Genetic Heritage of Wild Lake Trout in Lake Michigan

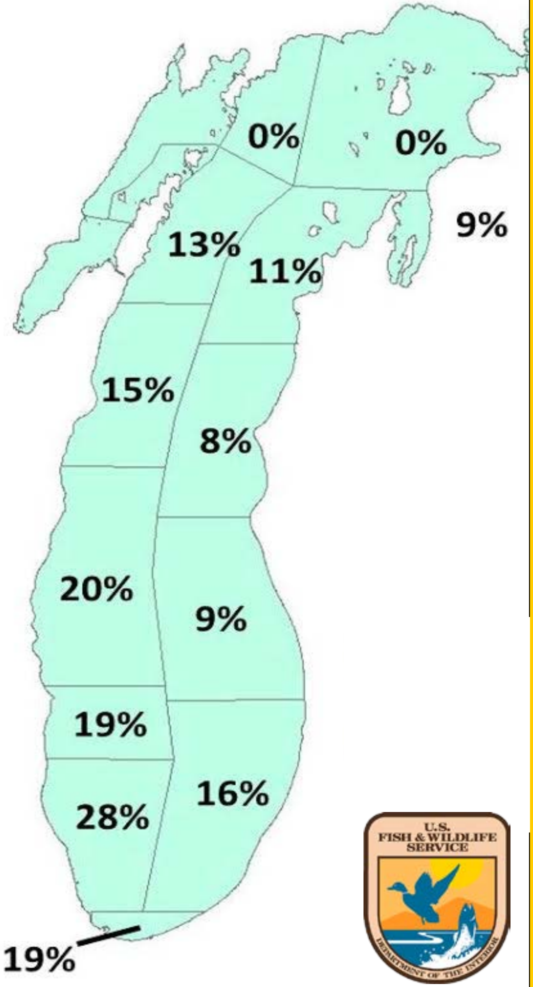
W.L Larson[1,2,3], K.N. Turnquist[1,2], C.R. Bronte[4], S.D. Hanson[4], T.J. Treska[4], M.S. Kornis[4], B.L. Sloss[2], and W. Stott[3,5]

[1]Wisconsin Cooperative Fishery Research Unit
[2]College of Natural Resources, University of Wisconsin – Stevens Point
[3]U.S. Geological Survey
[4]U.S. Fish and Wildlife Service, Green Bay Fish and Wildlife Conservation Office
[5]Great Lakes Science Center, Ann Arbor

Lake trout in Lake Michigan

- Historically supported large commercial fishery
- Extirpated in 1950's
- Stocked since 1960's
- No consistent natural recruitment until recently
  - Encountered in 2011 while targeting bloater
  - Multiple consecutive cohorts of suspected NR

% Wild lake trout, 2016



Courtesy of Great Lakes Mass Marking Program

Strains of gamete sources

Eight potentially different strains

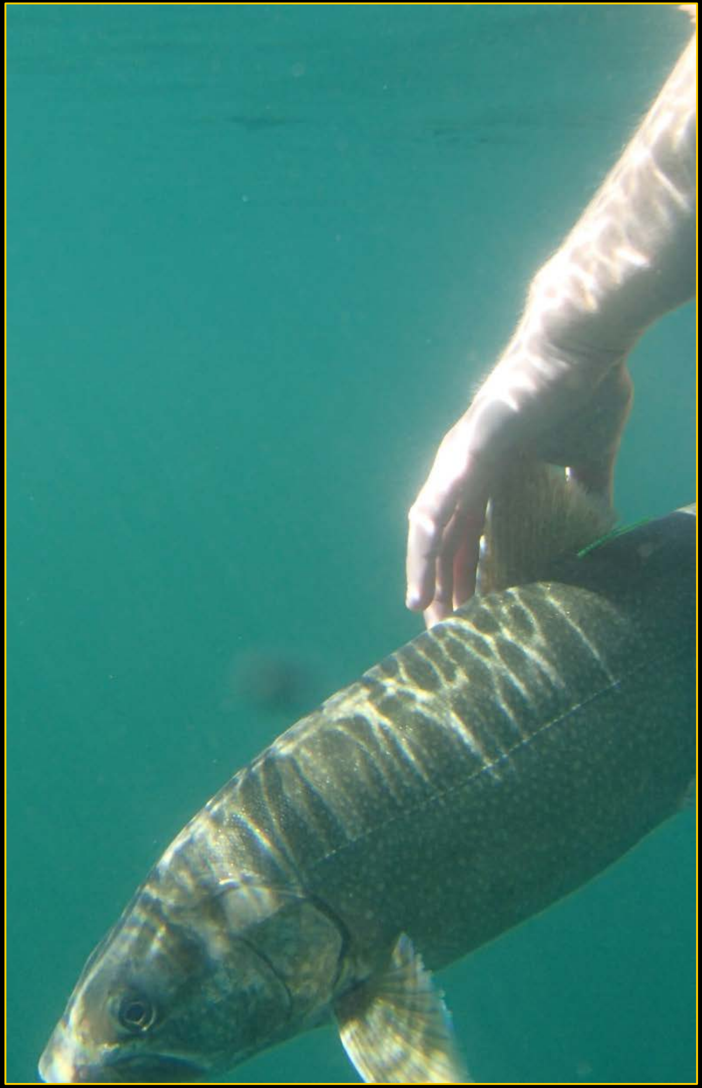
- Seneca Lake, Finger Lakes
- Isle Royal, Superior
- Marquette, Superior
- Apostle Islands, Superior
- Lewis Lake, Michigan historic
- Green Lake, Michigan historic
- Klondike Reef, Superior
- Parry Sound, Huron

Objectives

1) Identify suite of microsatellite markers that can delineate strains
2) Determine ability of microsatellites to assign pure strains and interstrain hybrids
3) Determine ancestry of wild recruits and compare to stocking records to investigate differential survival/reproduction

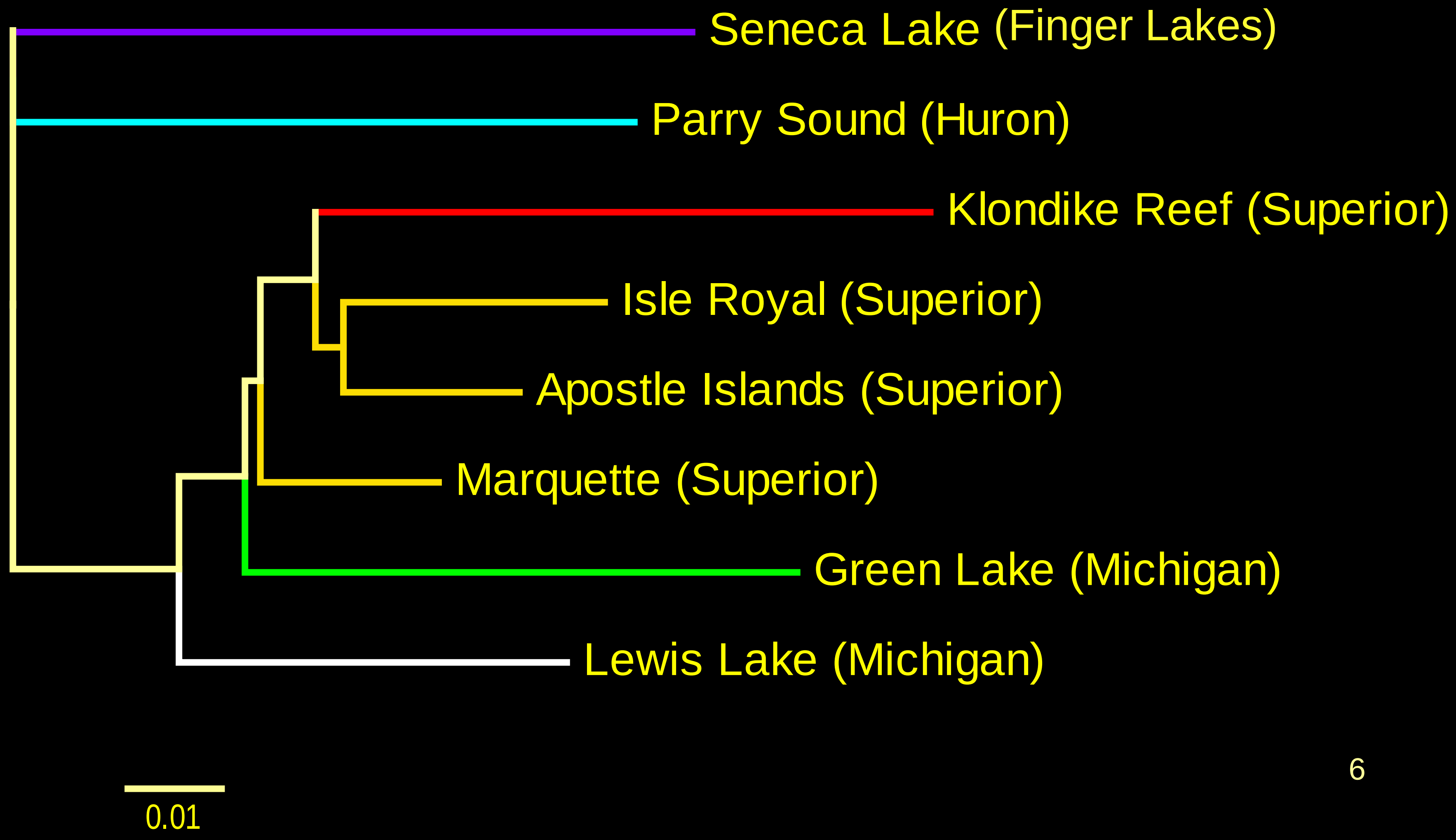
Study design – objective 1

- Strain differentiation
  - 8 sources tested
  - 561 Lake Trout
- Genotyped with 49 microsatellite loci
  - 36 loci used in final analysis
    - Removed loci: monomorphic, >70% missing data, failed HWE, showed LD
- Genetic structure
  - Genetic distance (tree)
  - Bayesian admixture (STRUCTURE)



Genetic structure of strains

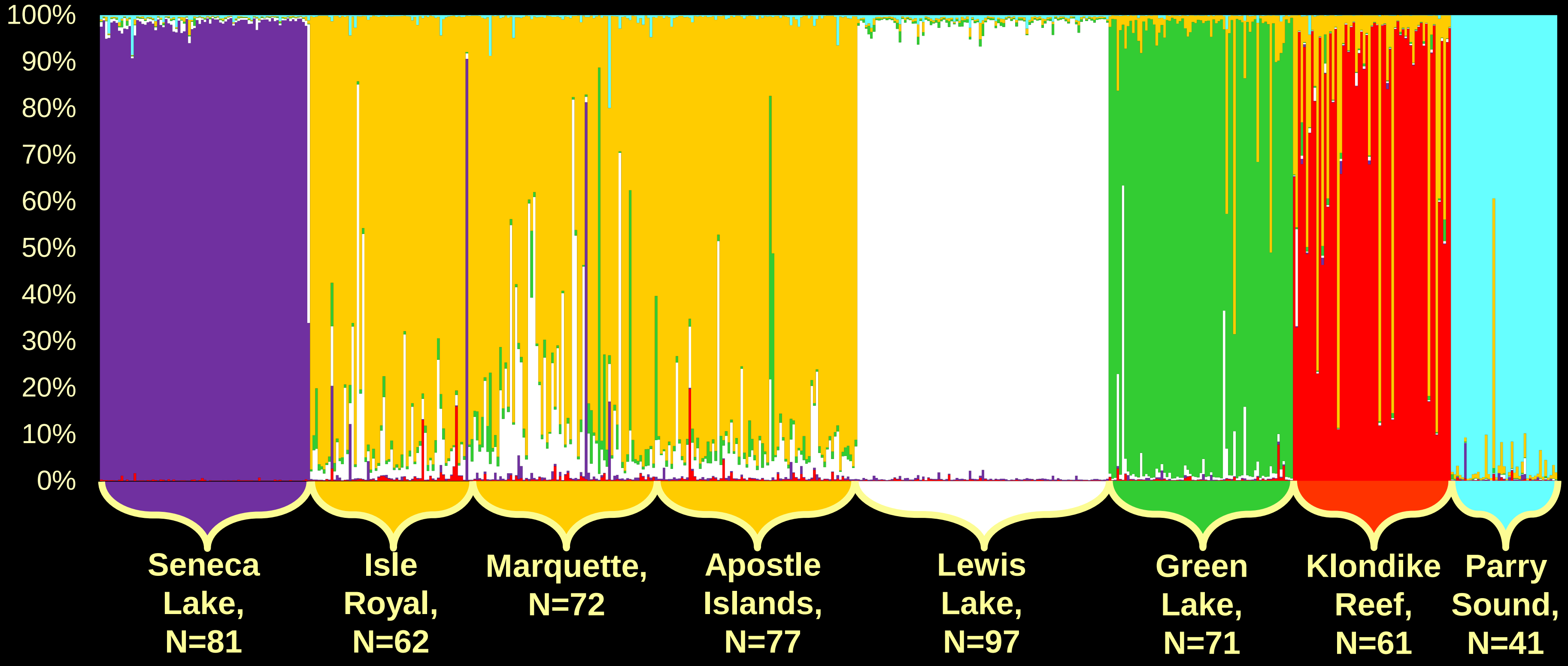
Nei’s genetic distance



Genetic structure of strains

Bayesian admixture (STRUCTURE)

36 microsatellites, 8 sources, 6 genetic units, N=561



Seneca	**Superior**	**Lewis**	**Green**	**Klondike**	**Parry**
🟪	🟨	⬜	🟩	🟥	🟦

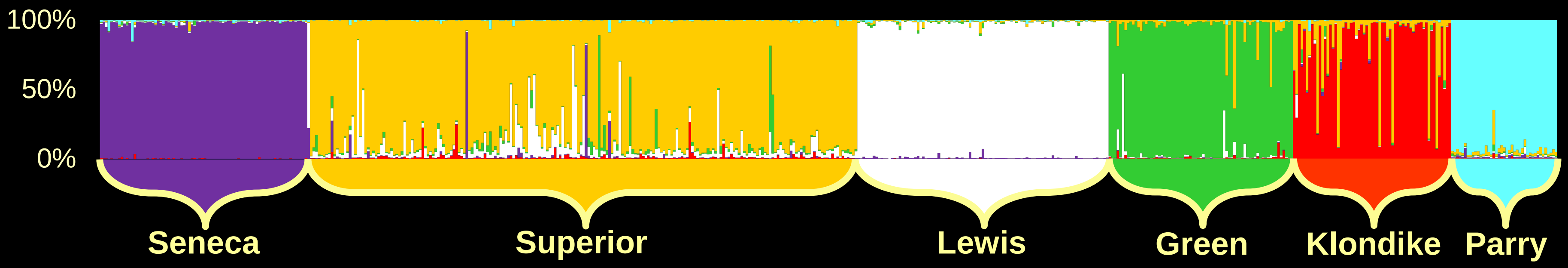
Strain analysis – takeaways

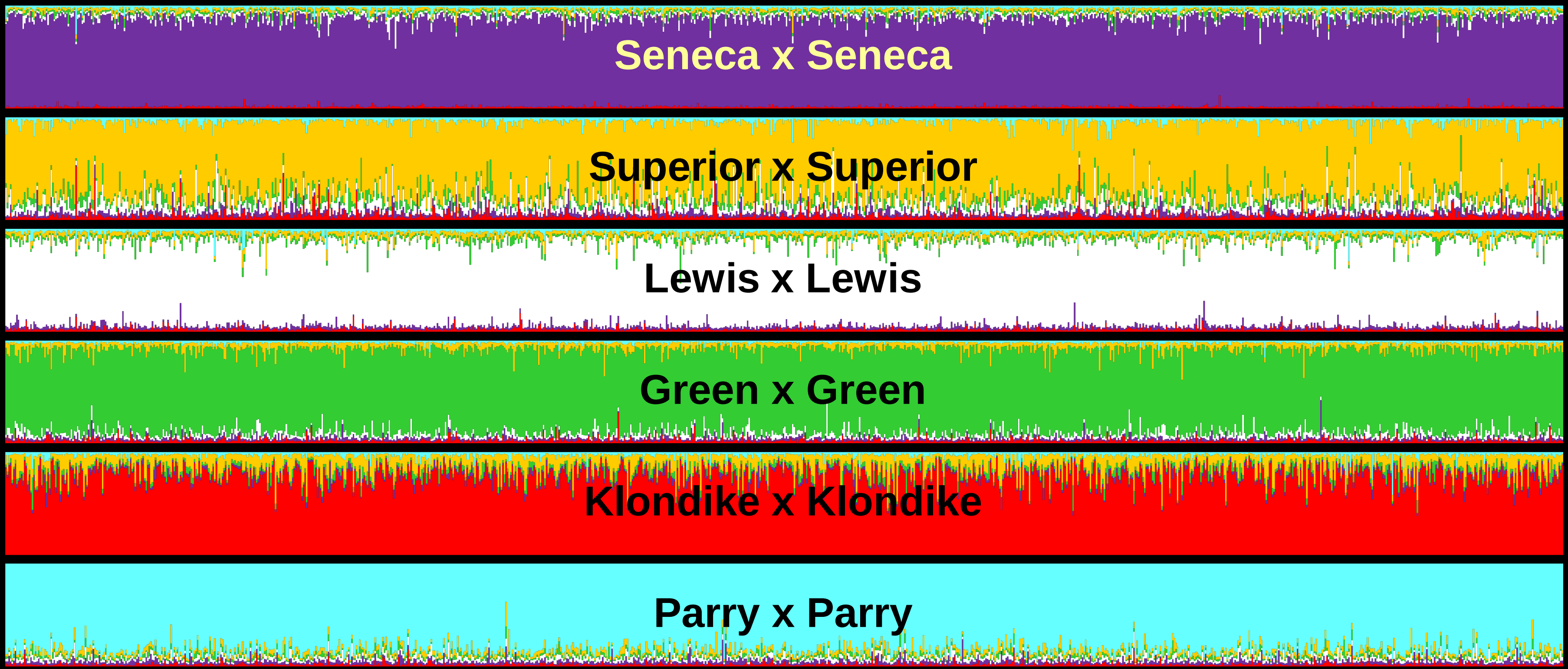
- Seneca and Parry Sound highly distinct
- Lewis and Green lakes mostly distinct, some overlap with other groups
- Superior populations similar, likely “polluted” with Lewis Lake (especially Marquette)
- Klondike likely mix of Superior leans and humpers
- Genetic diversity similar among strains, slightly higher in Superior

Study design – objective 2

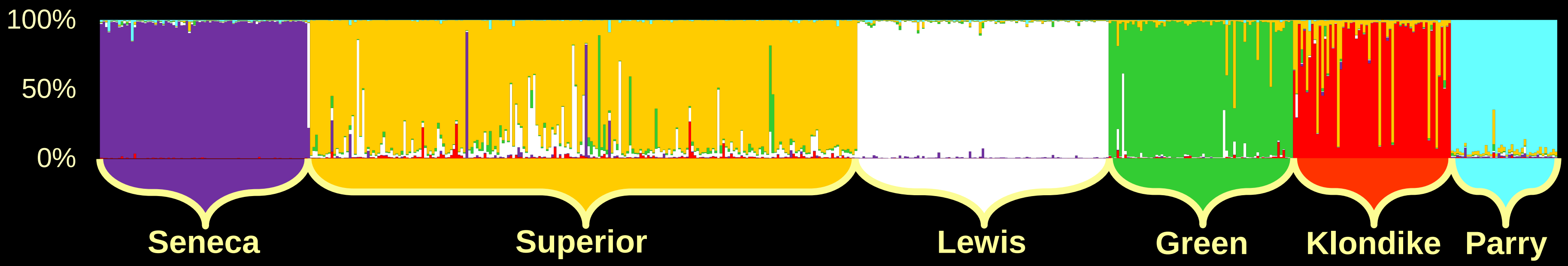
- Simulate pure and hybrid crosses
  - 6 purebred crosses
    - Eg. Seneca x Seneca
  - 14 interstrain crosses
    - Eg. Seneca x Green
- Identify ancestry of each individual
  - Bayesian admixture (STRUCTURE)
- Determine classification thresholds

Genetic structure of simulated pure crosses



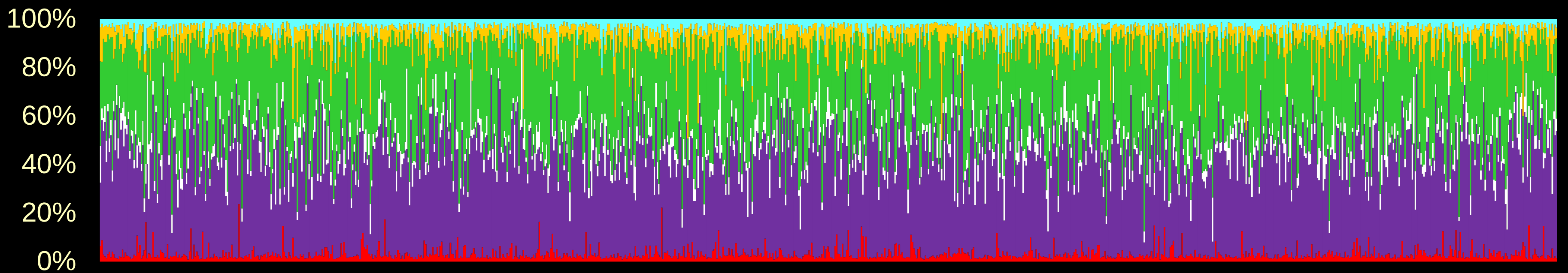


Genetic structure of simulated interstrain crosses



Eg. Seneca x Green

Green 🟩



Seneca 🟪

Classification thresholds

- Determined iteratively based on results from simulated crosses
- Designed to maximize assignment accuracy to both cross types
- Pure: > 70% ancestry from single strain
- Hybrid: < 70% ancestry from single strain, classified based on top two contributions
- Reporting groups: Seneca, Parry, Lewis, Green, Superior (includes Klondike)

Assignment accuracy: simulated pure crosses

Strain	% correct
Klondike	96%
Seneca	98%
Parry	97%
Lewis	94%
Green	91%
Superior	75%

Average 92% correct

Assignment accuracy: simulated hybrid crosses

Strain	% correct
Klondike x Seneca	0.94
Klondike x Parry	0.92
Klondike x Lewis	0.89
Klondike x Green	0.89
Seneca x Parry	0.91
Seneca x Lewis	0.88
Seneca x Green	0.85
Seneca x Superior	0.83
Parry x Lewis	0.83
Parry x Green	0.81
Parry x Superior	0.8
Lewis x Green	0.78
Lewis x Superior	0.79
Green x Superior	0.81

Average 85% correct

Classifying pures and interstrain hybrids: takeaways

- Assignment accuracy of pure individuals > 90% for all but Superior (75%)
- Assignment accuracy of F1 hybrids 85% on average, most crosses between 80% and 90%
- Historic pollution of Superior strains with fish from Lake Michigan reduces accuracy
- Almost all pure and hybrid crosses identifiable with > 80% accuracy

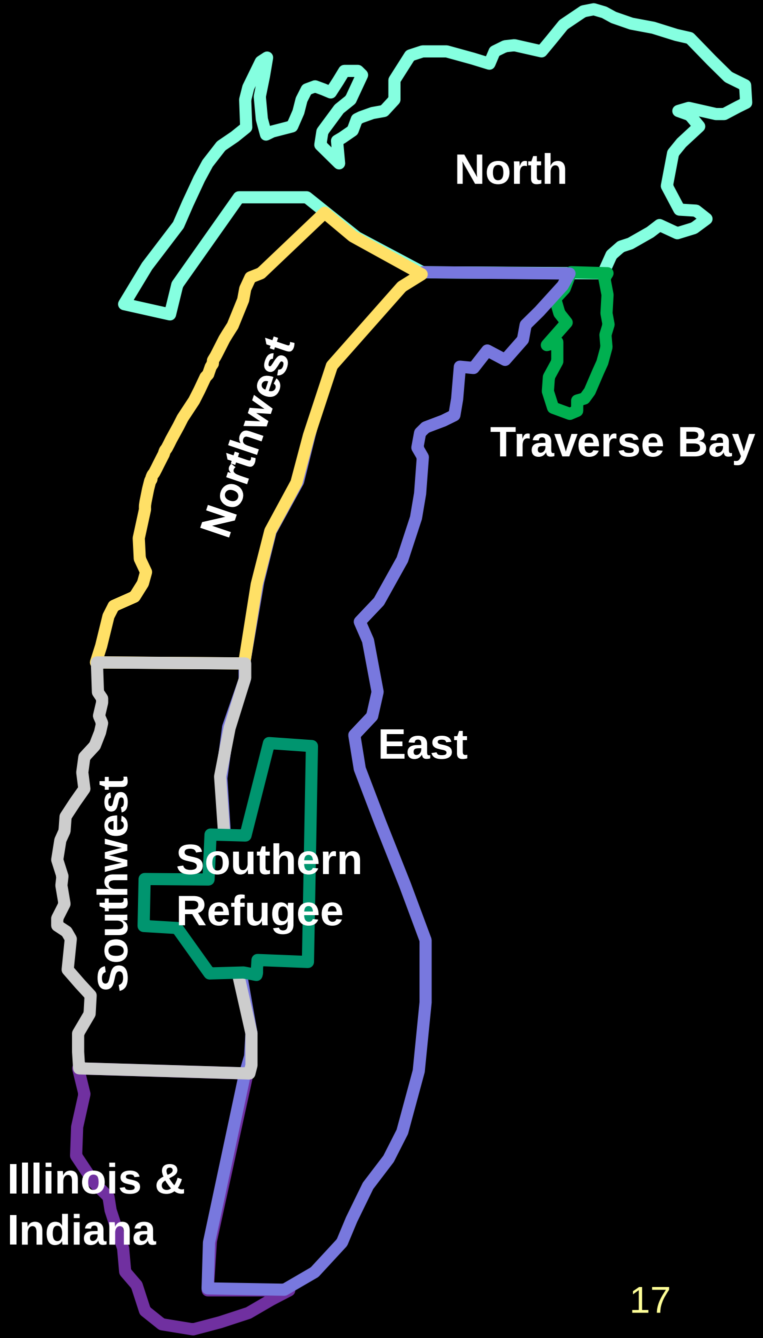
Study design – objective 3

- Analyzed wild recruits to assess reproductive success of strains
- Received 1,030 Natural Recruits from Lake Michigan (2009-2015)
  - Removed 126 incomplete genotypes or contaminated tissues
  - Removed 52 unknown sampling location
- Identified individual strain(s) of origin with STRUCTURE, hybrids counted as 50% each strain

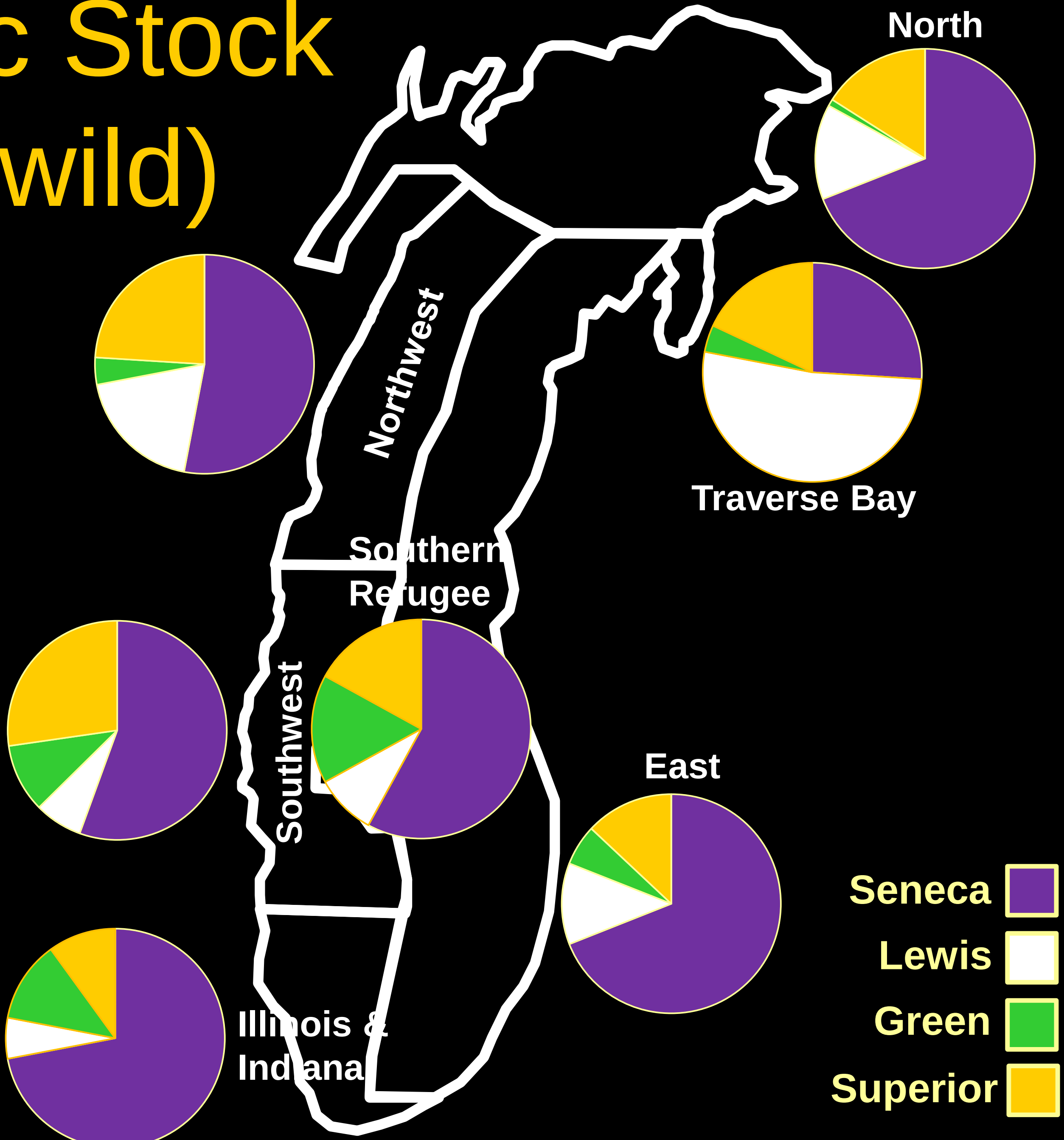
Spatial strata

Strata	Sample Size
North	216
Traverse Bay	85
Northwest	102
East	77
Southwest	91
Illinois & Indiana	160
Southern Refugee	116

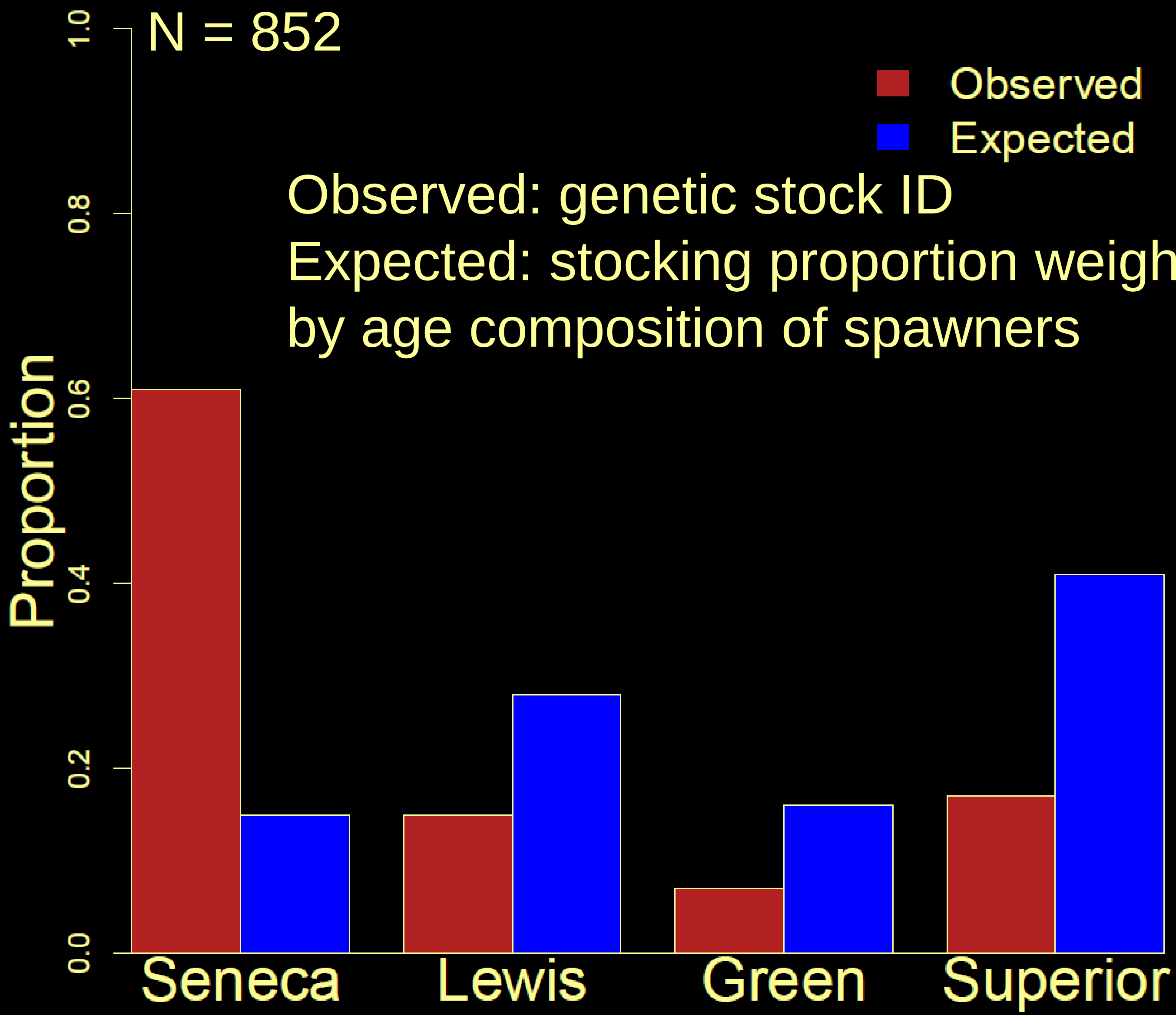
- ~100 samples/year from 2012-2014, 503 samples from 2015
- Assumptions: limited movement, homogenous spawning habitat



Genetic Stock IDs (wild)

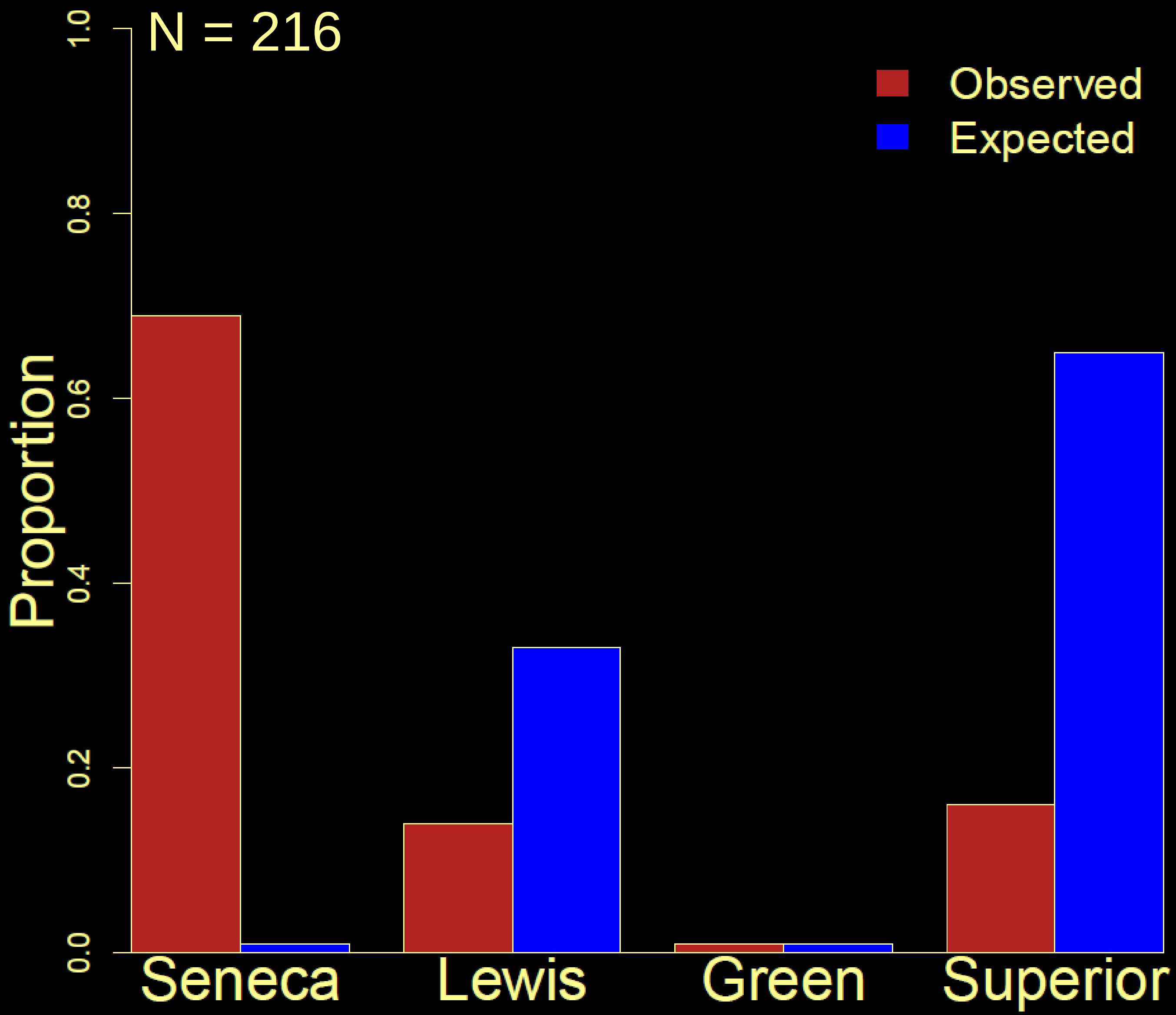


Stocked vs observed: all samples

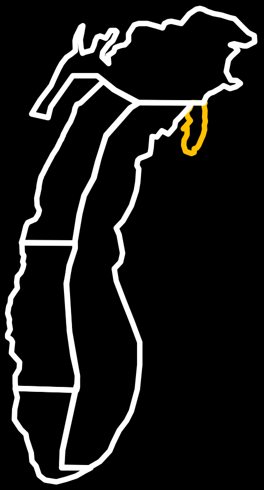


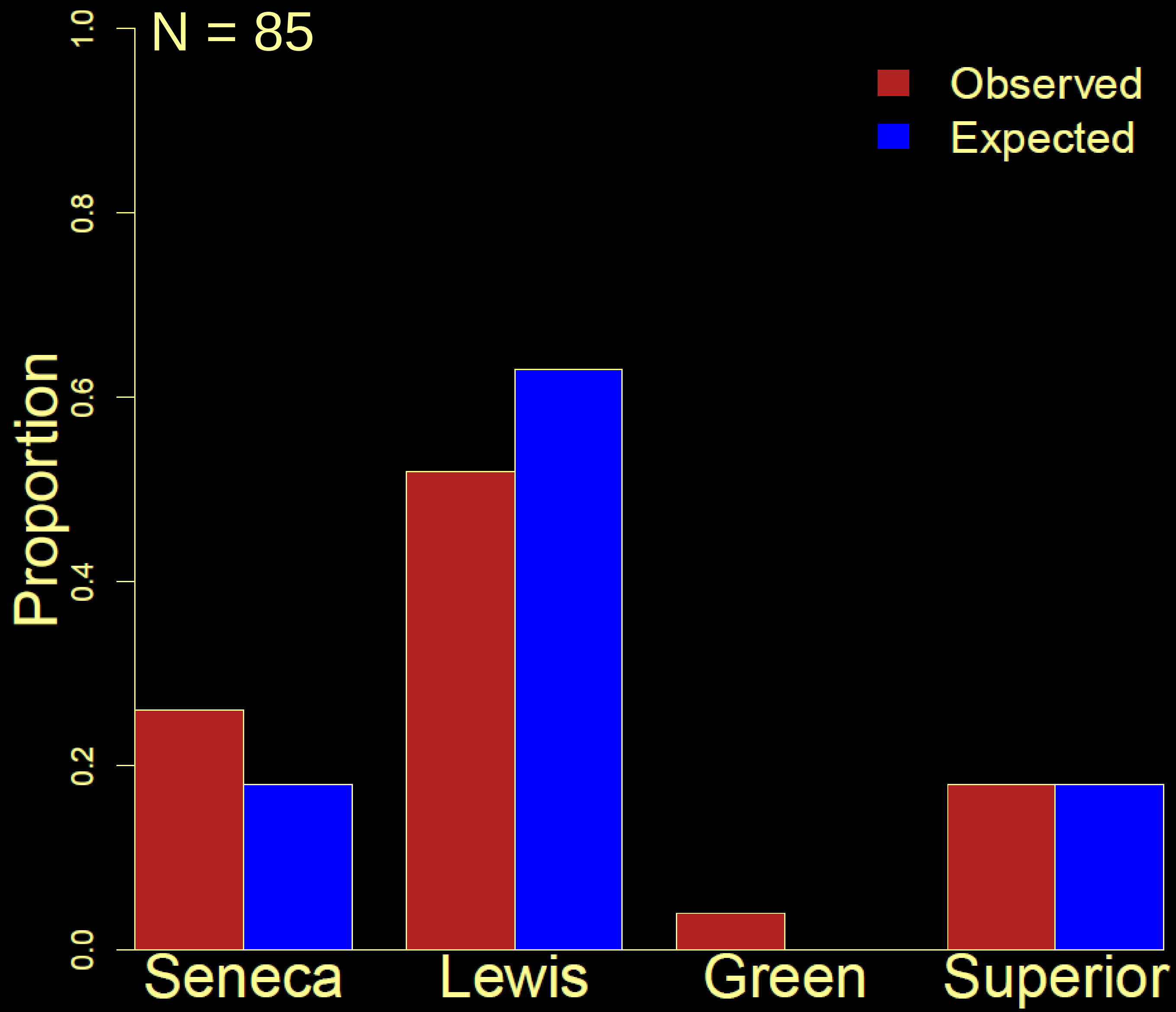
Observed: genetic stock ID
Expected: stocking proportion weighted by age composition of spawners

Stocked vs observed: North

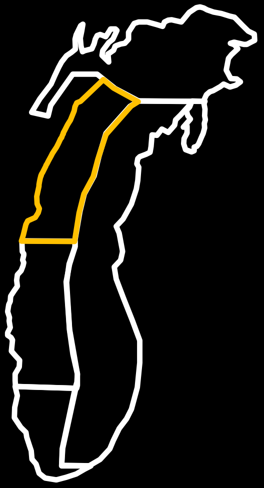


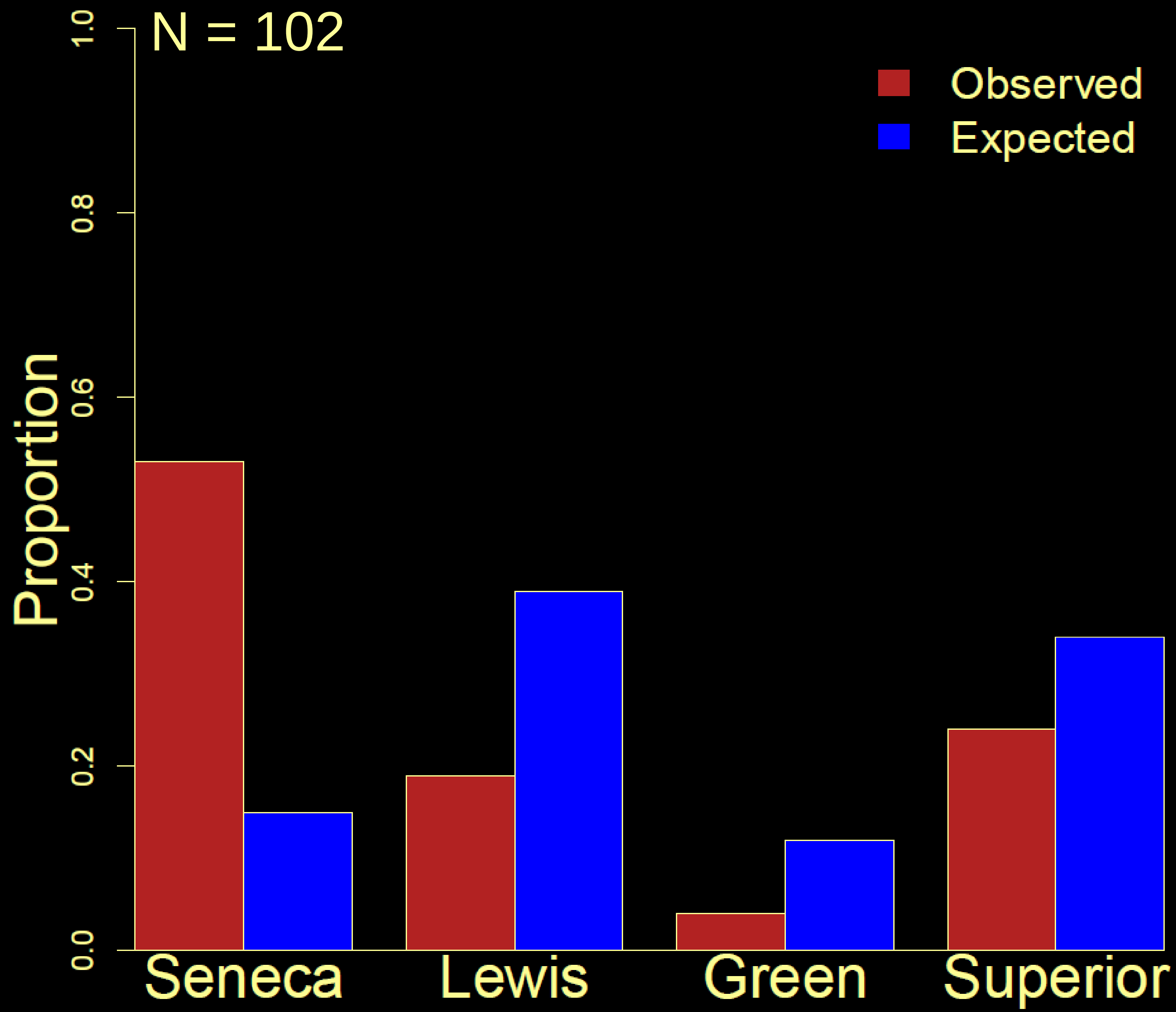
Stocked vs observed: Traverse



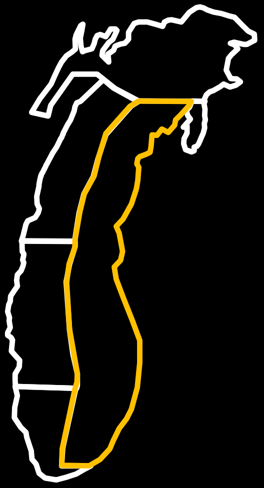


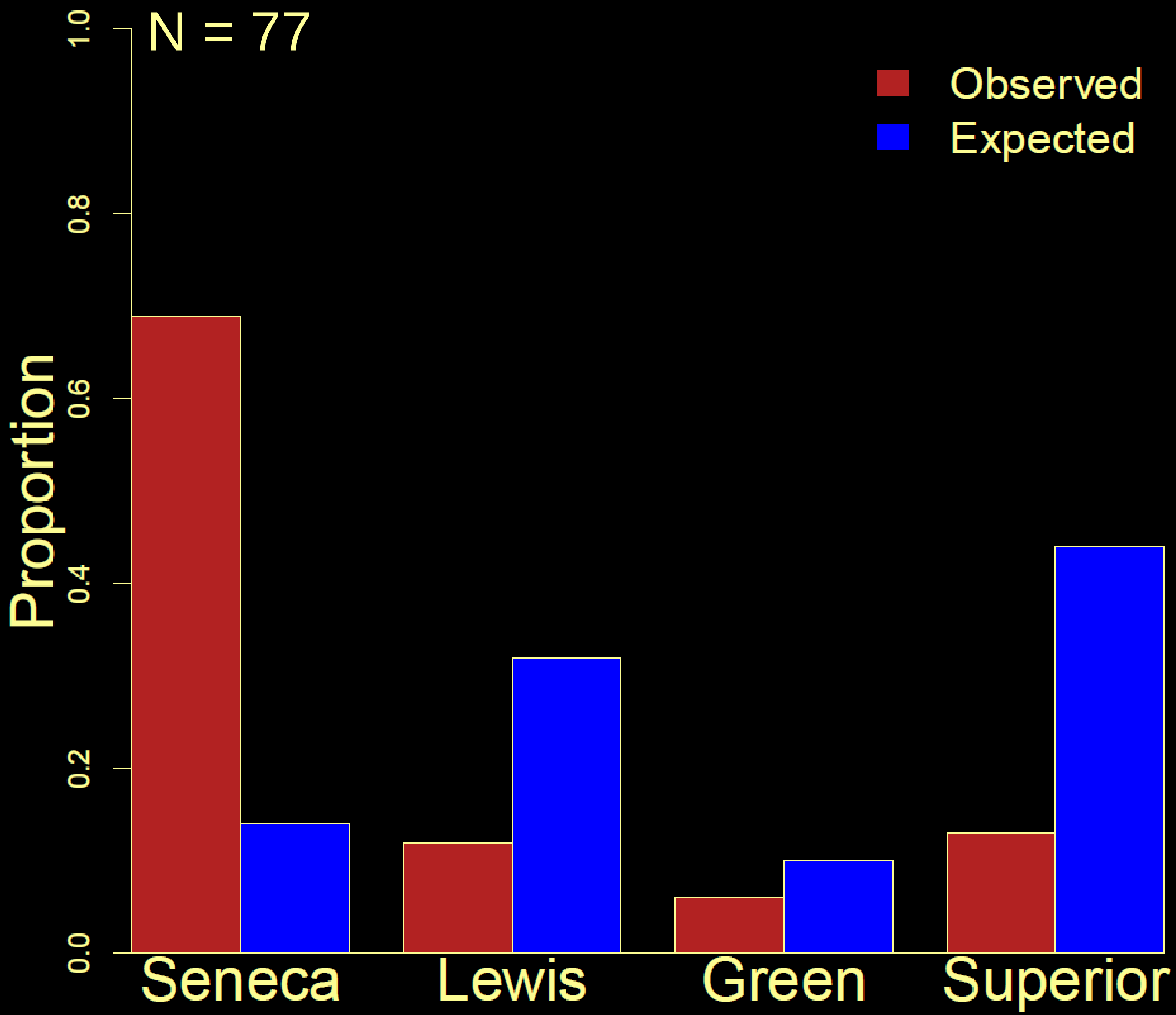
Stocked vs observed: Northwest



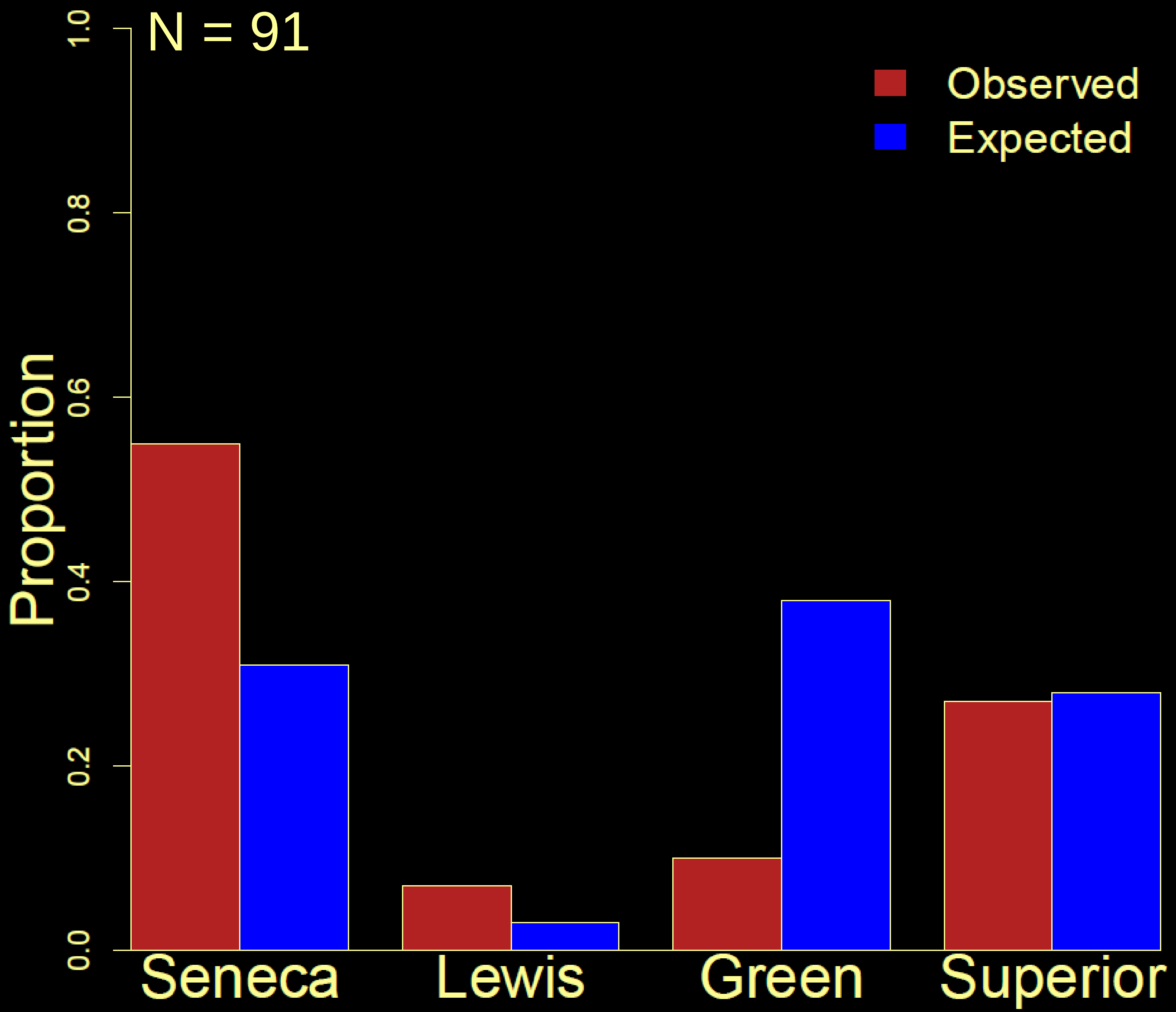


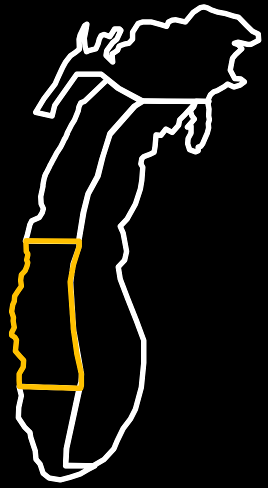
Stocked vs observed: East



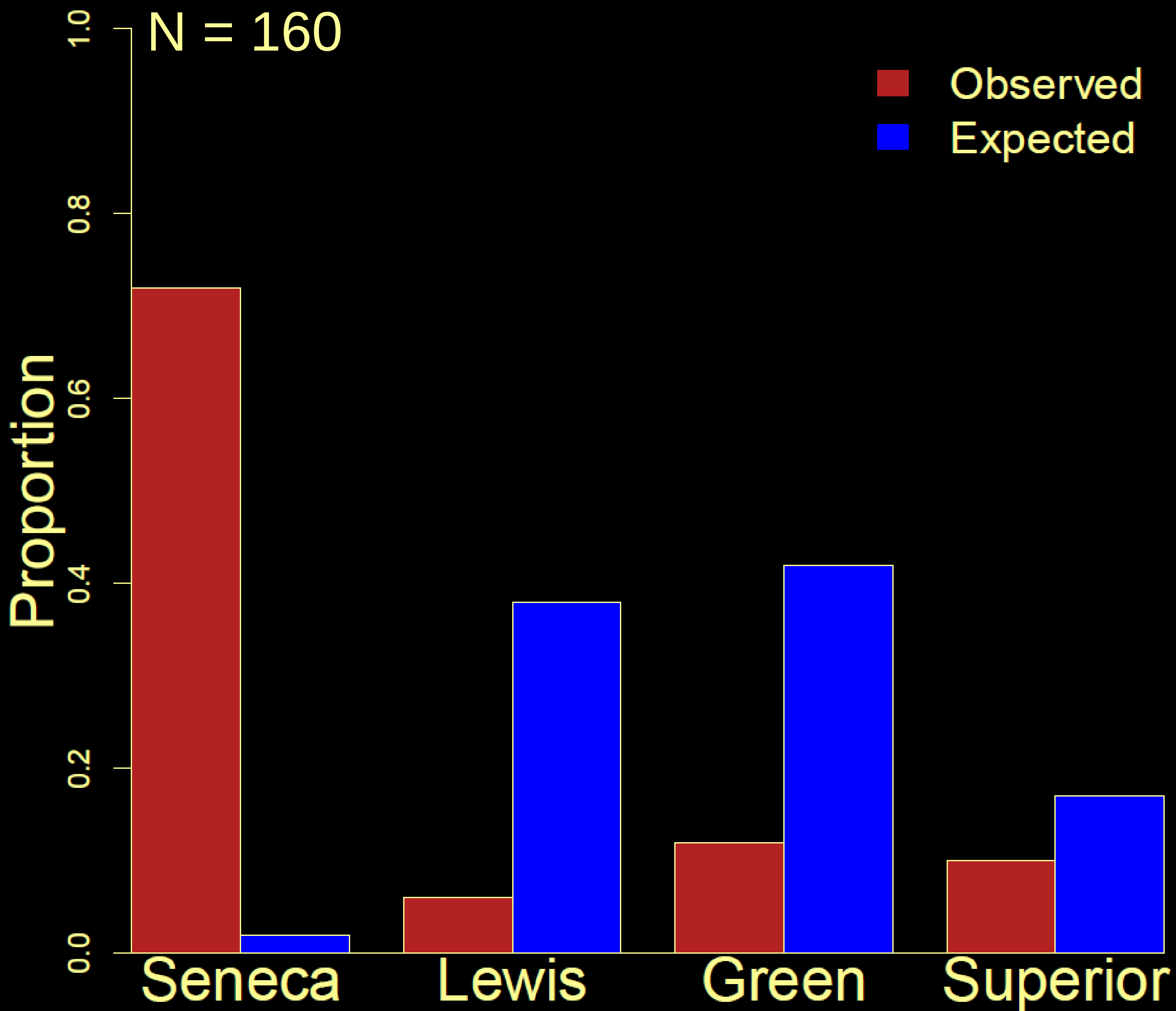


Stocked vs observed: Southwest

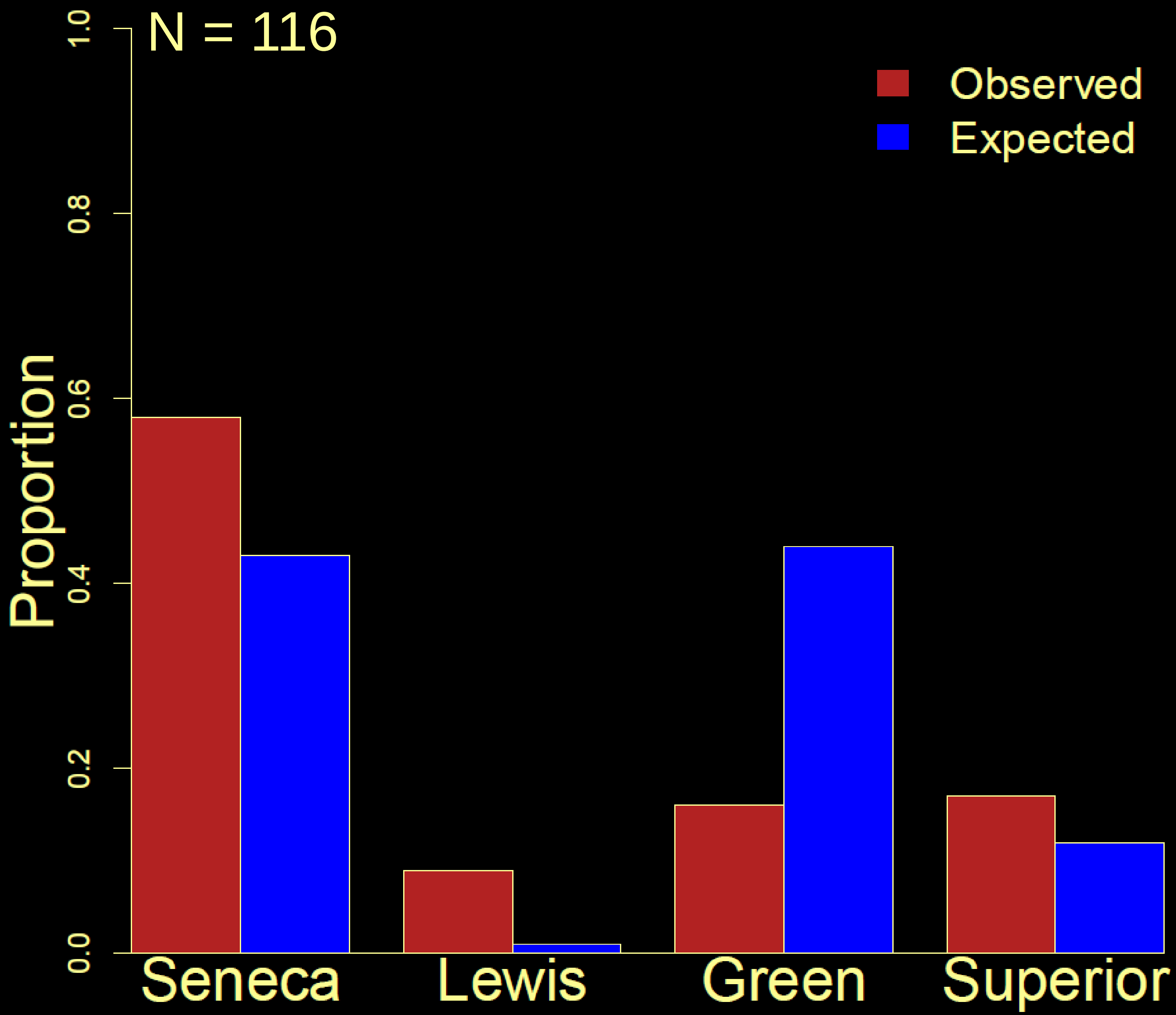




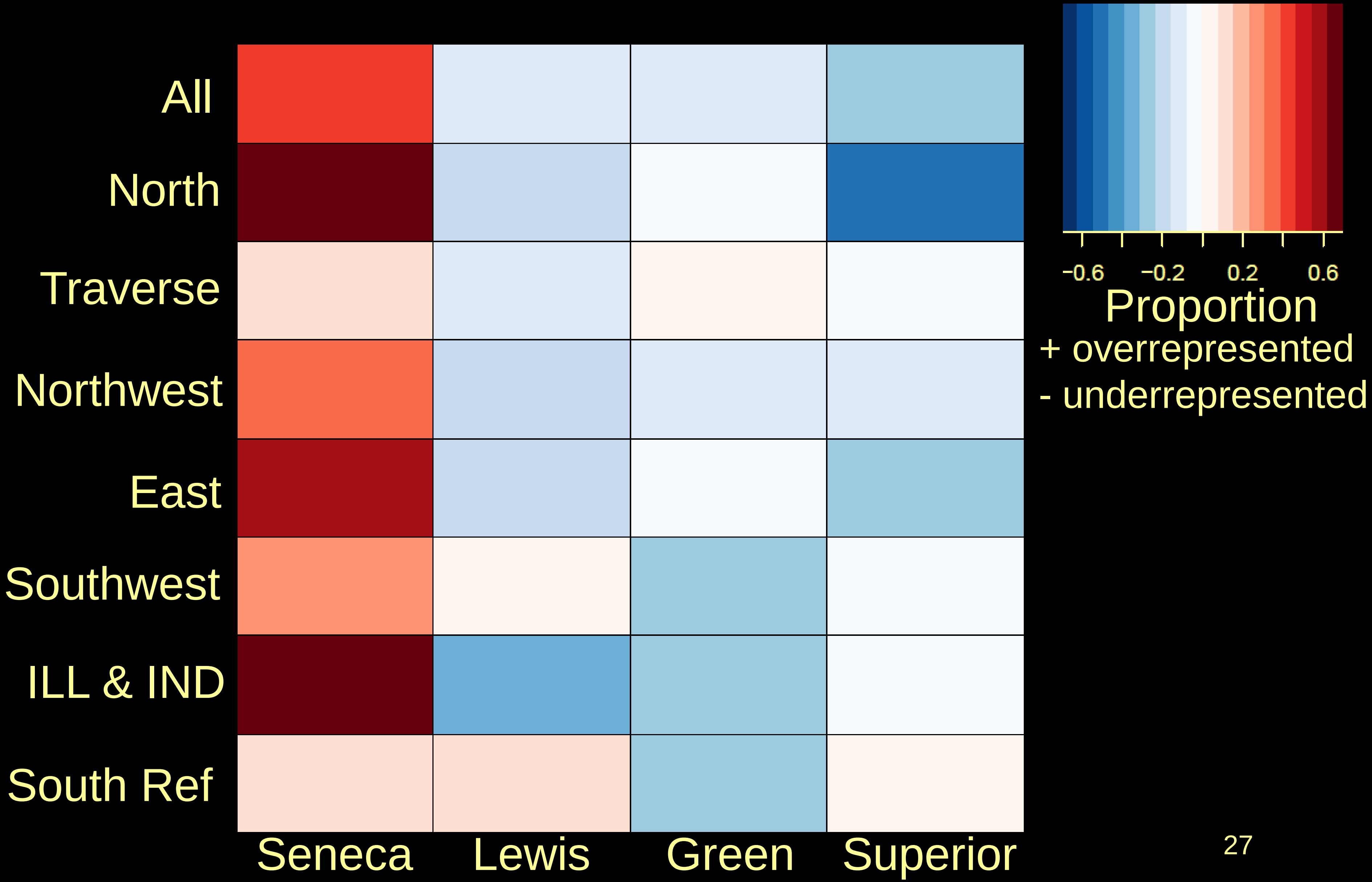
Stocked vs observed: Illinois and Indiana



Stocked vs observed: Southern Refugee



Observed - expected stock proportions



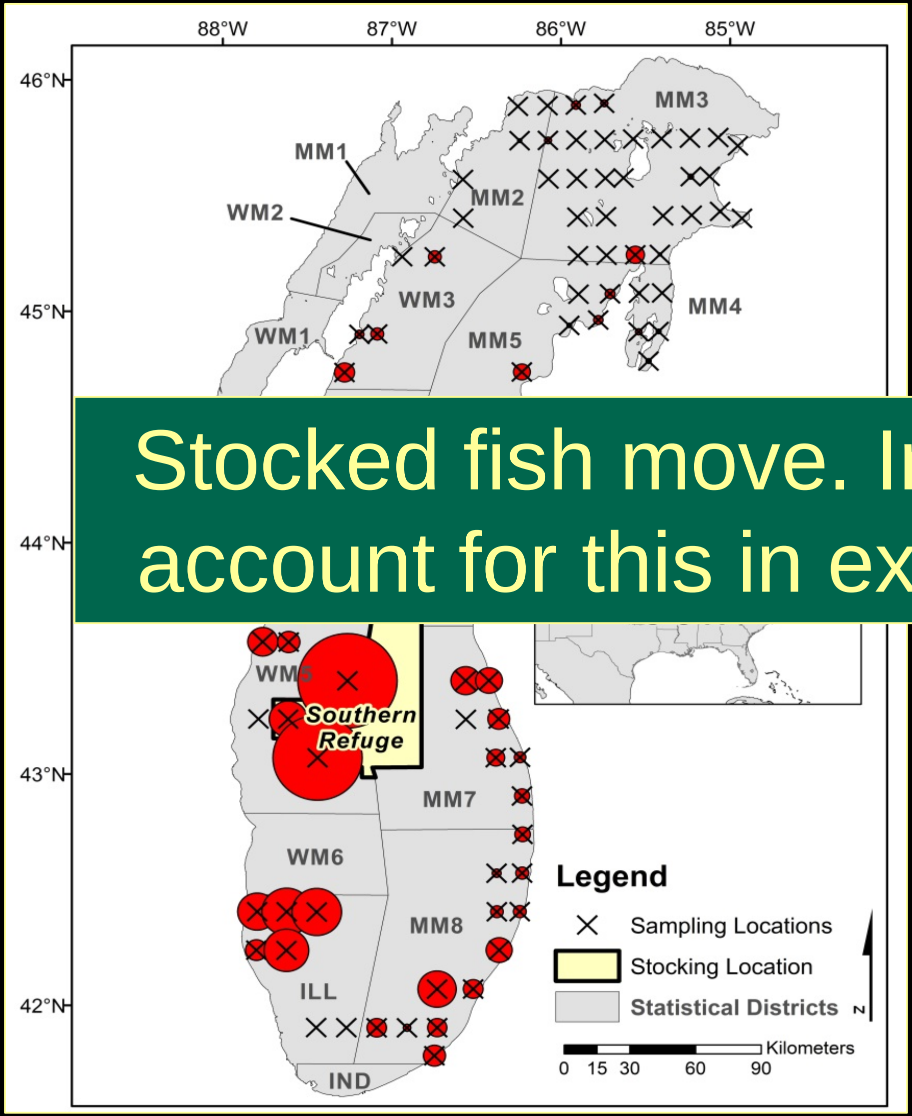
Origin of stocked lake trout recovered from open-water anglers in Lake Michigan

Origin	**Illinois**	**Indiana**	**Michigan**	**Wisconsin**	**Lake Michigan**
Nearshore	4%	30%	52%	13%	38%
Julian's Reef	53%	29%	5%	18%	16%
Northern Refuge	2%	0%*	10%	24%	9%
Southern Refuge	41%	41%	33%	46%	37%

*0% only due to rounding

Courtesy of Great Lakes Mass Marking Program

Movement of lake trout stocked offshore



- Location of recoveries of CWT lake trout released in the Southern Refuge

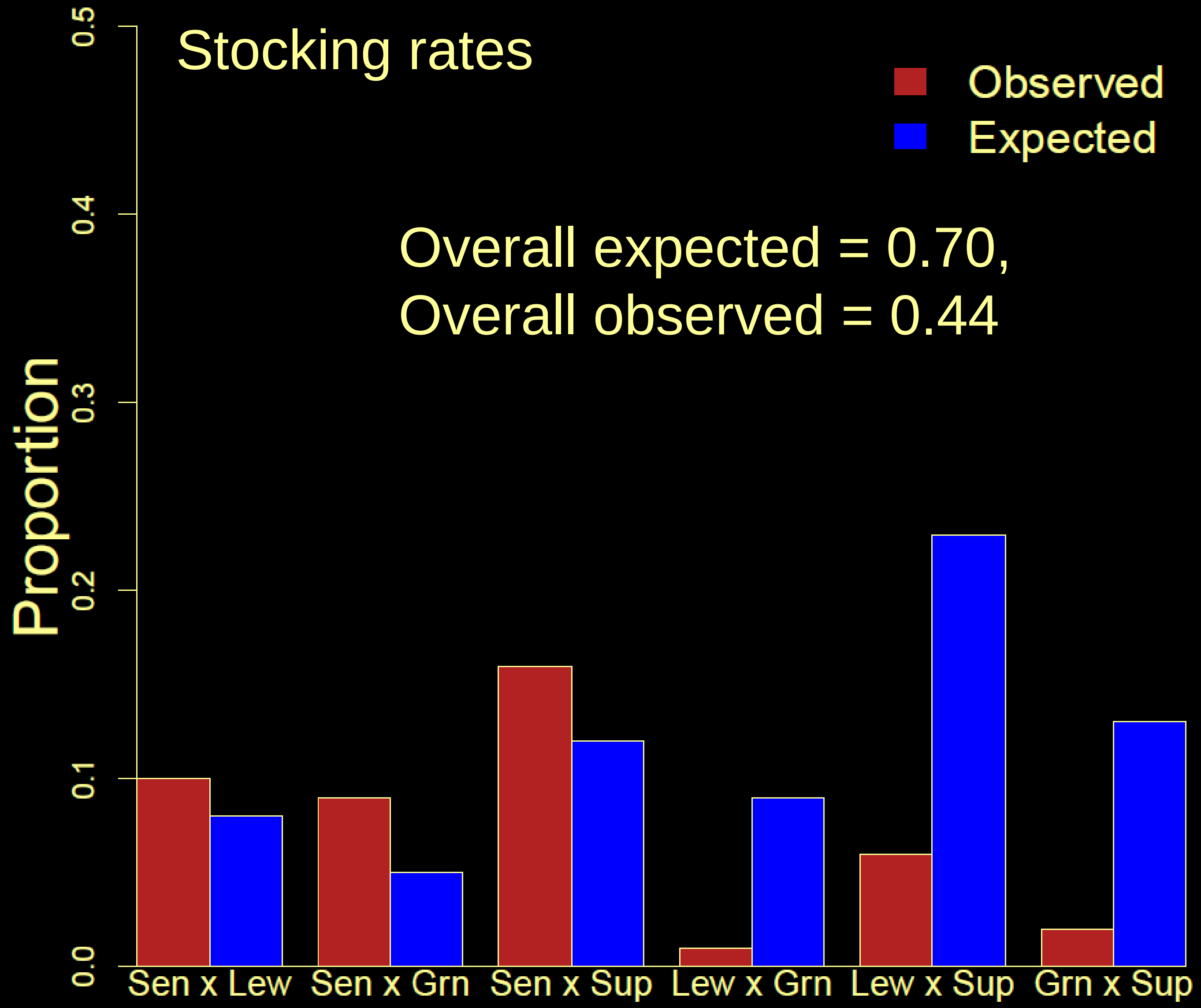
trout CPUE

- X's are sampling locations (LWAP and FIWS)

Stocked fish move. Important next step: account for this in expected proportions

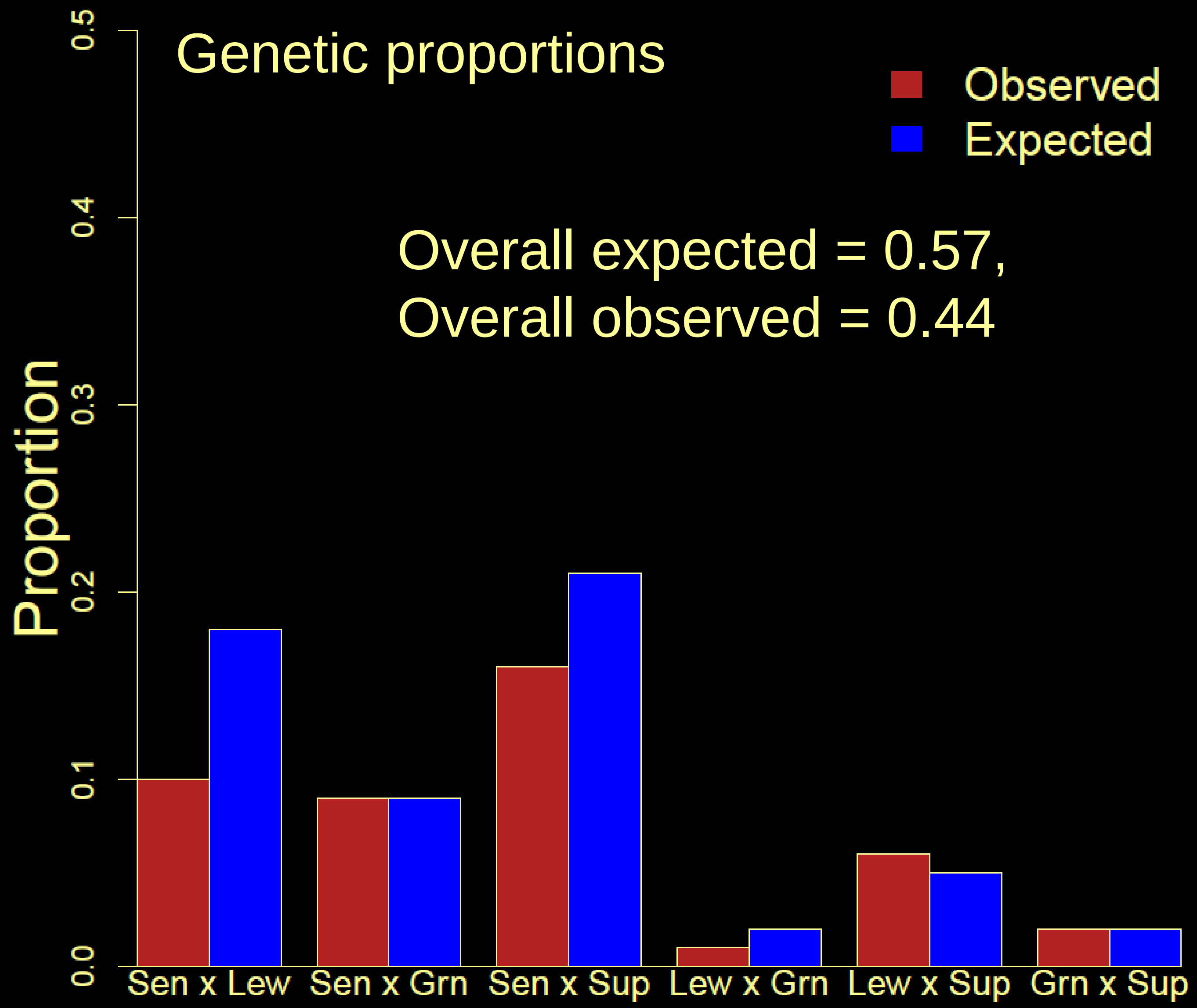
Courtesy of Great Lakes Mass Marking Program

Frequency of hybridization

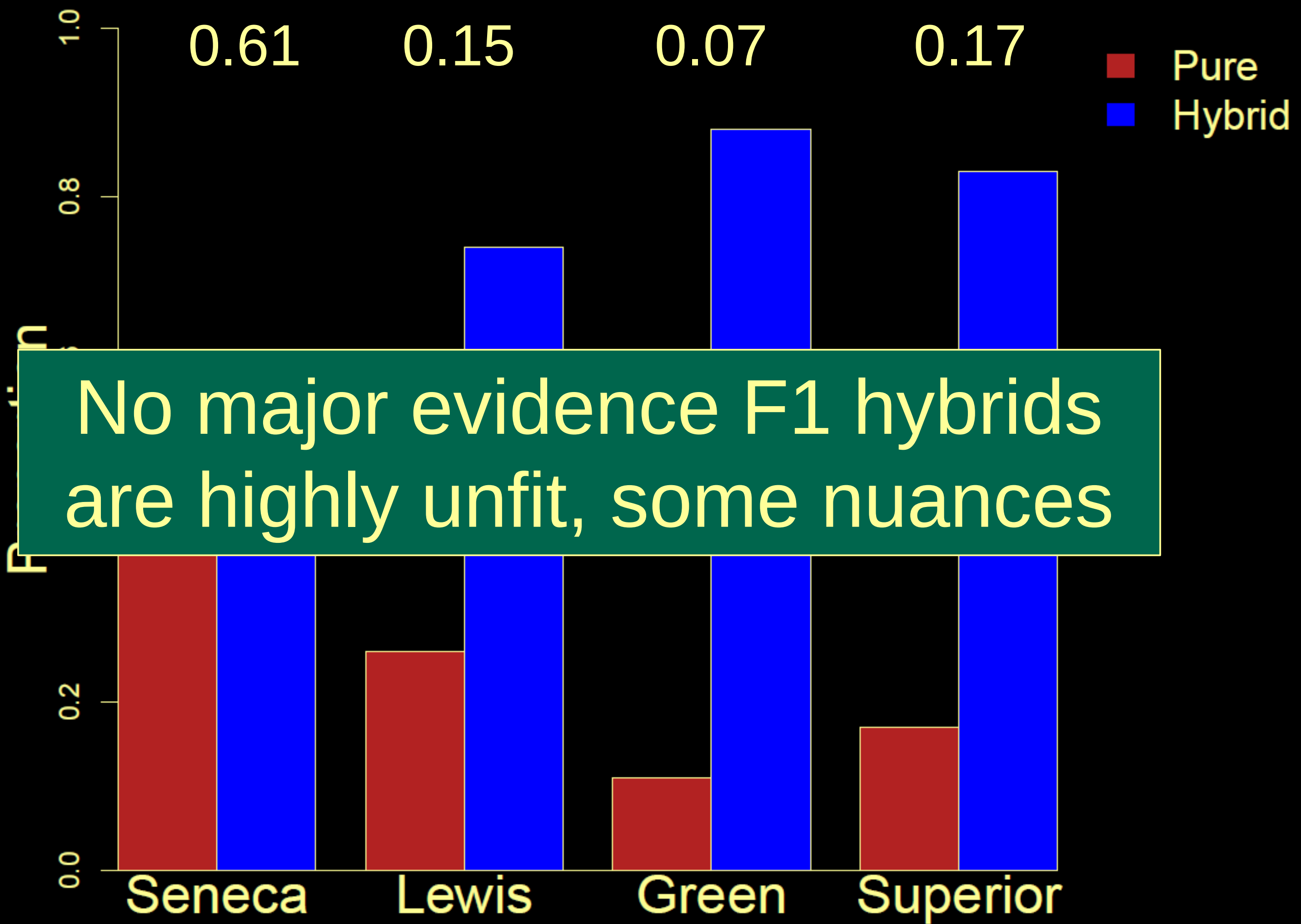


Overall expected = 0.70,
Overall observed = 0.44

Frequency of hybridization



Proportion of pures vs hybrids



No major evidence F1 hybrids are highly unfit, some nuances

- Seneca hybrids frequent but similar to expectations
- Superior heavily stocked, pures rare

Conclusions

- Strains and inter-strain hybrids can be differentiated relatively well (SNPs may improve)
- Some variation in stock proportions across space, but Seneca usually dominant (exception: Traverse)
- Seneca is highly overrepresented compared to past stocking history, other stocks perform more poorly
- Performance of other stocks varies by area (e.g. Superior in North, Lewis/Green in Traverse)
- Hybridization rates similar to expectations based on genetic data (exception: Superior pures rare)

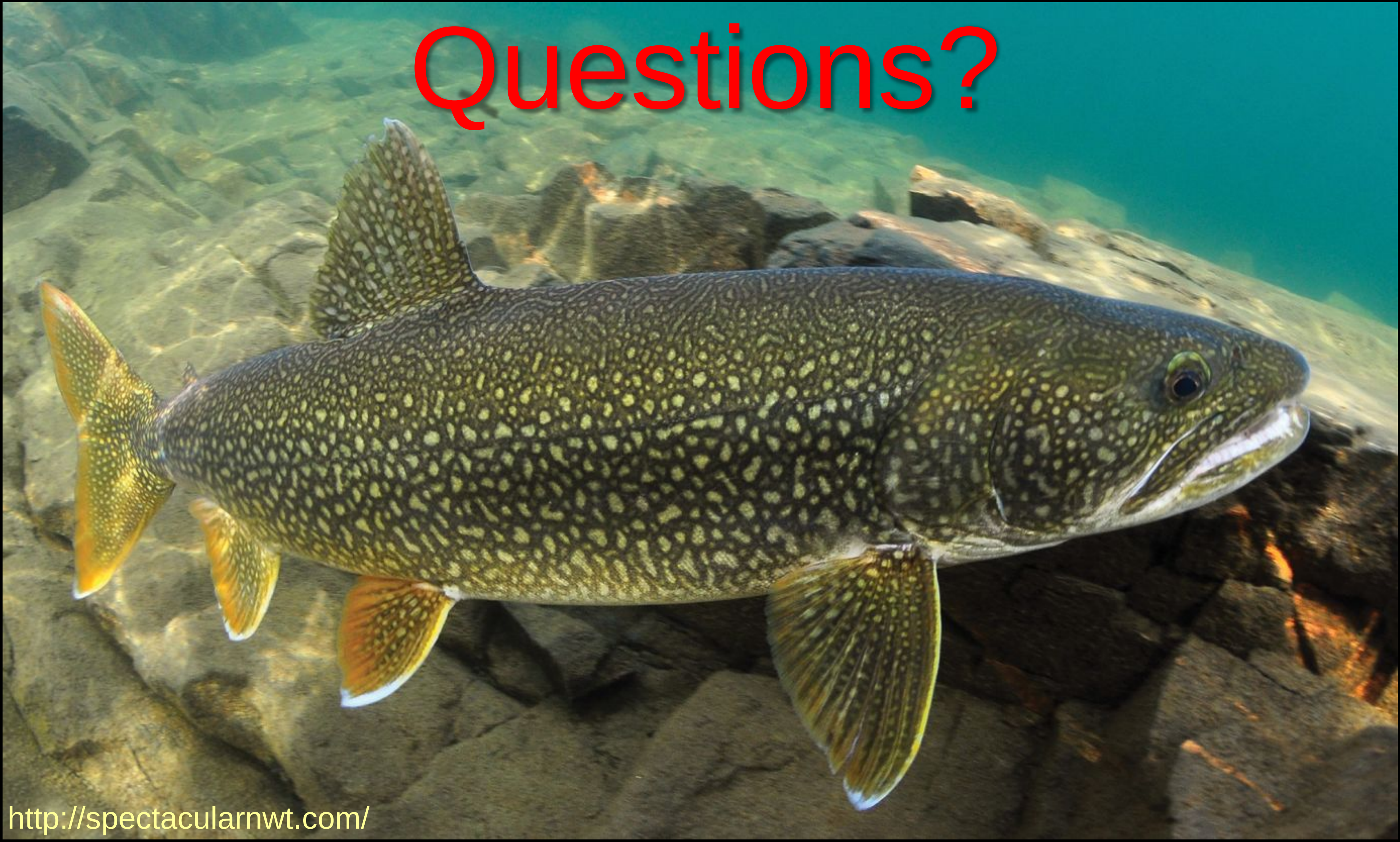
Management recommendations

- Continue stocking Seneca
  - Clearly well adapted to Lake Michigan and successfully reproducing
- Continue stocking strains derived from Lake Michigan
  - Possible adaptive advantages in certain areas (Traverse)
  - Avoid putting all eggs in one basket, environment could favor remnant native alleles
- Evaluate reasons to continue stocking Superior strains
  - Appears to be maladapted to many areas of Lake Michigan (sea lamprey, other factors?) but does well where mortality is low.
- Future: determine stock proportions of spawners to investigate survival vs reproductive success

Acknowledgements

- Great Lakes Fishery Trust
- MCGL Technicians
- Lake Michigan Lake Trout Working Group
- Lake Michigan Technical Committee
- Great Lakes Mass Marking Program Recovery Technicians (USFWS)
- Great Lakes Restoration Initiative
- U.S. Fish & Wildlife Service
- Mark Holey, USFWS
- Kim Scribner (MSU)

Questions?



http://spectacularnwt.com/

Wes.Larson@uwsp.edu