Wild Rice Protection and Restoration

Panel Presentation to the
Governor's Task Force on Wild Rice
NCROC
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Collaborators

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- Dr. David Biesboer

  Professor Emeritus, University of Minnesota

  Past Director, Itasca Biological Station and Laboratories

Scope of Work

- Developing DNA marker (SSR) tools for wild rice
- Measuring wild rice genetic diversity at the population level
- Assisting in decisions pertaining to restoration (re-seeding or new introduction)

What is an SSR?

ATCGATTGCCGTATTACGCAGATTCGCTACGG
ACCCATAGCGAGTACGCTATAGTGTACGCTAT
CTACGCTGGGCCACTAGATCTAGCGAGGCTA
CTTGCTATTATTATTATTATTATTATTATTGCT
GCGGCACGGAAGTCGTAGATTCGTCCGATCT
TACTGCAGCTCTACGACGTACTACGACGTGTG
ATAGCCAAGTAATCGTATTGAATTTTGCGAGAC
TACTACGGGGAACCACCCAGTACTG

(Genomic DNA Sequence)

What is an SSR?

ATCGATTGCCGTATTACGCAGATTCG
CTACGGACCCATAGCGAGTACGCTAT
AGTGTACGCTATCTACGCTGGGCCAC
TAGATCTAGCGAGGCTACTTGCTATTA
TTATTATTATTATTATTATTATTATTGCTGCG
GCACGGAAGTCGTAGATTCGTCCGAT
CTTACTGCAGCTCTACGACGTACTAC
GACGTGTGATAGCCAAGTAATCGTAT
TGAATTTTGCGAGACTACTACGGGGA
ACCACCCAGTACTGTTTACTA

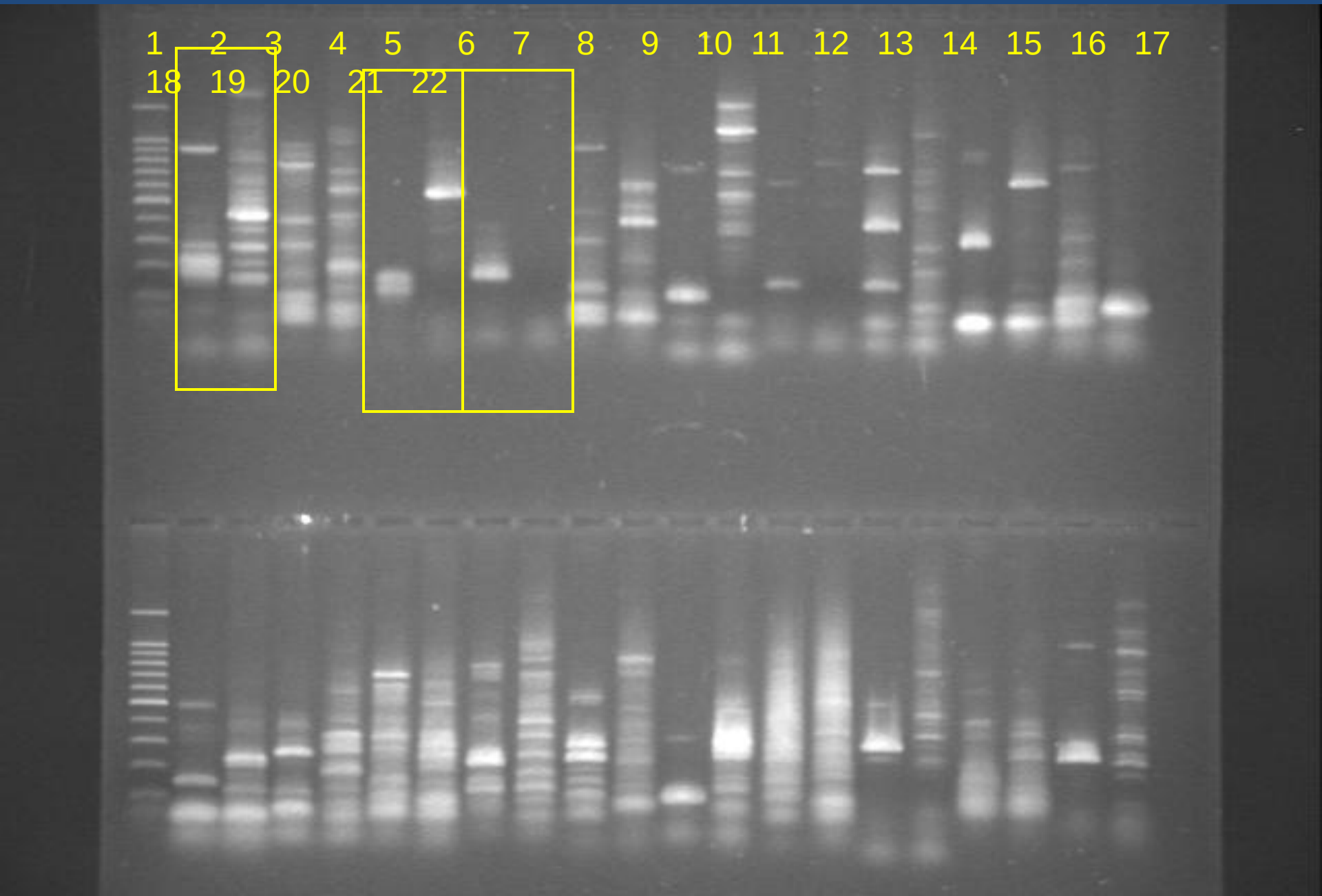
What is an SSR?

ATCTAGCGAGGCTACTTGC
TATTATTATTATTATTATTATT
ATTATTGCTGCGGCACGGA
AGTCGTA

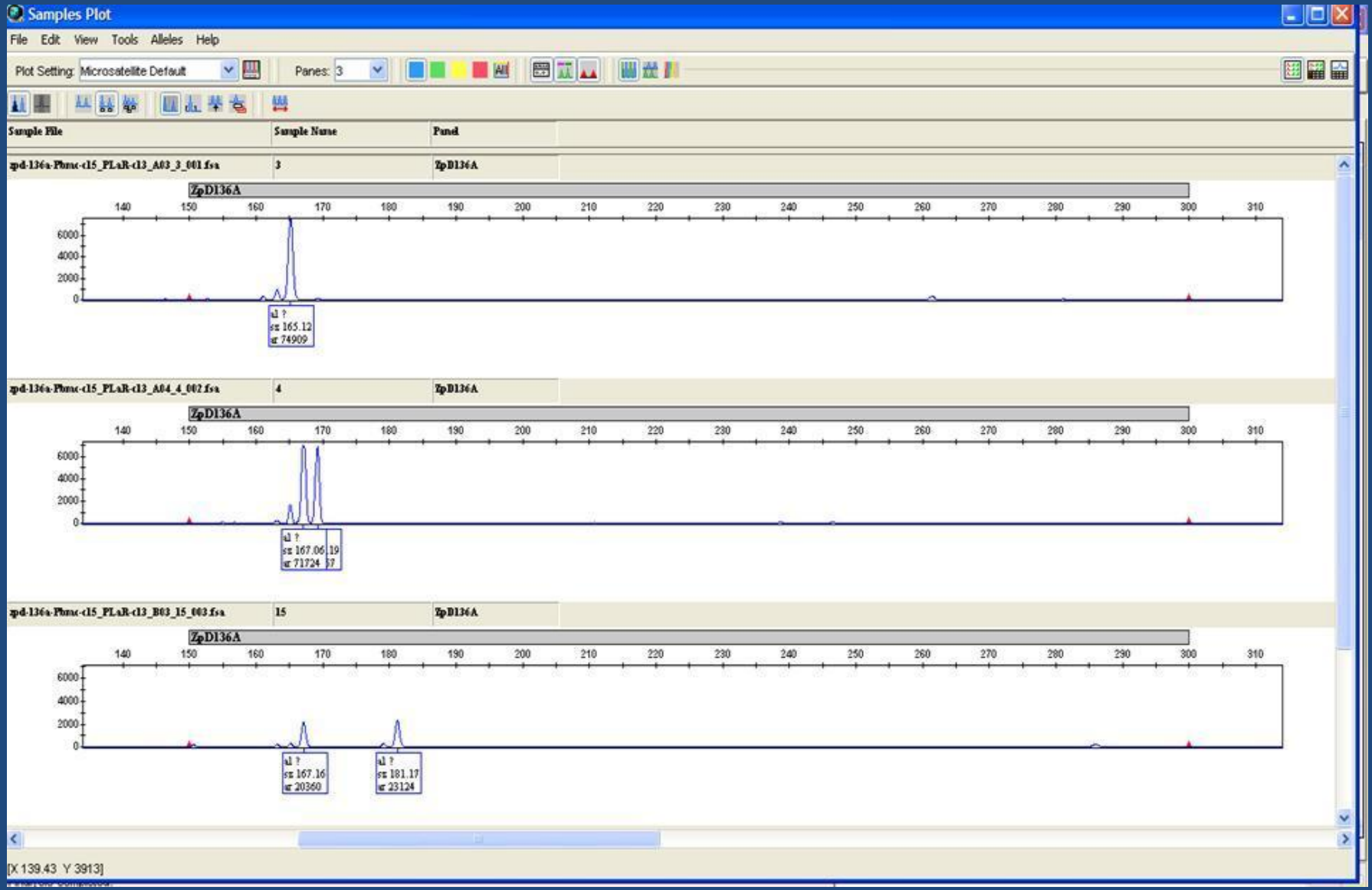
(9 “ATT” repeats)

SSRs are highly polymorphic and can be used in fingerprinting as well as marker assisted selection.

SSR markers assayed on agarose gels



SSR markers assayed on a Genetic Analyzer

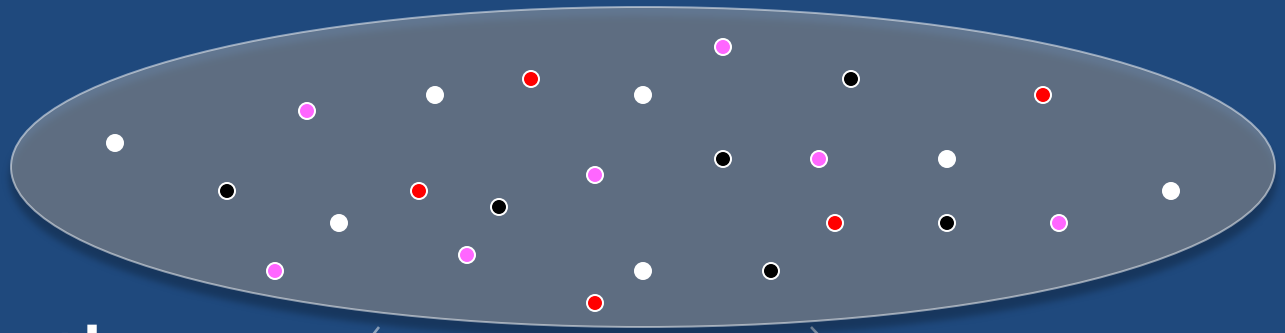


Sources of genetic diversity

- **Migration**
  - Physical movement (*i.e.*, ducks, flowing water)
- **Drift****
  - Random change in allele frequency
  - Non-random mating in a population
- **Mutation**
  - Change in DNA sequence (gene or marker)
- **Selection**
  - Natural (adaptation) or imposed (human)

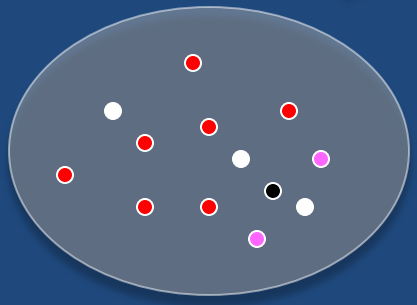
Sources of genetic diversity

Drift

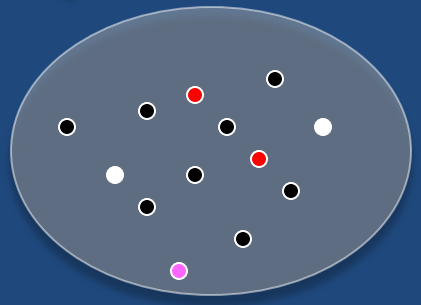


Separation
(time or space)

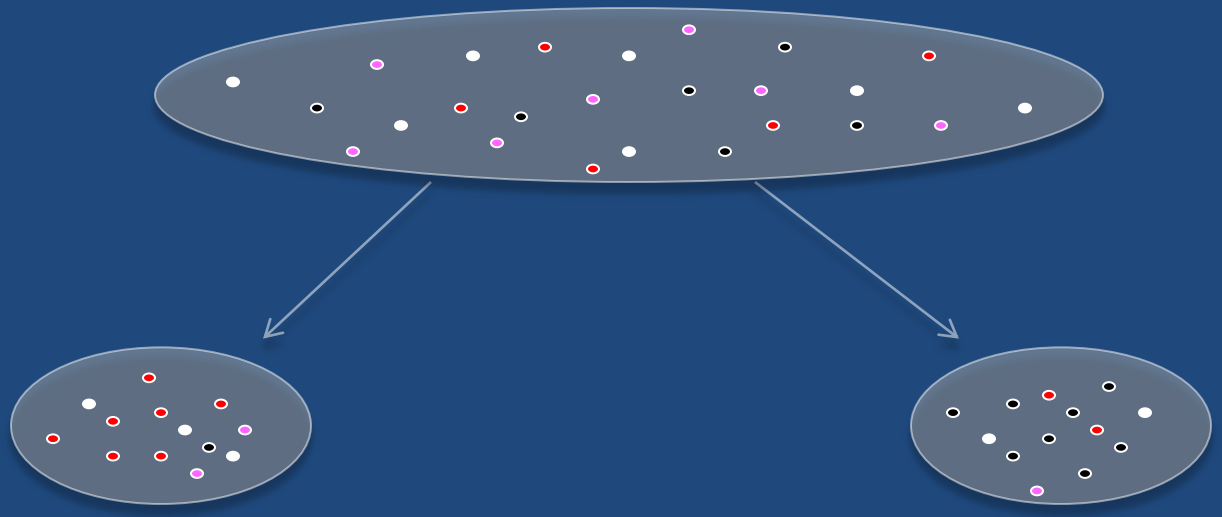
Separation
(time or space)



“Founders”

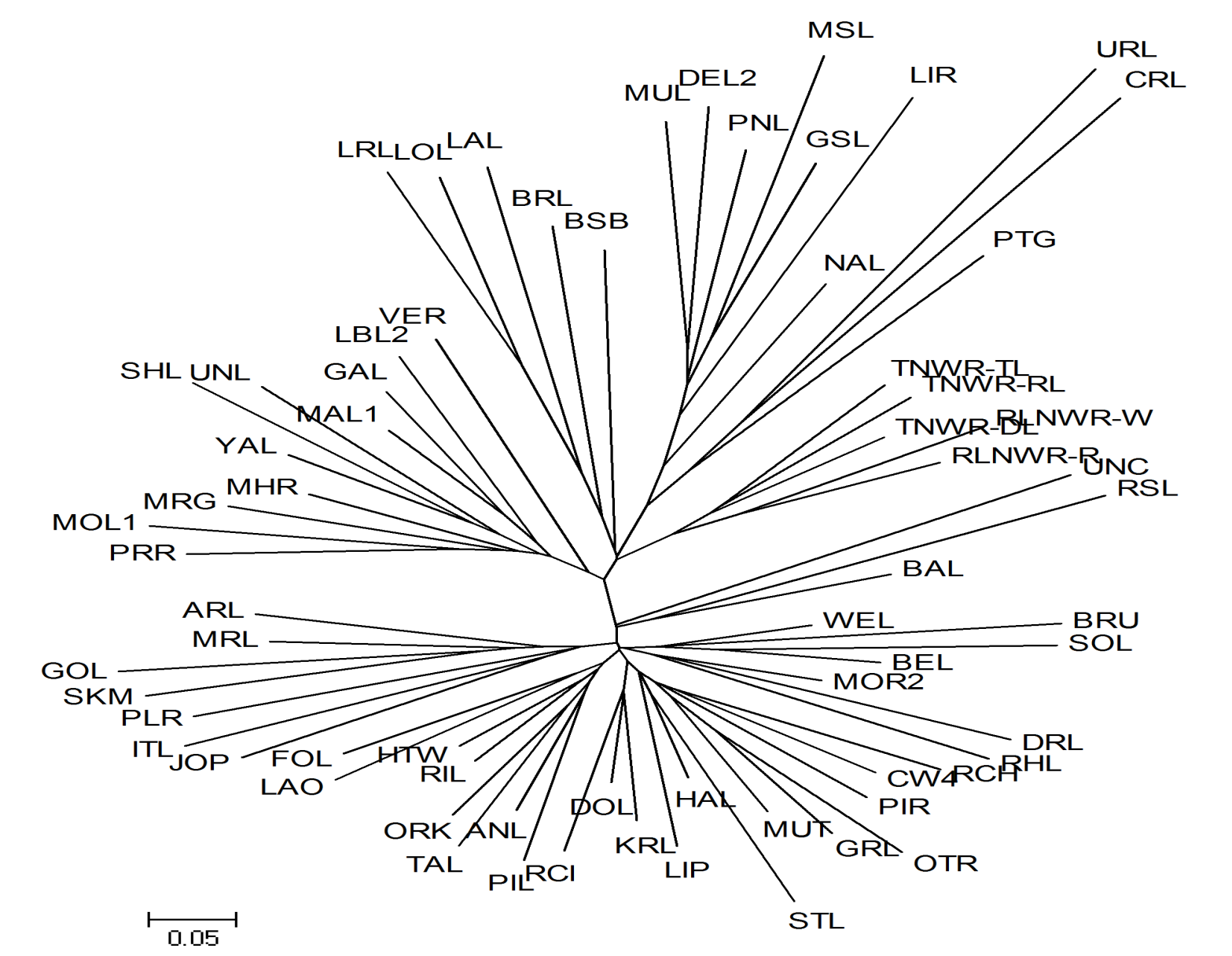


Sources of genetic diversity



- Genetic drift
  - Random, sampling bias or “founder effect”
  - Greater effect in small populations
  - Generally considered important evolutionary effect

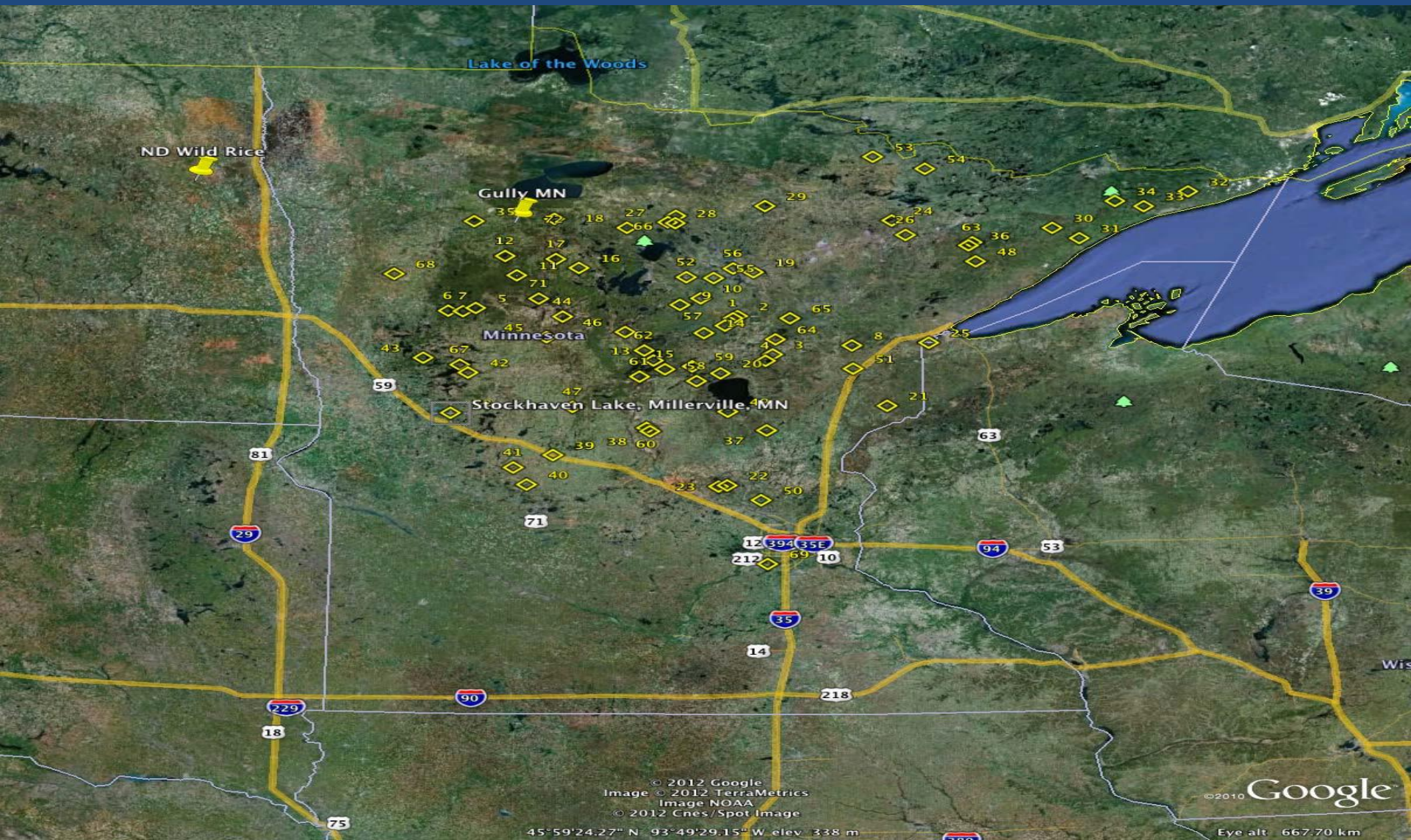
Wild Rice population genetic distance dendogram



Past Funding

- State of Minnesota, LCCMR **
- USDA, ARS cooperative agreement
- MN Cultivated Wild Rice Council

Project Geography



Barriers to Our Work

- Funding
- Lack of understanding / misdirection
- Political climate surrounding scientific understanding of our natural world

“Lowest Hanging Fruit”

- More inclusive database of MN wild rice population genetic diversity
  - Population of 1 acre or more
- Development of more DNA markers
  - Larger coverage of the wild rice genome
- Correlating environmental data with genetic data from same water body
  - Water temp., depth, color, sediment type, etc.

Top 3 Priorities and Their Funding

- Provide consistent, long-term funding dedicated to high quality, scientific research projects ($500,000 - $1M per year)

- Create an open and transparent culture around wild rice research through regular reporting with stakeholders ($30,000 - $50,000 per year)

- Treat each wild rice population as unique and irreplacable (priceless)