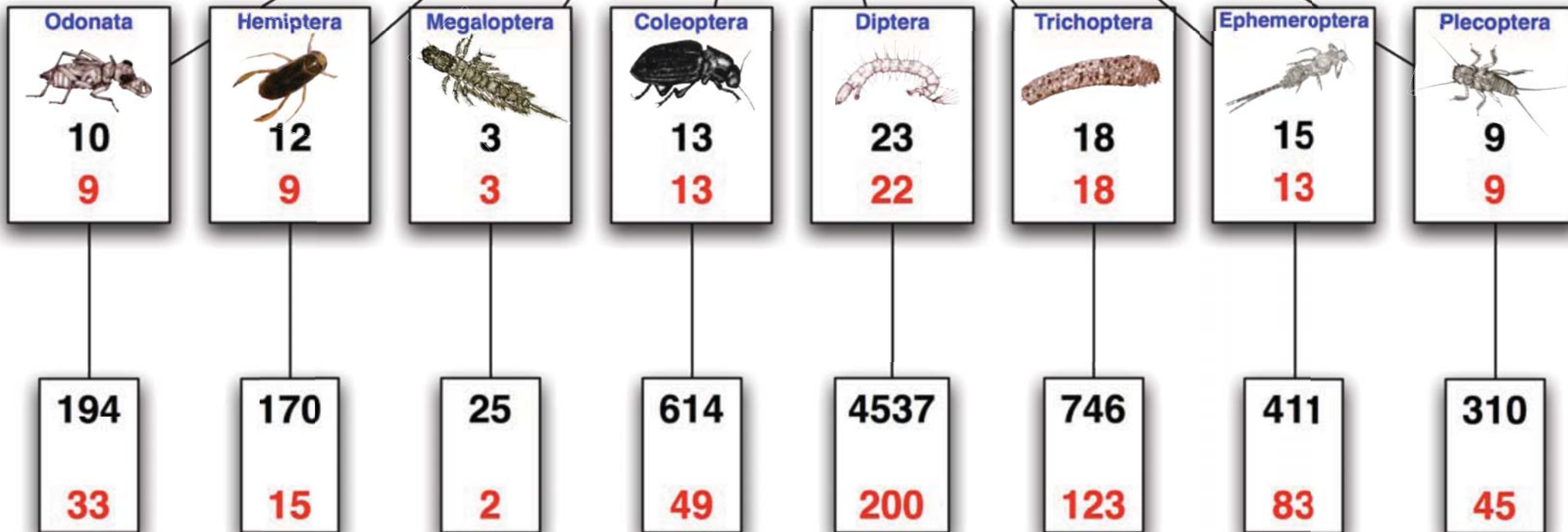
Do we have enough data?

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Yes, but we know little about temporal variability.
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Possible, but restricted geographic range limits analysis.
- Data to observe trends in biodiversity?

Insecta

CANADA
CABIN

Number of families



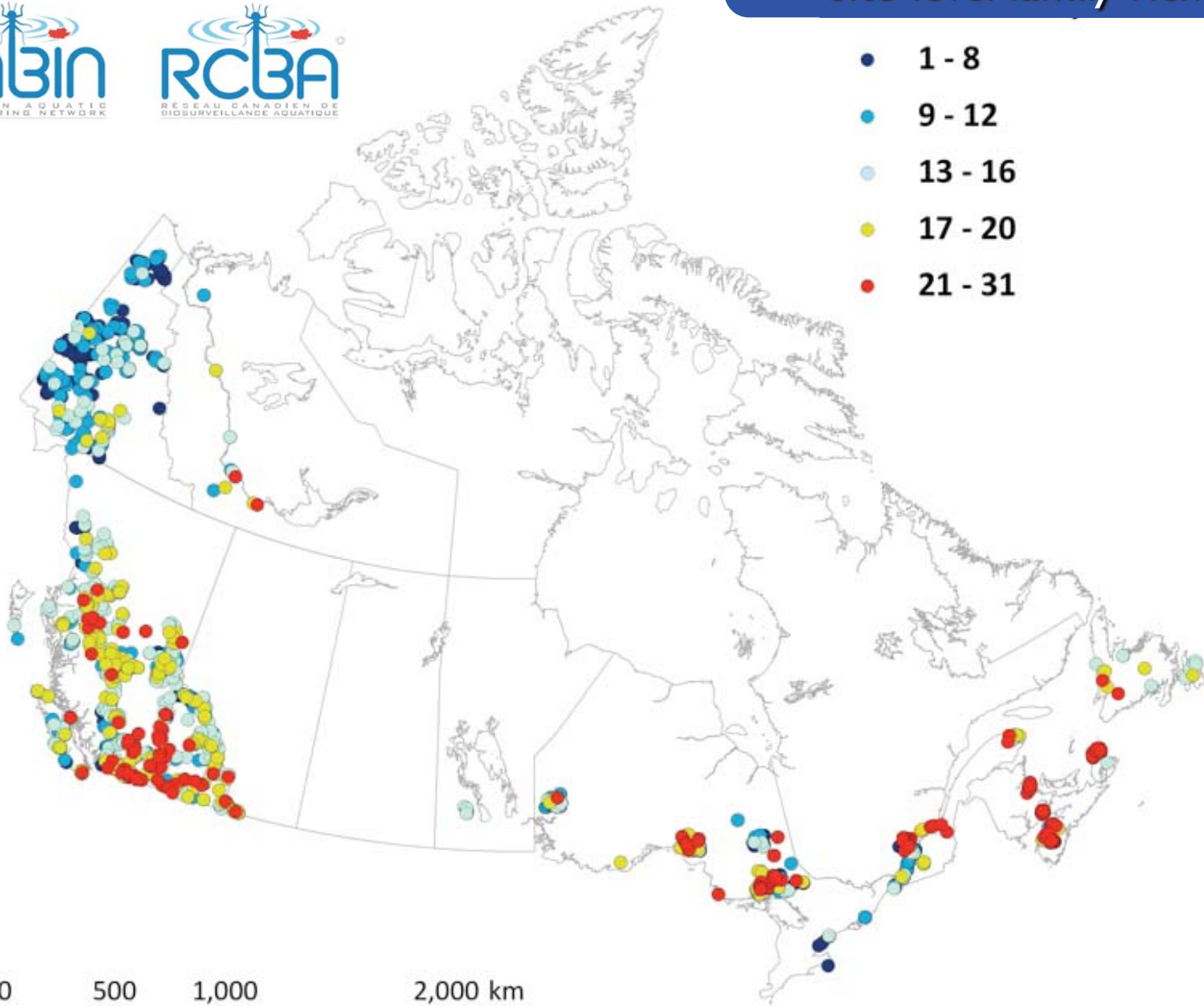
Number of species

CABIN database & reference collection



Site-level family richness

- 1 - 8
- 9 - 12
- 13 - 16
- 17 - 20
- 21 - 31



N

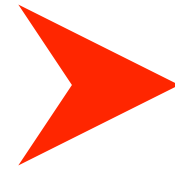
0 500 1,000 2,000 km

Do we have enough data?

- Data to build reference condition models?
Yes, but we know little about temporal variability.
- Data to develop new diagnostic tools?
Possible, but restricted geographic range limits analysis.
- Data to observe trends in biodiversity?
*No, as poor taxonomic resolution limits scope
[see also talk by Colin Curry this morning]*

Data bottleneck: **Taxonomy**

Phylum - Class - Order - **Family** - Genus - **Species**

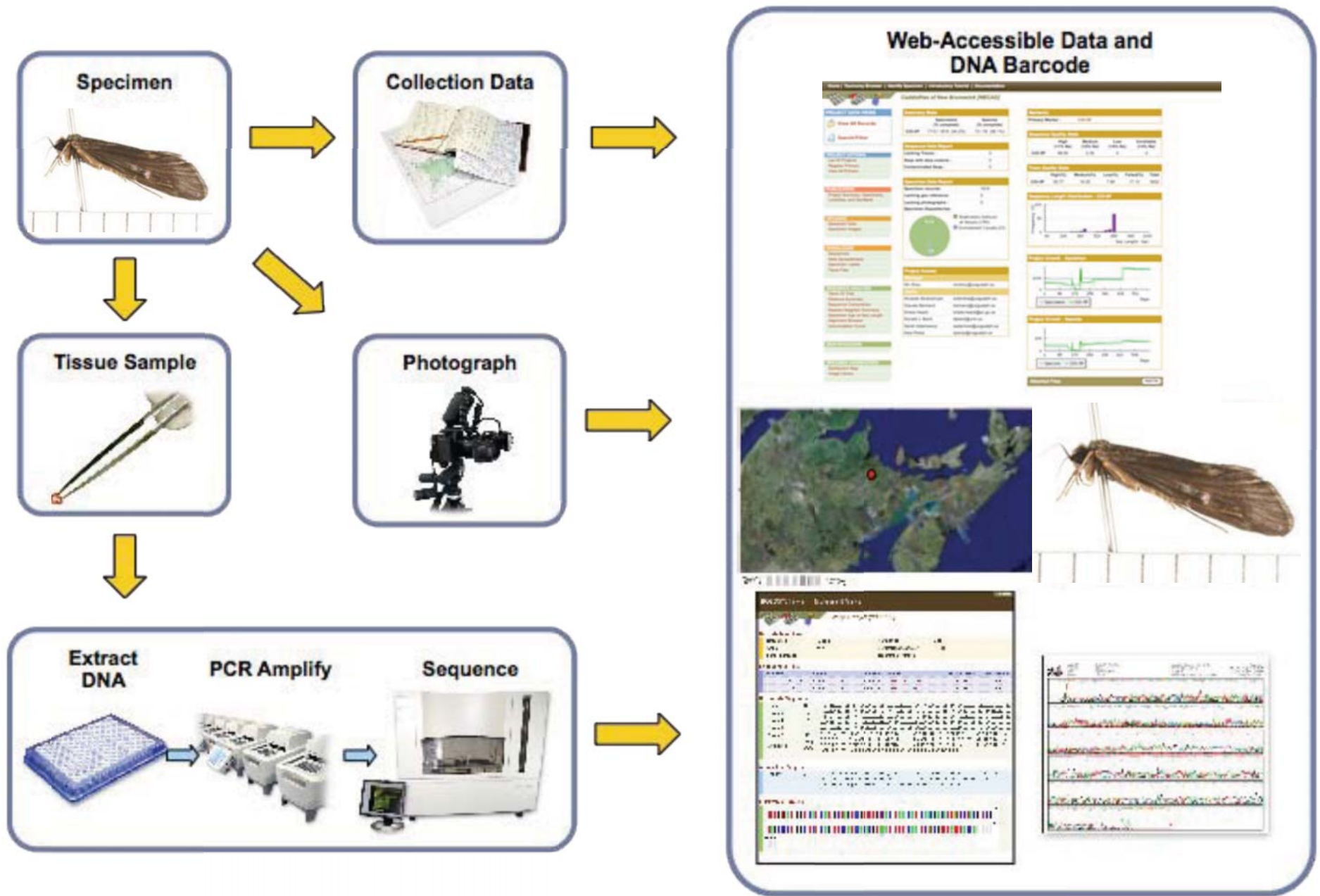


Increasing analytical power

Increasing cost of processing sample

Solution: DNA-based identification?

DNA barcoding



Atlantic Canada BioBlitz Studies

Focus: Ephemeroptera / Plecoptera / Trichoptera / Odonata
2008/2009



6765 specimens / 2891 COI sequences / 458 species

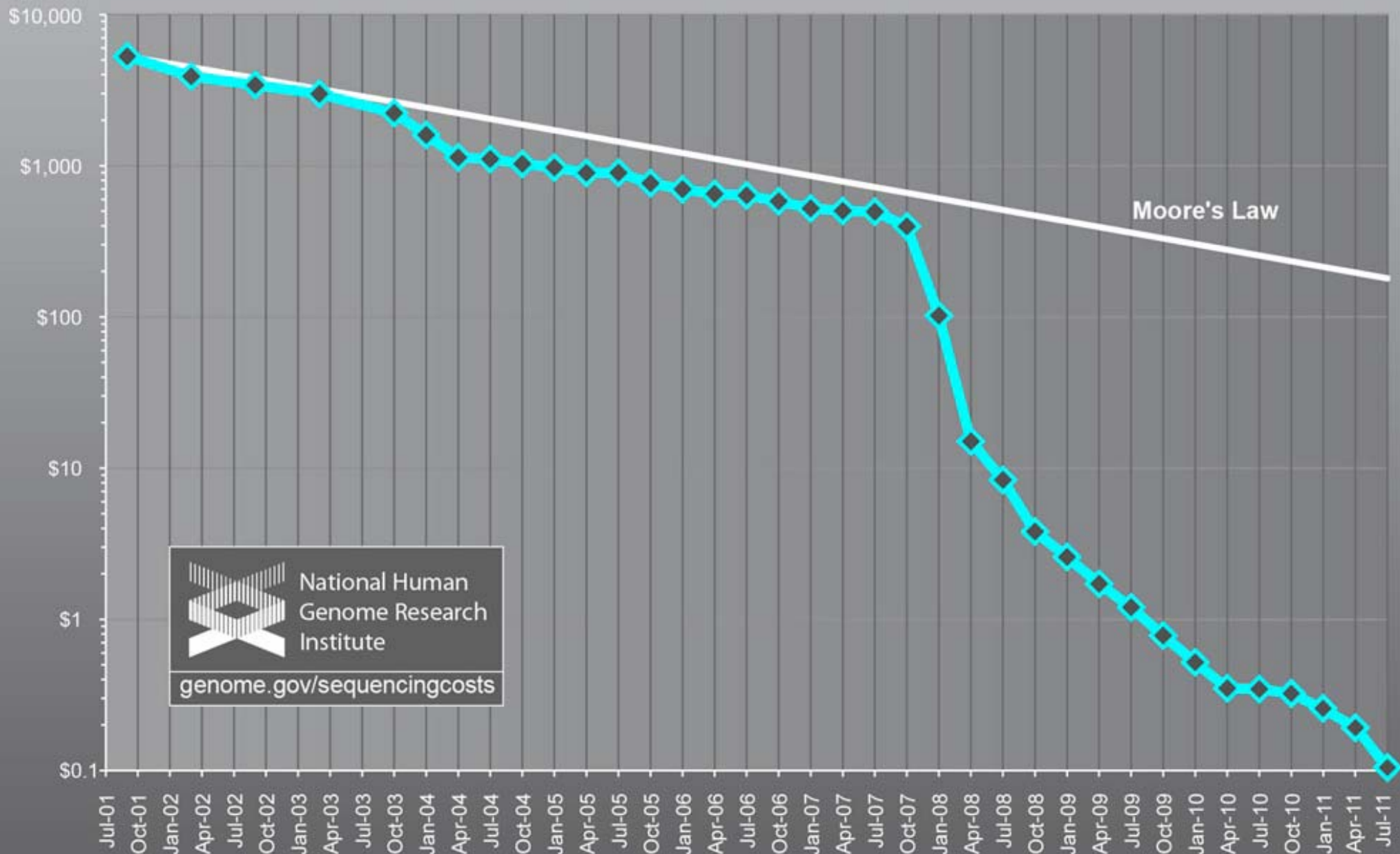
UNB Biology / Canadian Rivers Institute, Environment Canada, Parks Canada,
Miramichi River Environmental Assessment Committee, Biodiversity Institute of Ontario,
local volunteers in Miramichi and Cape Breton

Web 2.0 / 3.0: six big ideas

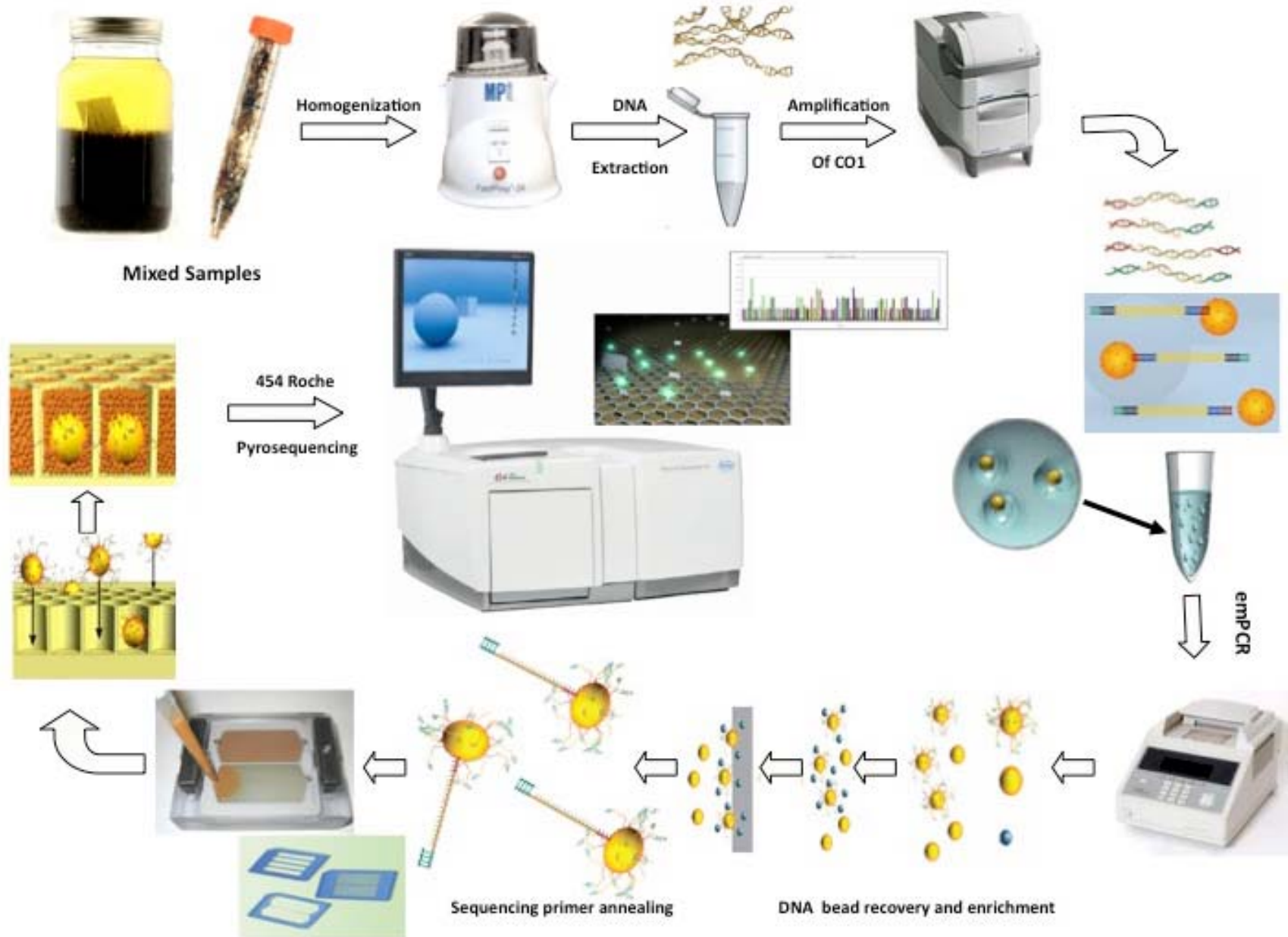
1. Individual production and user-generated content
2. Harnessing the power of the crowd
3. **Data on an epic scale**
4. Architecture of participation
5. Network effects, power laws and the Long Tail
6. Open-ness

Paul Anderson, 2007

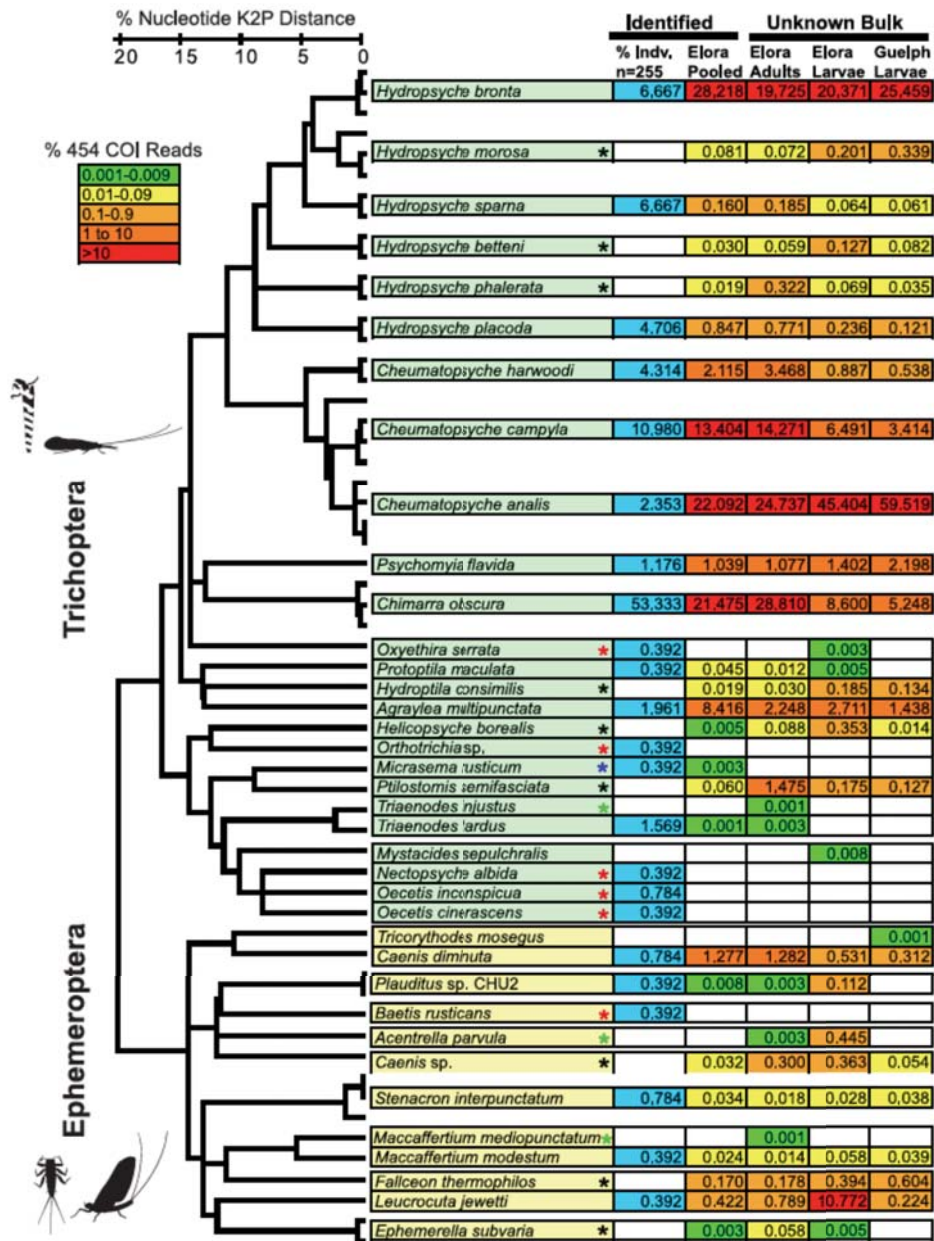
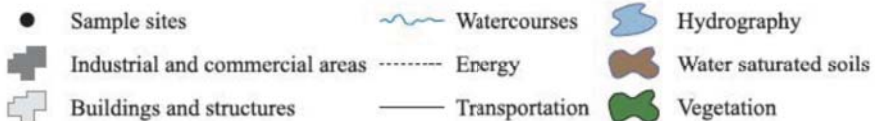
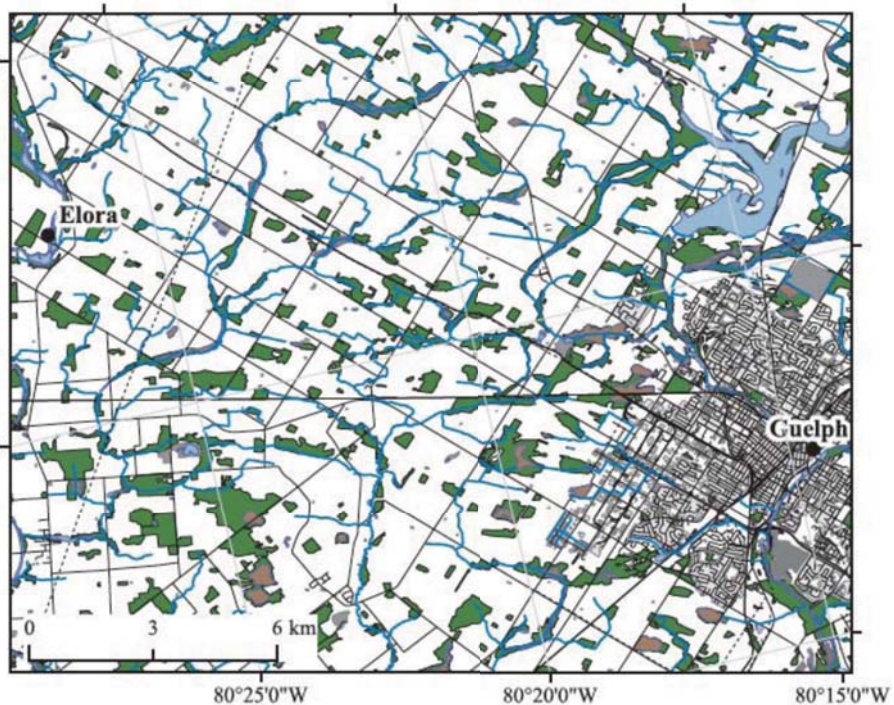
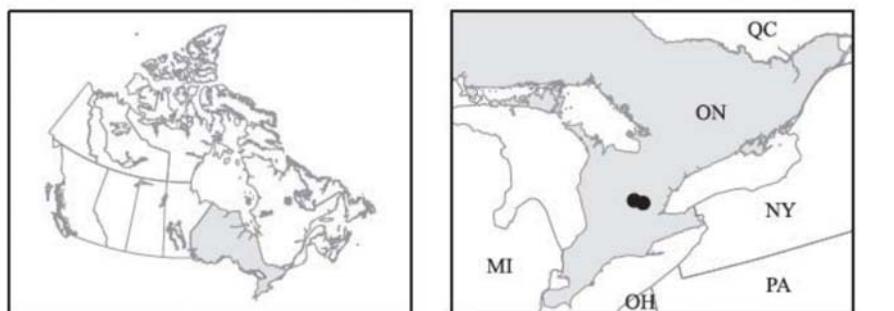
Cost per Megabase of DNA Sequence



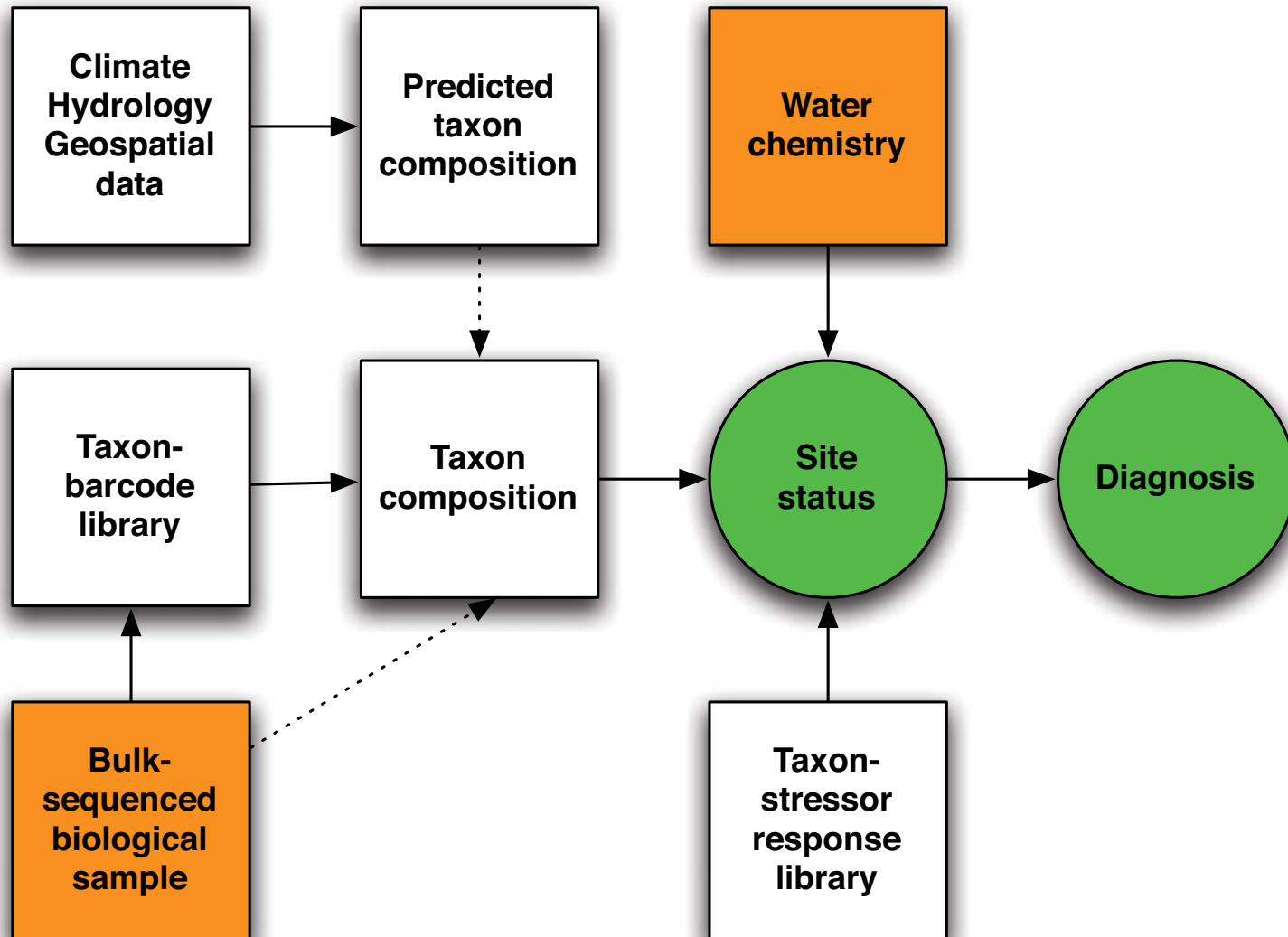
Next generation DNA sequencing



Proof of concept

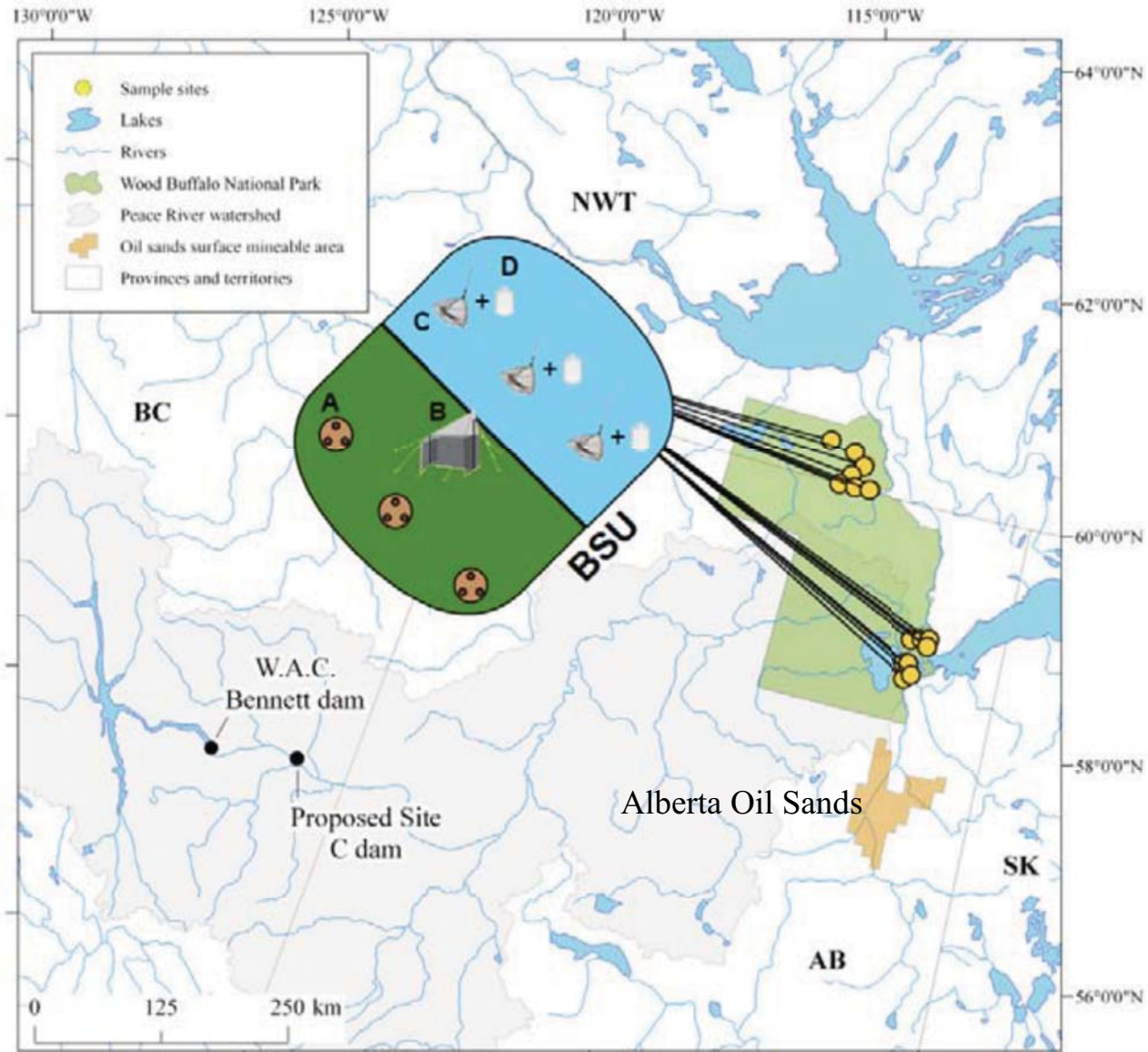


Biomonitoring 2.0



Biomonitoring 2.0: remote region biodiversity analysis

(Environment Canada, Parks Canada, Universities of Guelph, McMaster & Dalhousie, Aurora Research Institute)



Biomonitoring 2.0: Next Steps

- Development of a bioinformatics platform for Bio2 application
- Development of analytical methods compatible with taxonomic and raw biodiversity data streams
- Development of field-friendly sampling methods for DNA-based biodiversity discovery
- Linkage with national efforts for biological survey?



Thanks

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