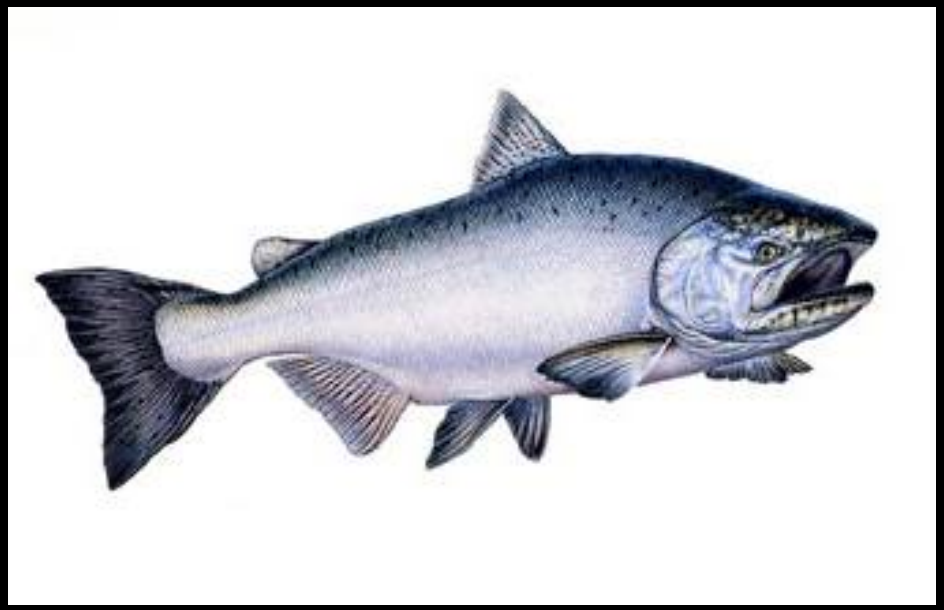
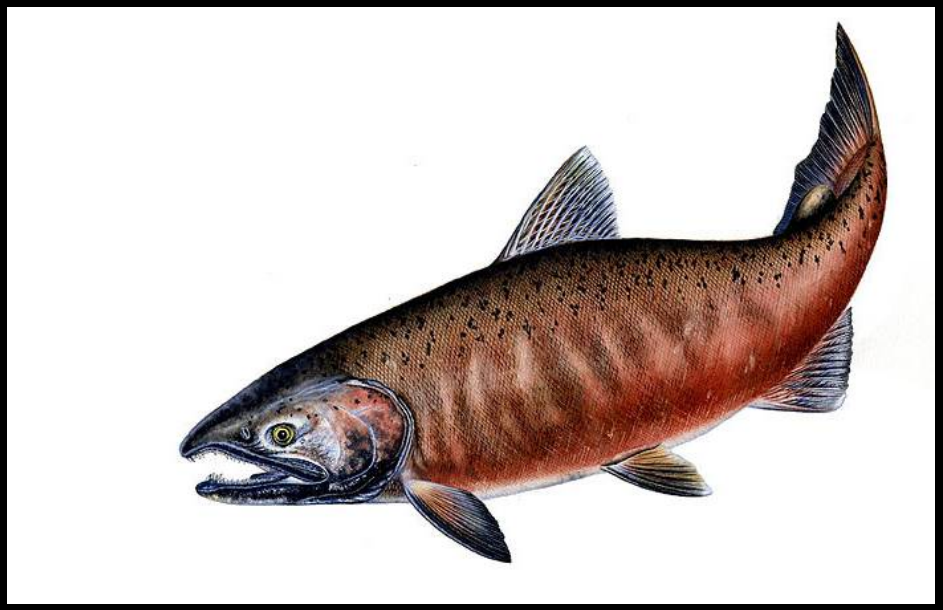
Use of genetic data to estimate salmonid stock composition and migration patterns





Jon Hess and Shawn Narum
CRITFC Conservation Geneticists
Collaborative Center for Applied Fish Science
Hagerman, Idaho

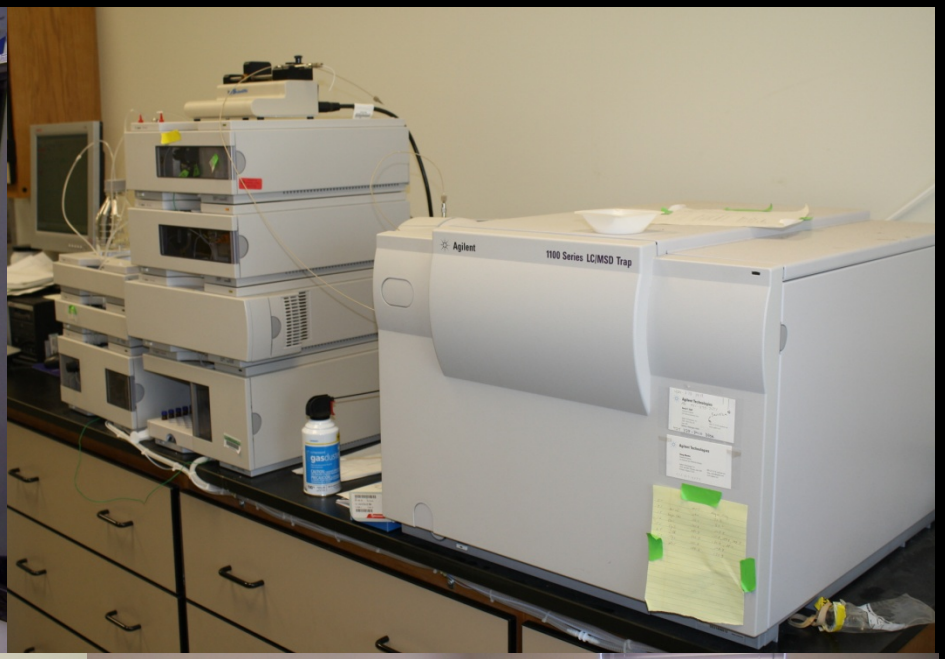
Highly Collaborative

- Four Member Tribes
- University of Idaho
- USDA – ARS
- Salmon genetics community (state and federal agencies, universities)

Collaborative Center for Applied Fish Science, Hagerman, Idaho – Opened 2006

Offices, Cubicles, Conference Room

Laboratory Space



Dorm Facilities (6 rooms)

Experimental Aquaculture Facilities

CRITFC Staff

- 5 Scientists
  - Shawn Narum
  - Andrew Matala
  - Nate Campbell
  - Jeff Stephenson
  - Jon Hess

- 4 Lab Techs (UI)
  - Vanessa Jacobson
  - Justin Parker
  - Lori Maxwell
  - Amanda Matala

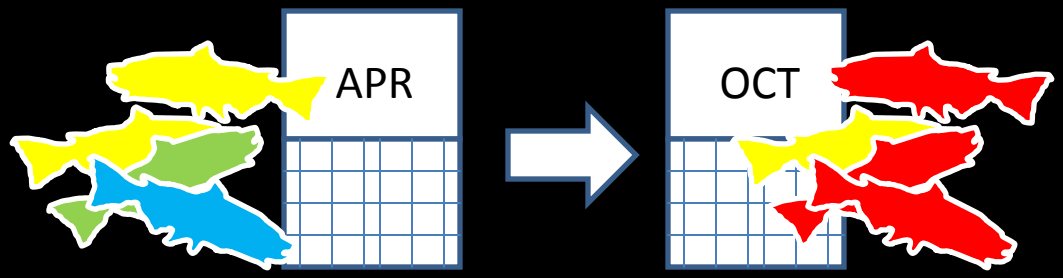
Basic information needed for management of fisheries:

1)What is the general stock composition of the total return of fish in the Columbia River?

Basic information needed for management of fisheries:

1)What is the general stock composition of the total return of fish in the Columbia River?

2)How does stock composition vary across time, space, and harvest?



Basic information needed for management of fisheries:

1)What is the general stock composition of the total return of fish in the Columbia River?

2)How does stock composition vary across time, space, and harvest?

Basic information needed for management of fisheries:

1)What is the general stock composition of the total return of fish in the Columbia River?

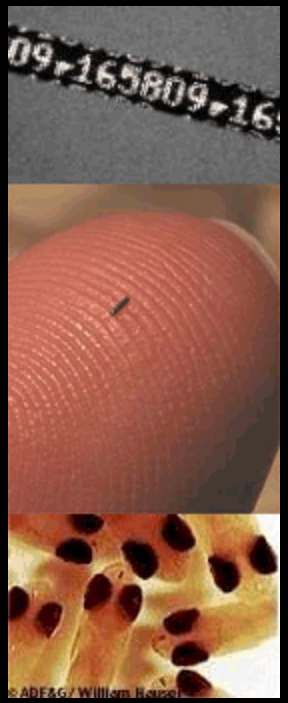
2)How does stock composition vary across time, space, and harvest?

Tools used to address these questions

1) What is the general stock composition of the total return of fish in the Columbia River?

2) How does stock composition vary across time, space, and harvest?

Tools used to address these questions



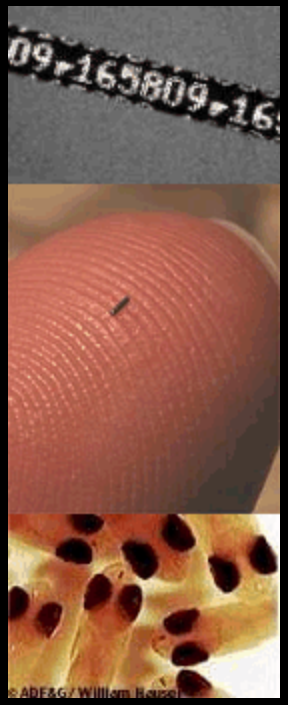
Coded Wire Tags (CWT)

Passive Integrated Transponder (PIT) Tags

1) What is the general stock composition of the total return of fish in the Columbia River?

2) How does stock composition vary across time, space, and harvest?

Tools used to address these questions



Coded Wire Tags (CWT)

Passive Integrated Transponder (PIT) Tags

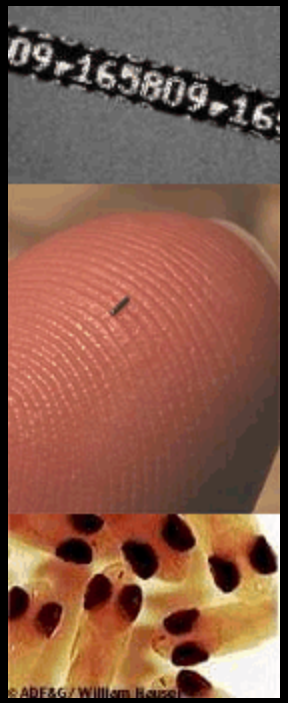
- Only hatchery fish are tagged

- Must recapture previously marked fish in order to collect data

1) What is the general stock composition of the total return of fish in the Columbia River?

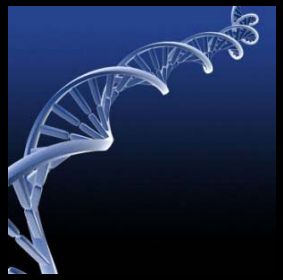
2) How does stock composition vary across time, space, and harvest?

Tools used to address these questions



Coded Wire Tags (CWT)

Passive Integrated Transponder (PIT) Tags

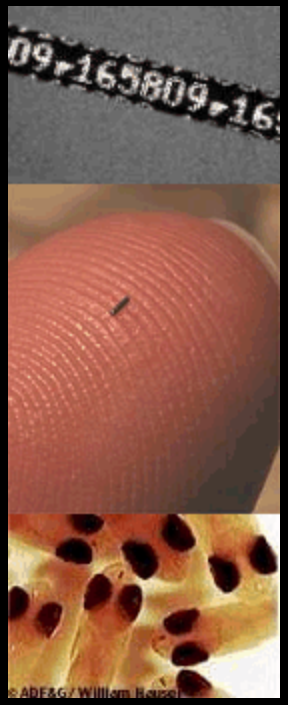


Genetic Information

1) What is the general stock composition of the total return of fish in the Columbia River?

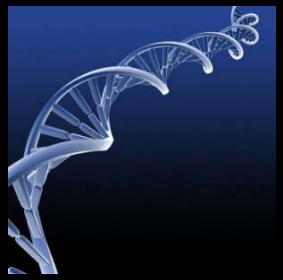
2) How does stock composition vary across time, space, and harvest?

Tools used to address these questions



Coded Wire Tags (CWT)

Passive Integrated Transponder (PIT) Tags



Genetic Information

- All fish contain genetic information

1) What is the general stock composition of the total return of fish in the Columbia River?

2) How does stock composition vary across time, space, and harvest?

CRITFC is addressing stock questions in Chinook and Steelhead

1)What is the general stock composition of the total return of fish in the Columbia River?

2)How does stock composition vary across time, space, and harvest?

CRITFC is addressing stock questions in Chinook and Steelhead

SPECIFICALLY

1)What is the general stock composition of the total run of Chinook and Steelhead as they pass Bonneville Dam?

2)How does stock composition of Chinook vary throughout the run, sampled at two main locations above and below Bonneville Dam, and across three types of fisheries (tribal, sport, and commercial)?

CRITFC is addressing stock questions in Chinook and Steelhead

SPECIFICALLY

1)What is the general stock composition of the total run of Chinook and Steelhead as they pass Bonneville Dam?

2)How does stock composition of Chinook vary throughout the run, sampled at two main locations above and below Bonneville Dam, and across three types of fisheries (tribal, sport, and commercial)?

How is this accomplished?

How is this accomplished?

Three main steps

1) Collect baseline genetic information on streams throughout Columbia River

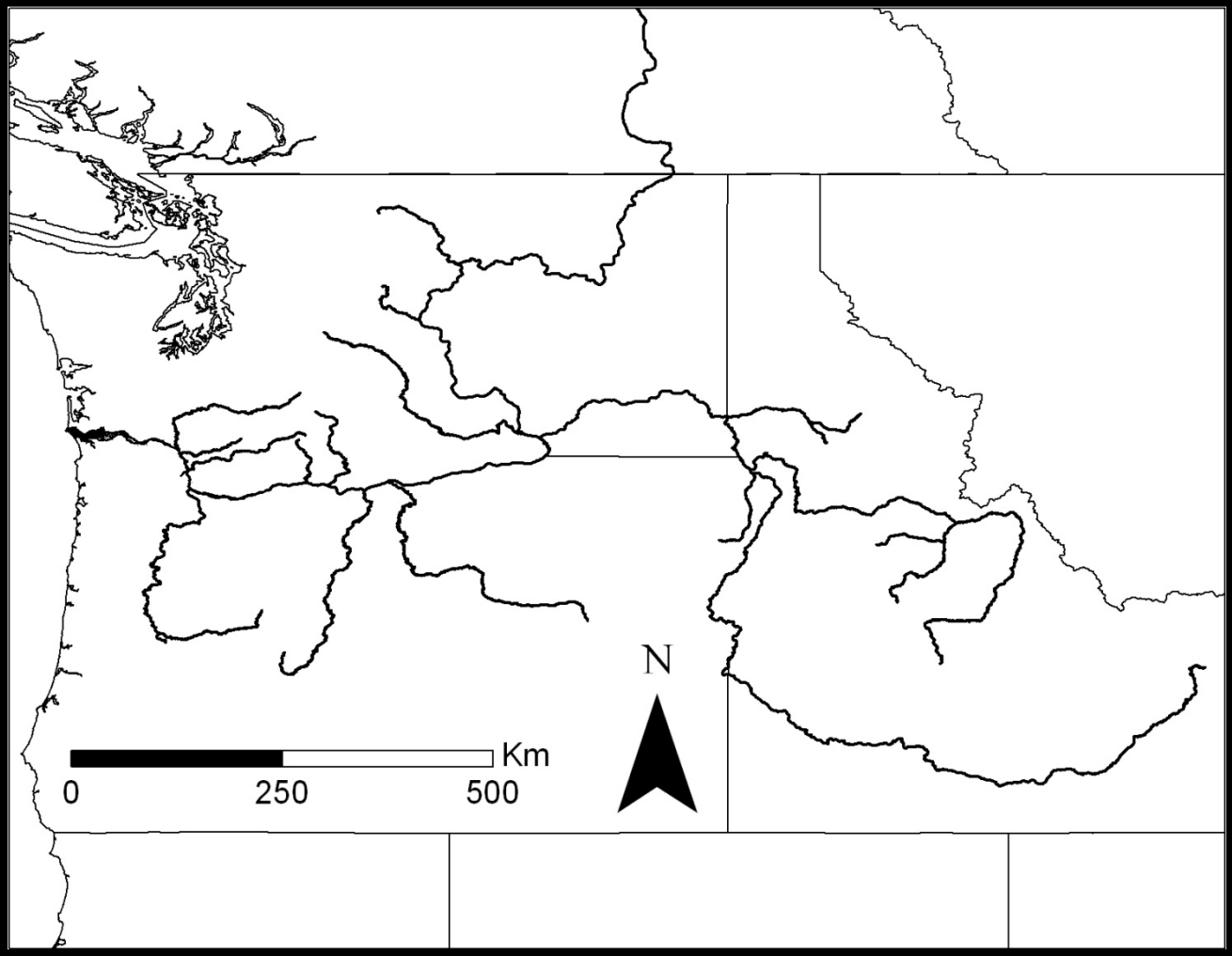
2) Collect genetic information on the unknown mixture of fish

3) Conduct analyses of this information to match unknown fish with its likely stream of origin.

Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

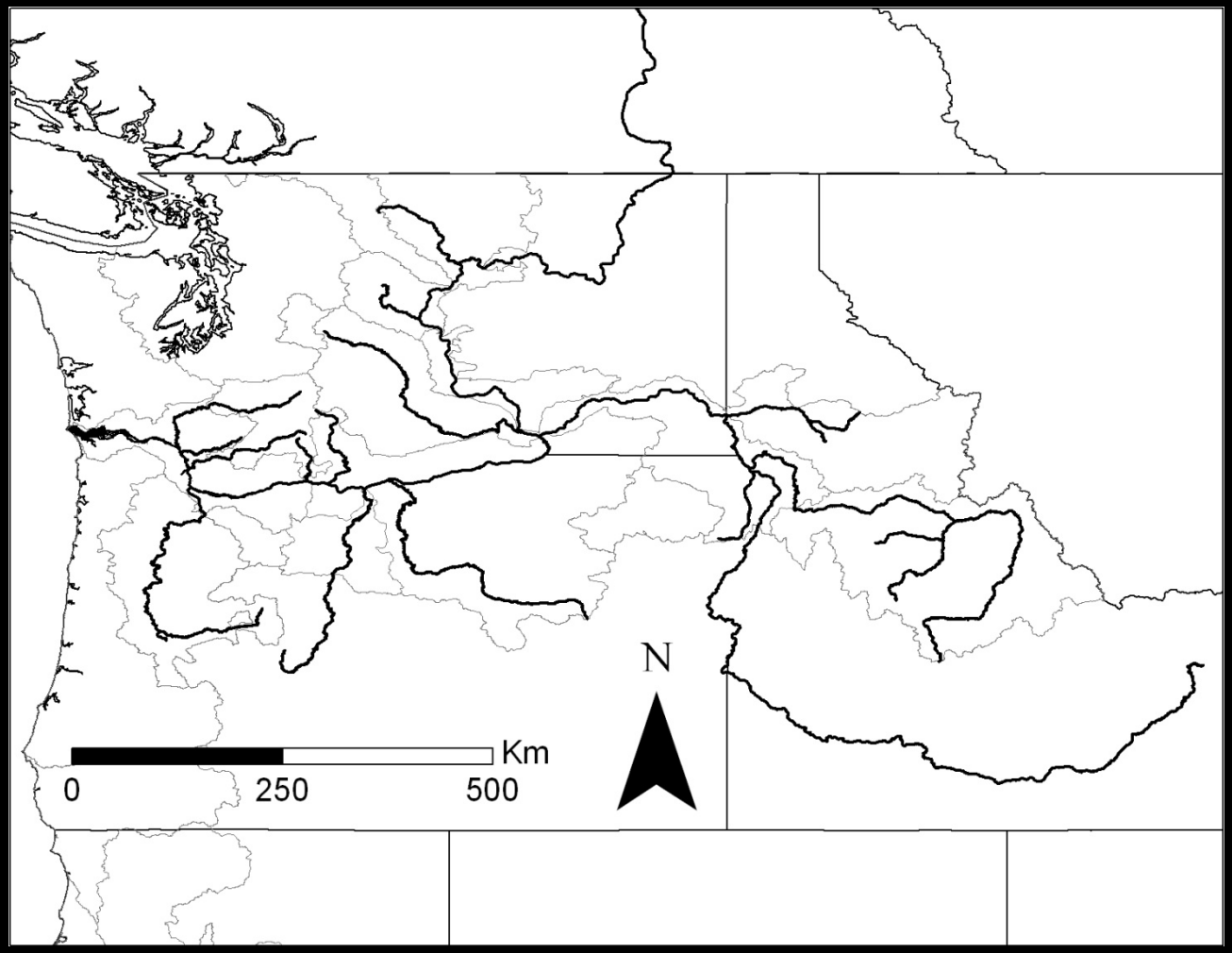
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

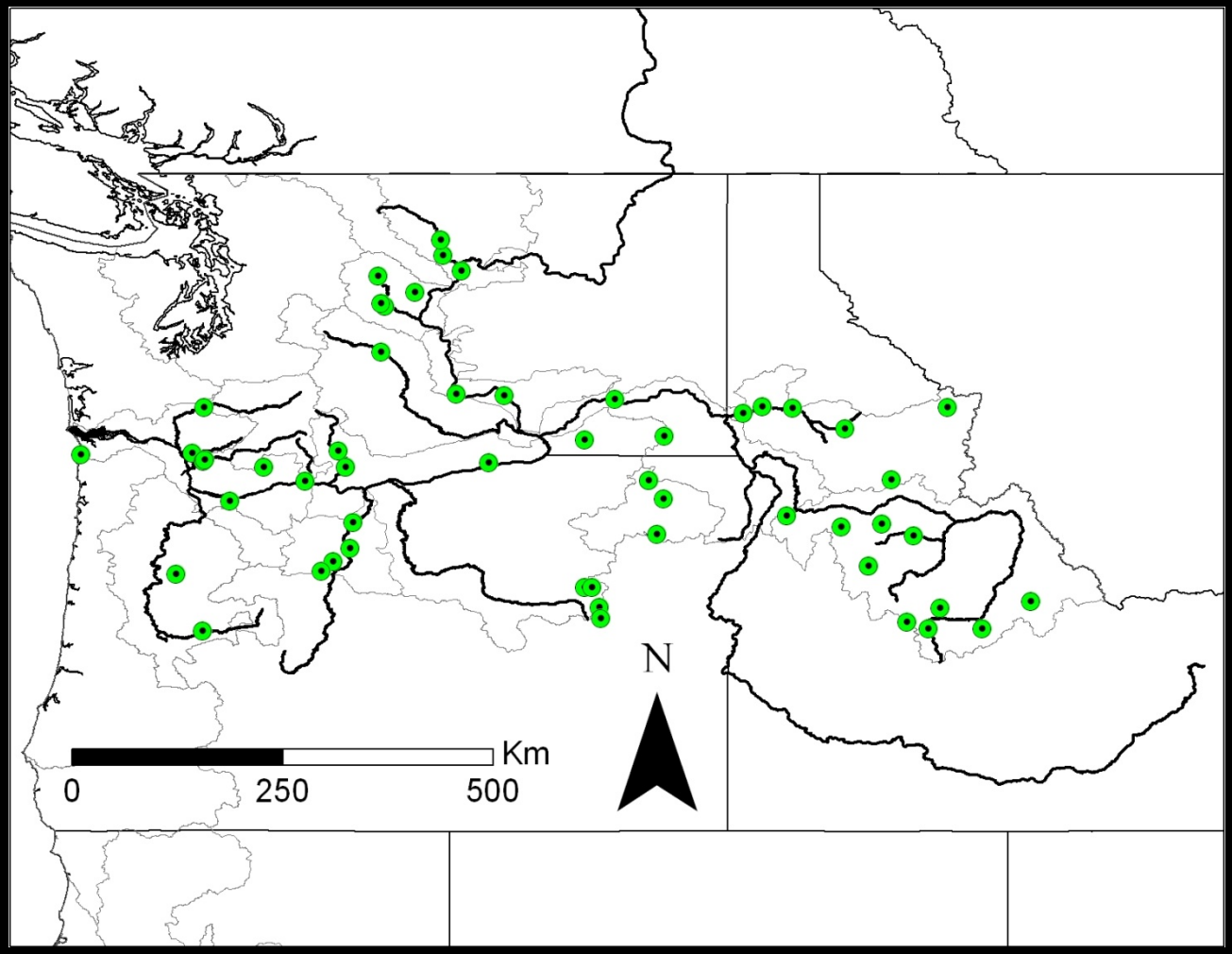
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

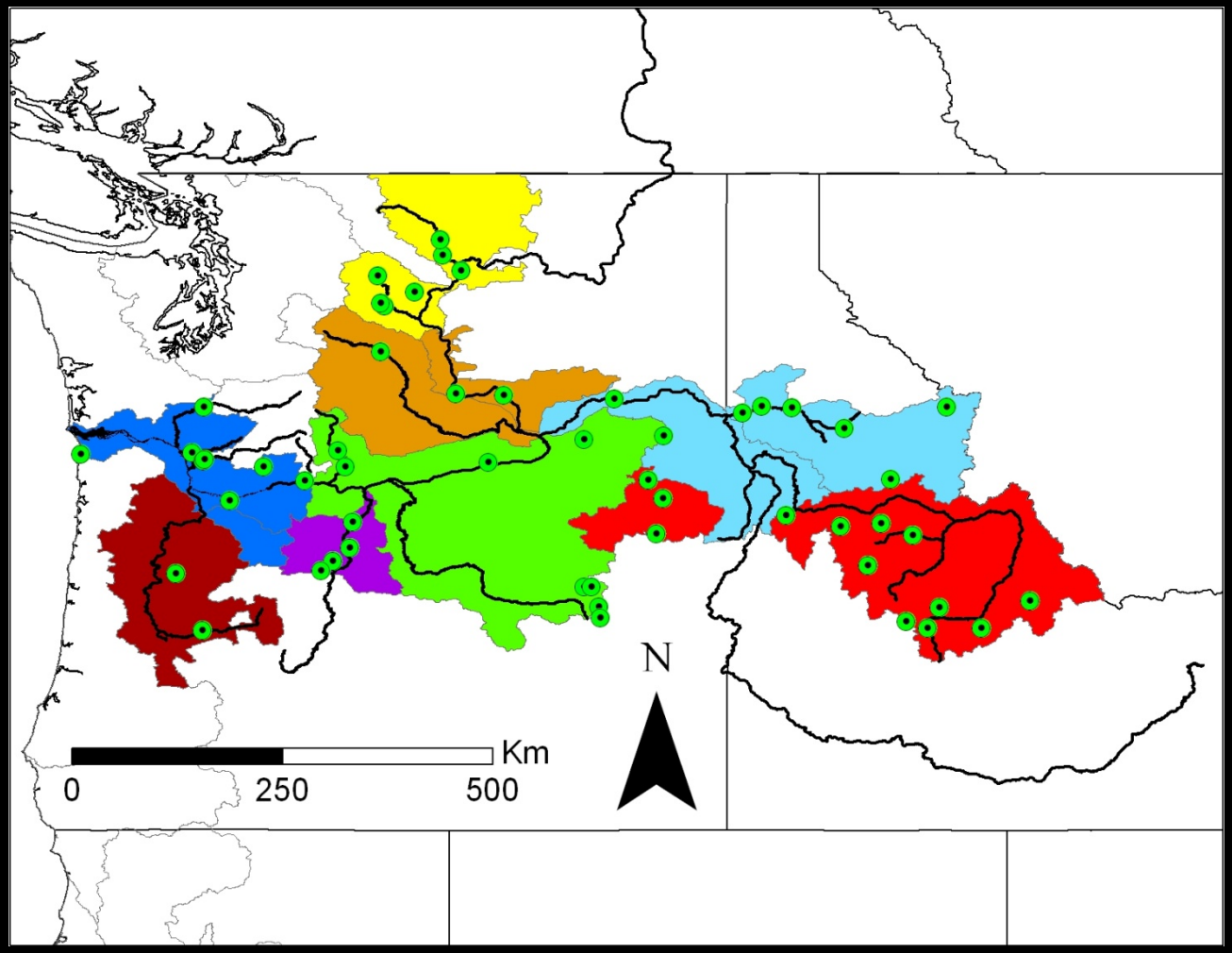
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

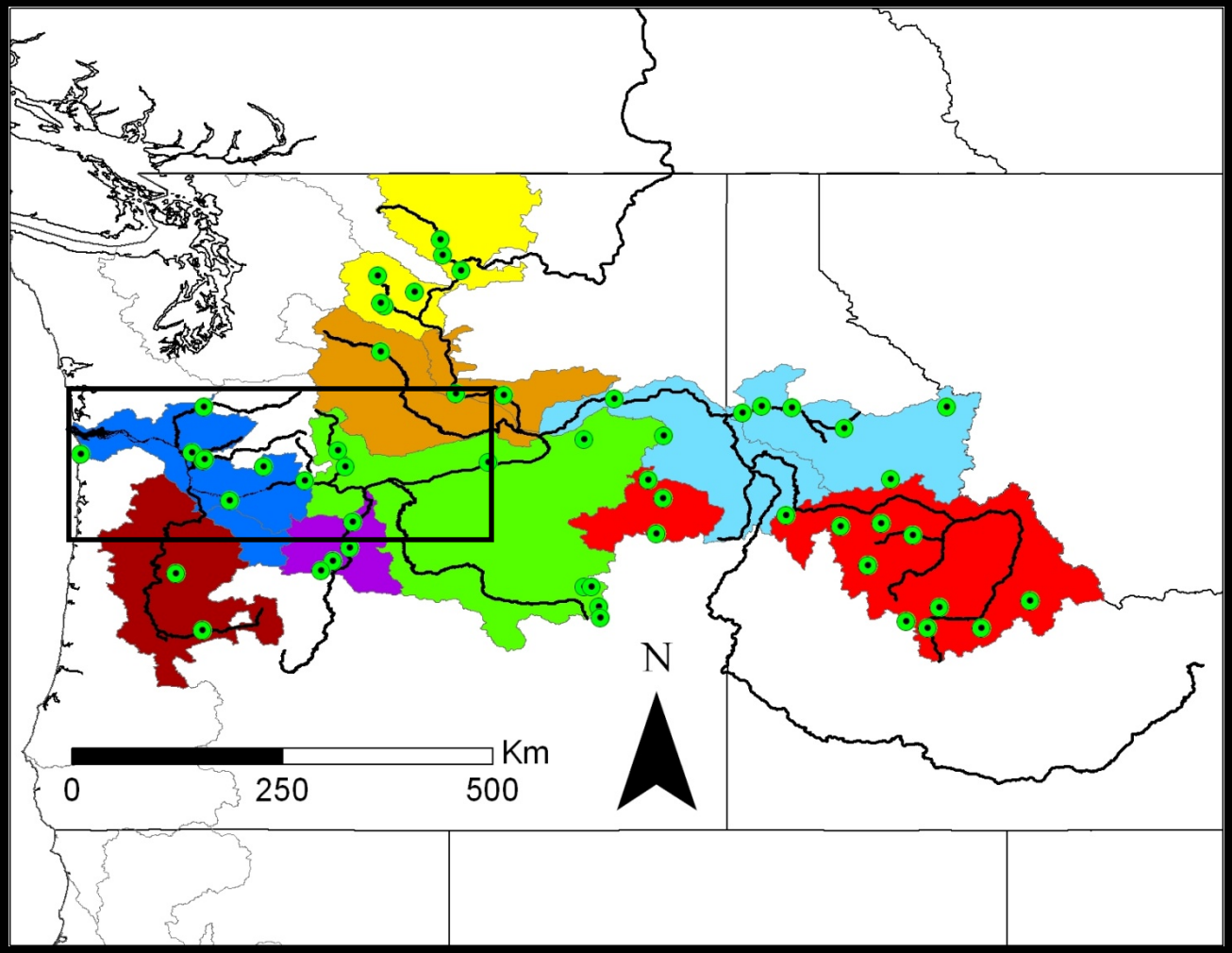
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

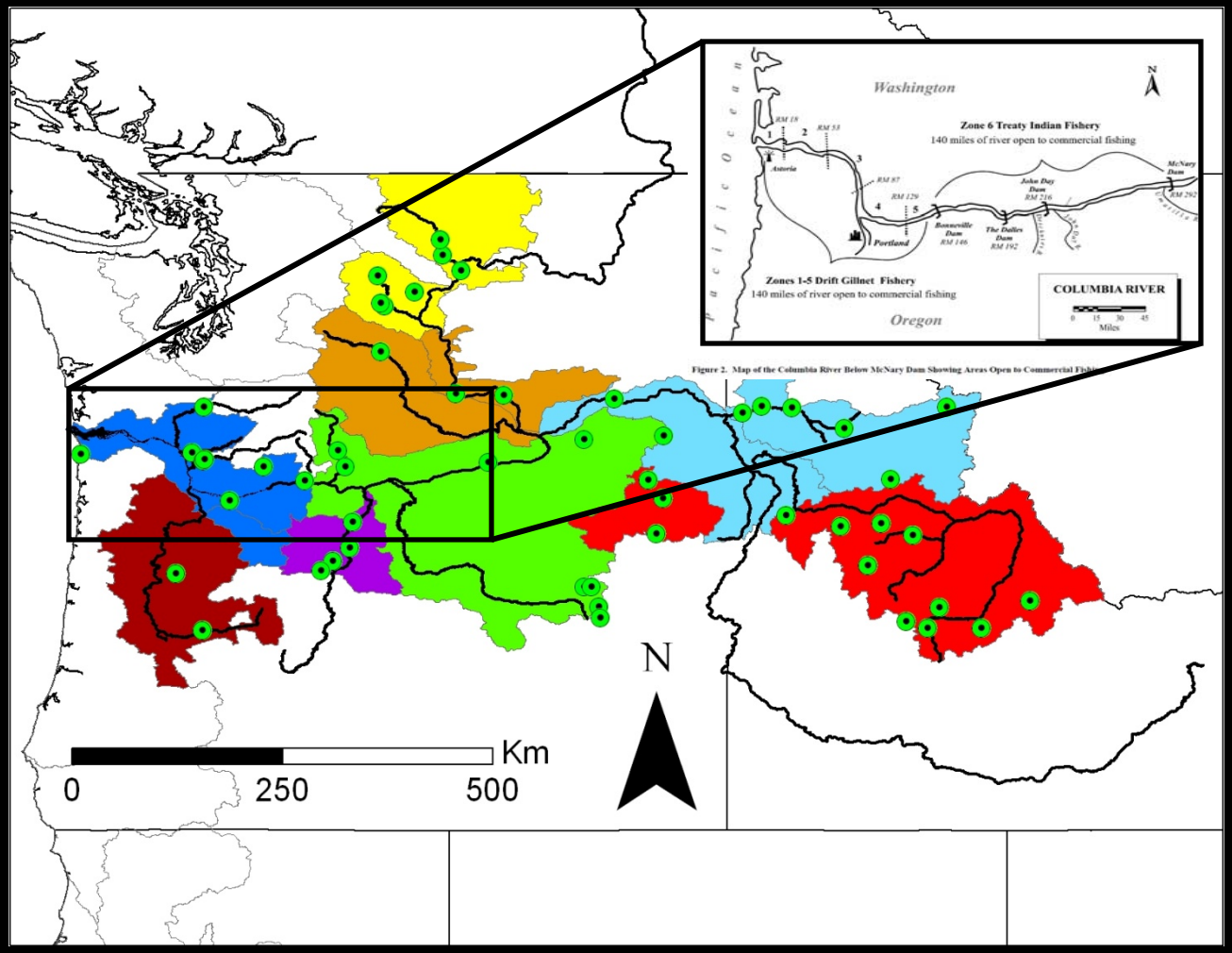
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

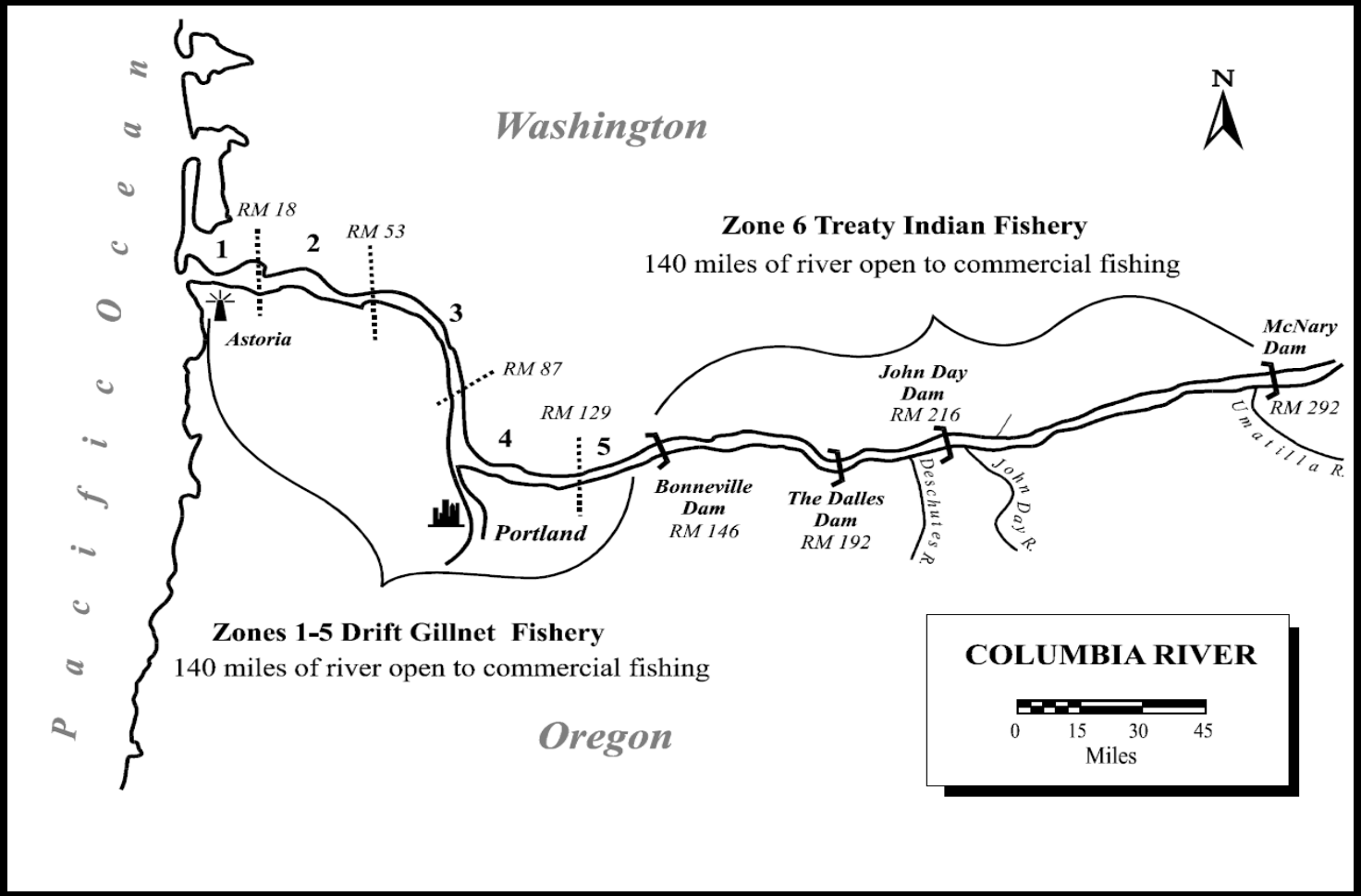
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

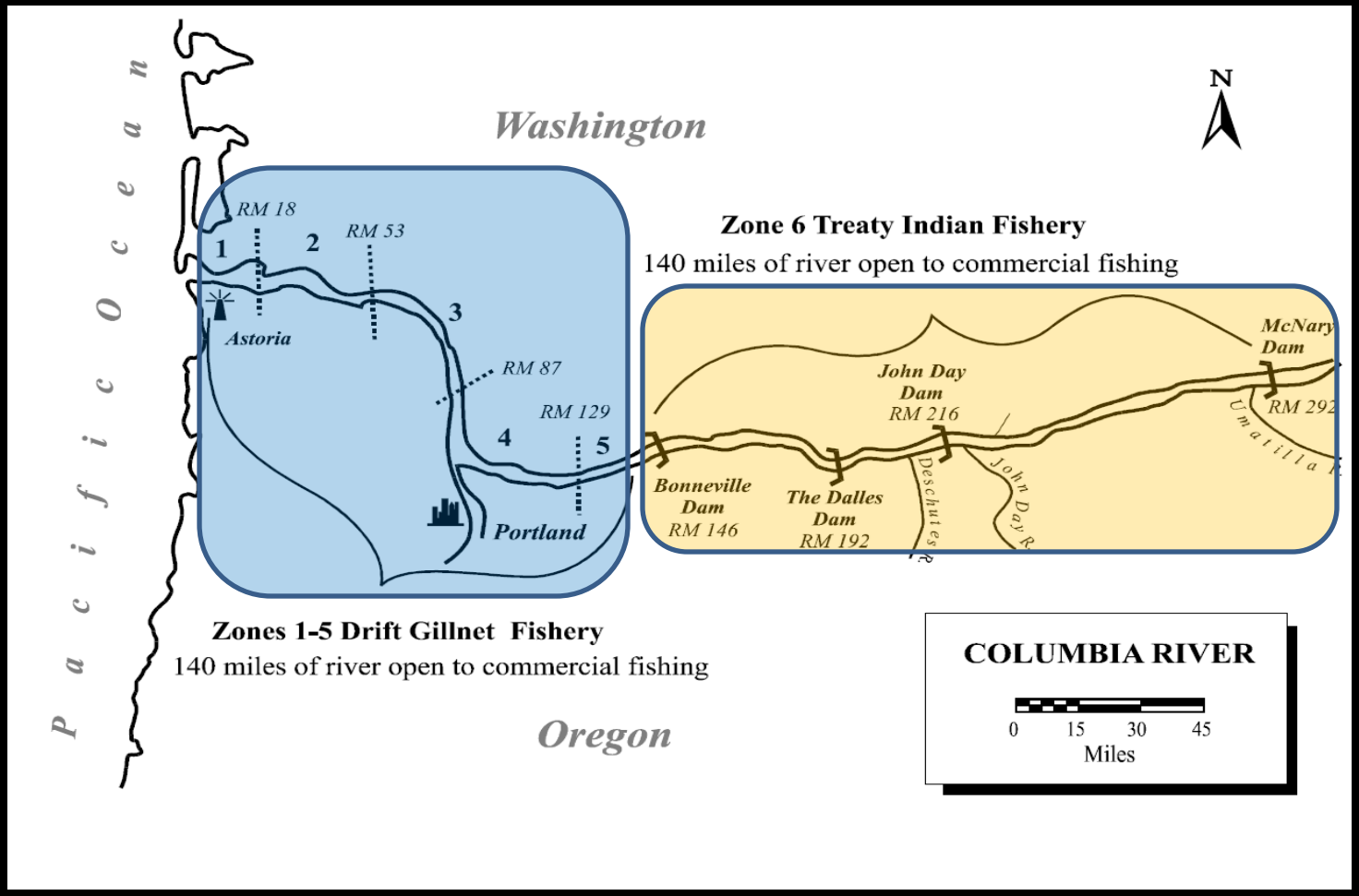
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

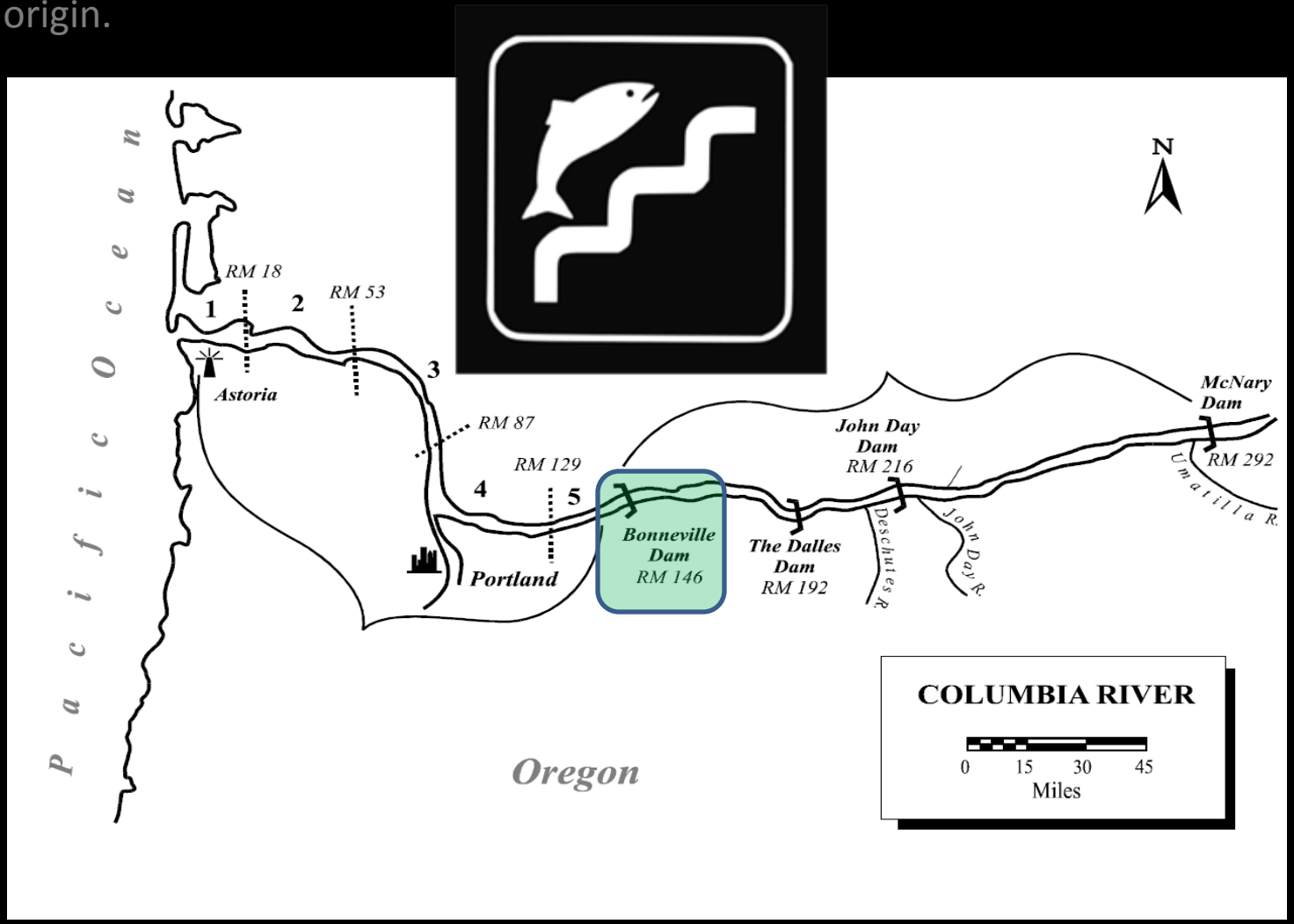
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

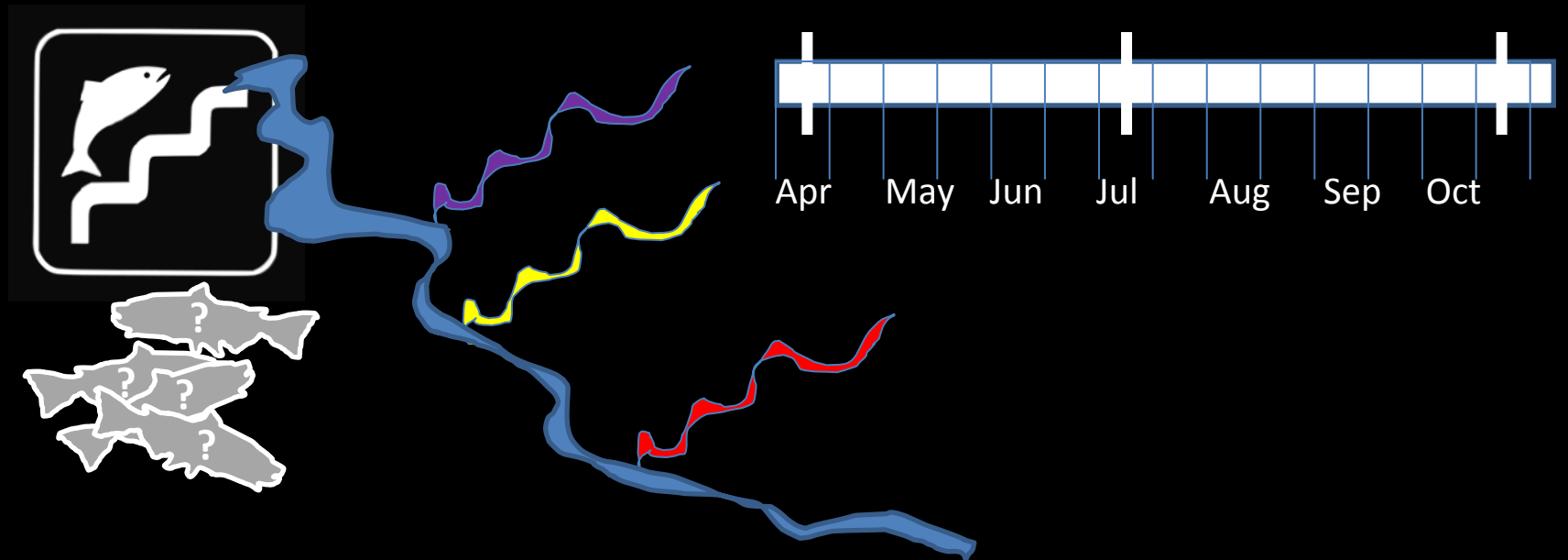
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

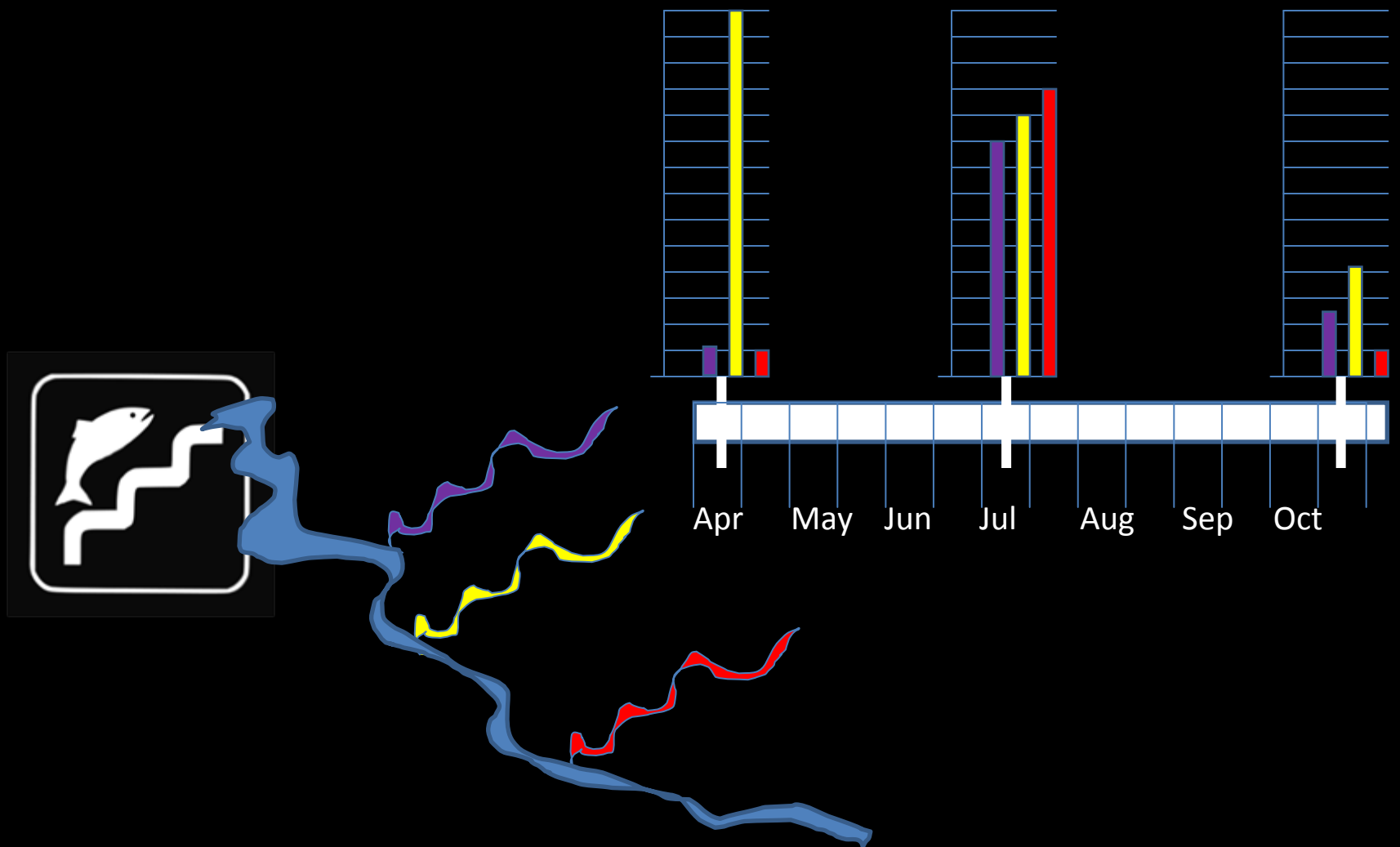
Conduct analyses of this information to match unknown fish with its likely stream of origin.



Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

Conduct analyses of this information to match unknown fish with its likely stream of origin.

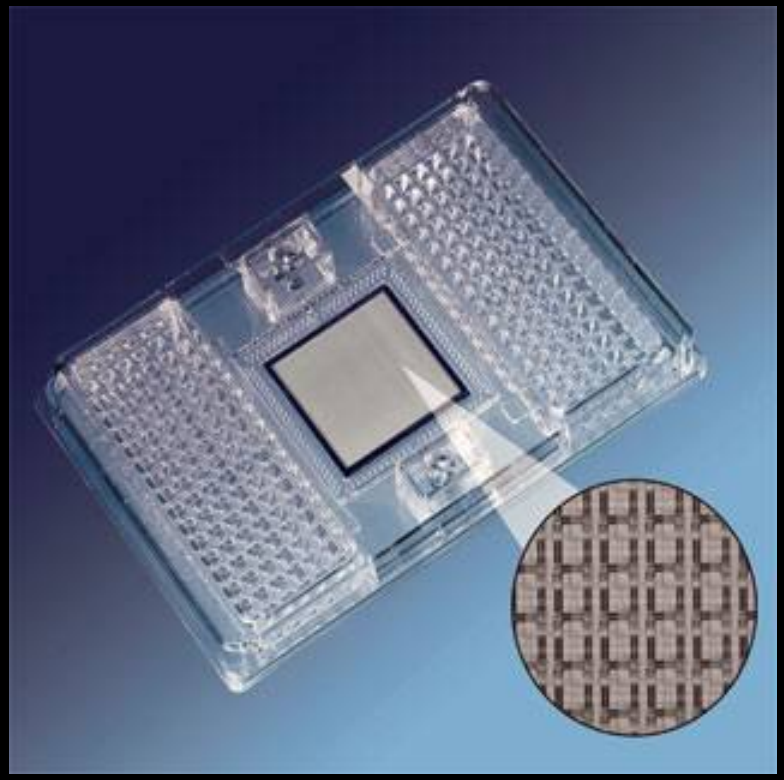


Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

Conduct analyses of this information to match unknown fish with its likely stream of origin.

Potential for in-season analyses.

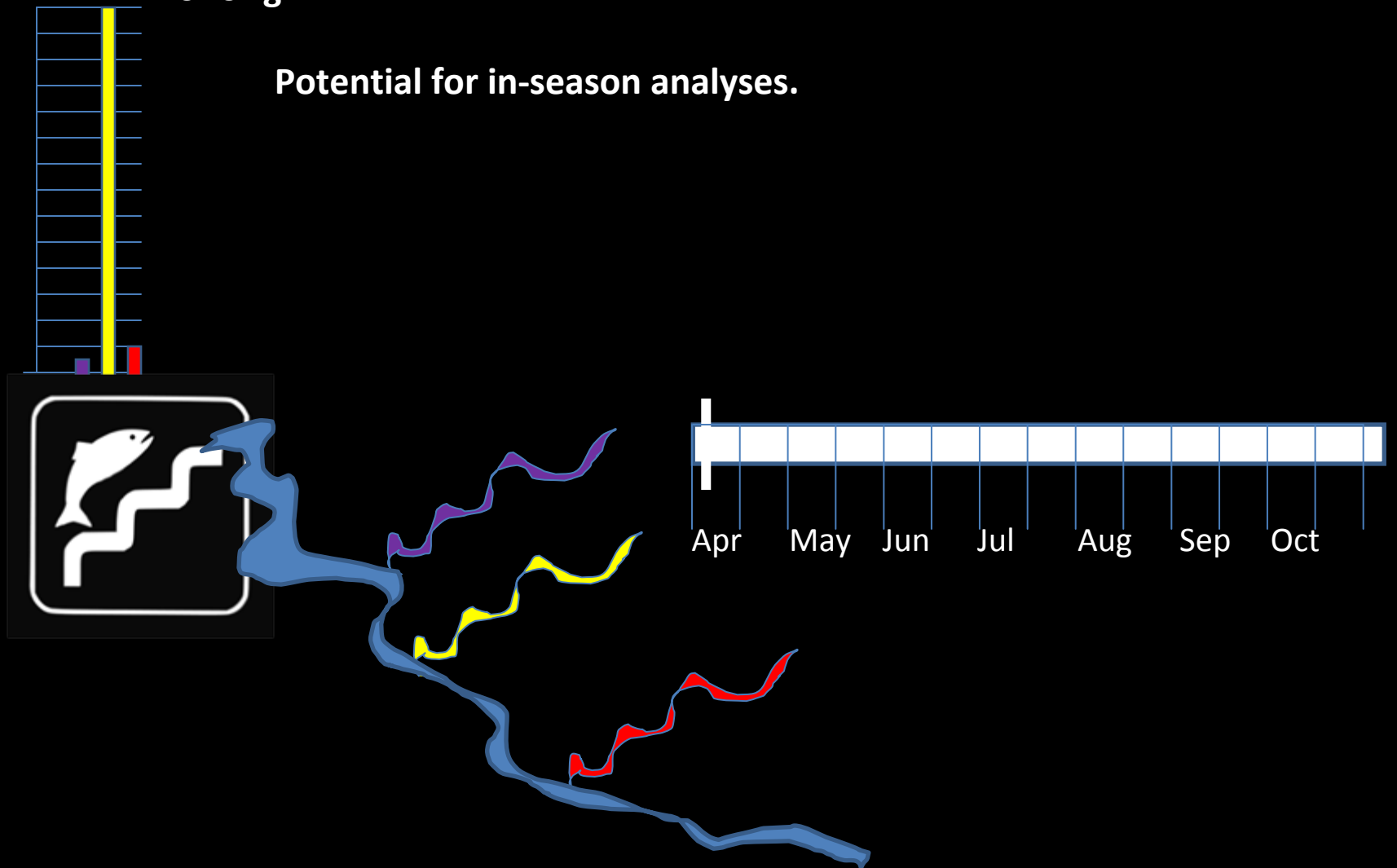


Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

Conduct analyses of this information to match unknown fish with its likely stream of origin.

Potential for in-season analyses.

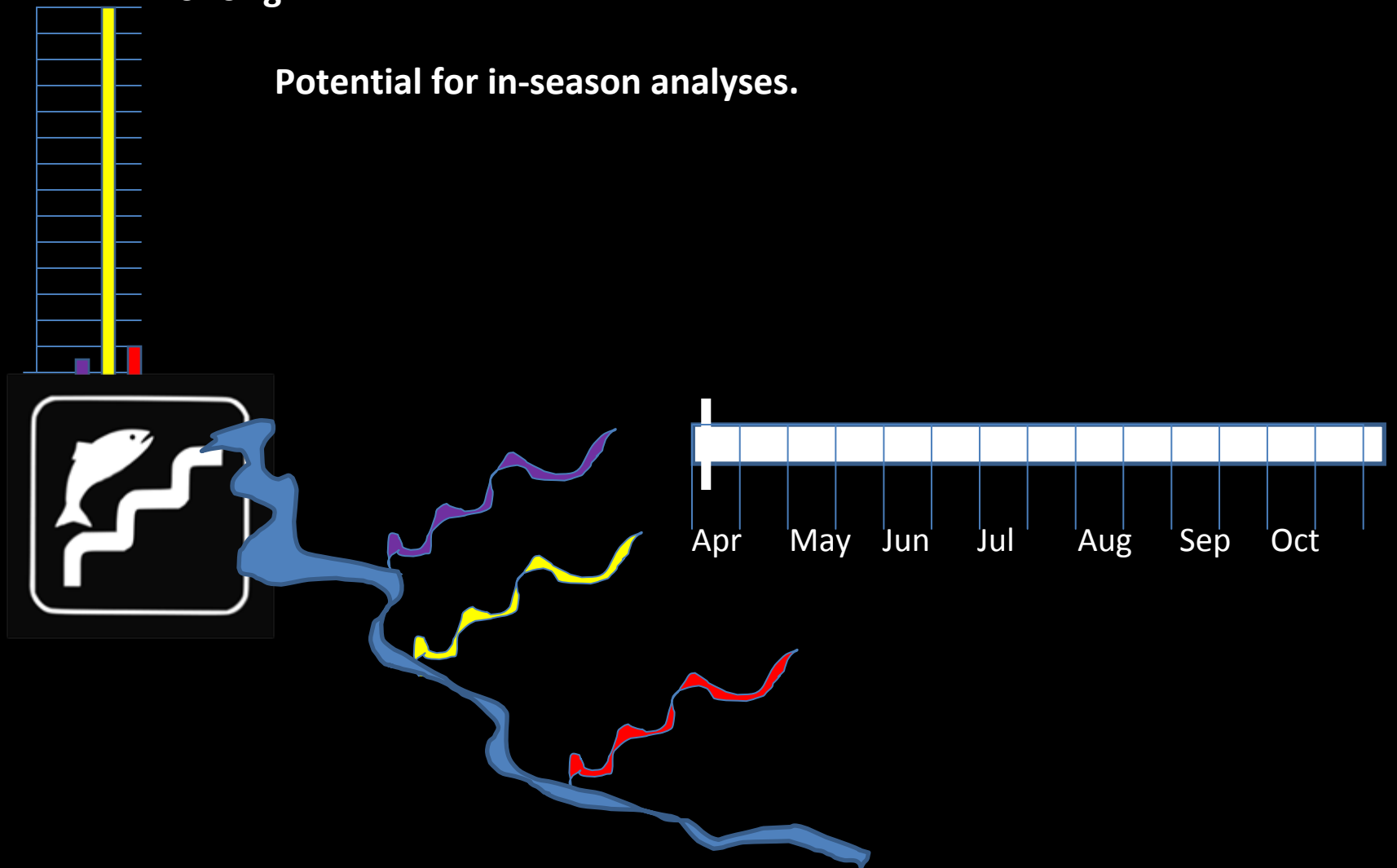


Collect baseline genetic information on streams throughout Columbia River

Collect genetic information on the unknown mixture of fish

Conduct analyses of this information to match unknown fish with its likely stream of origin.

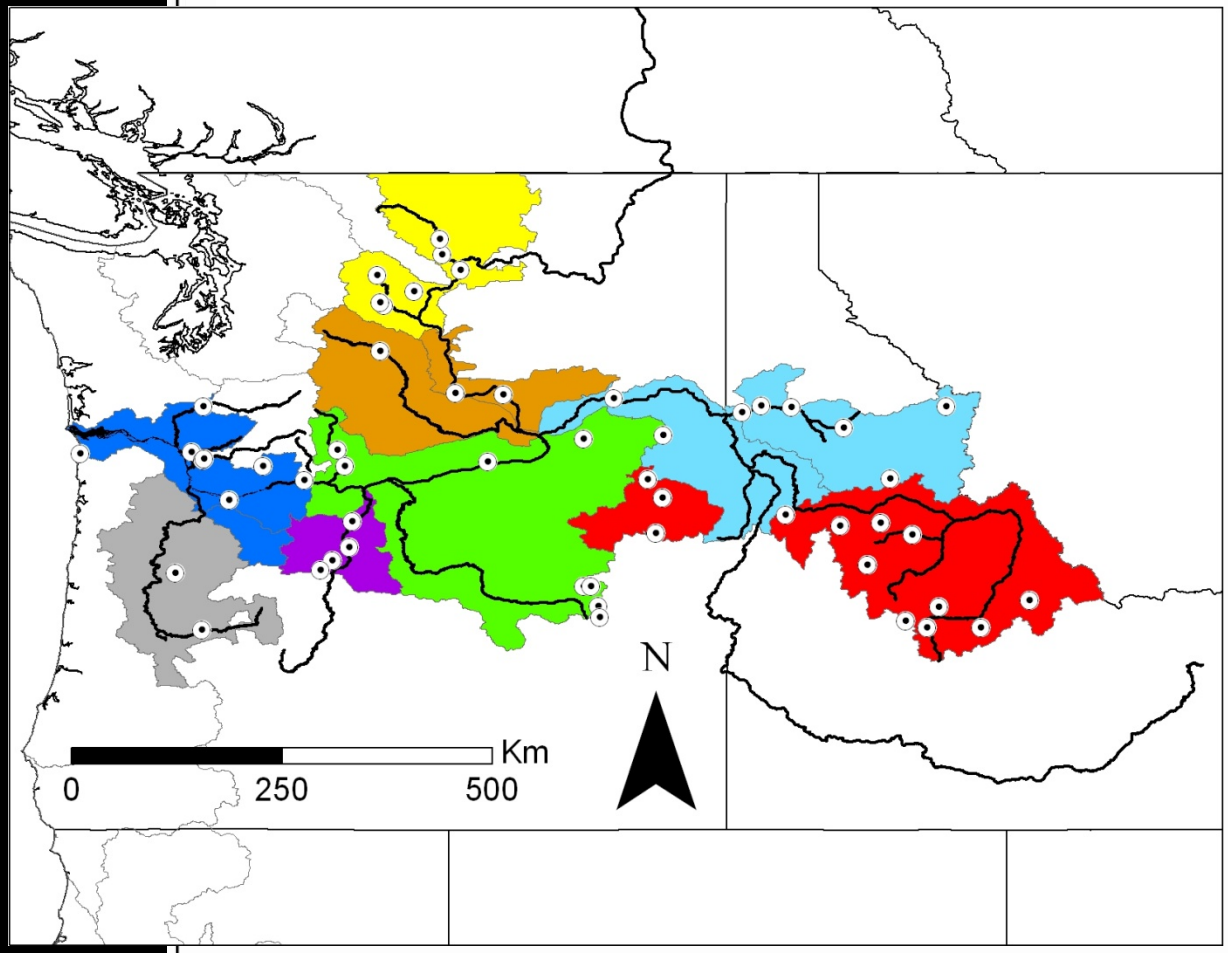
Potential for in-season analyses.



Bonneville Chinook weekly stock composition from 2004-2006

A Real Example of Genetic Stock Identification Results

Bonneville Chinook weekly stock composition from 2004-2006



Columbia River Stocks

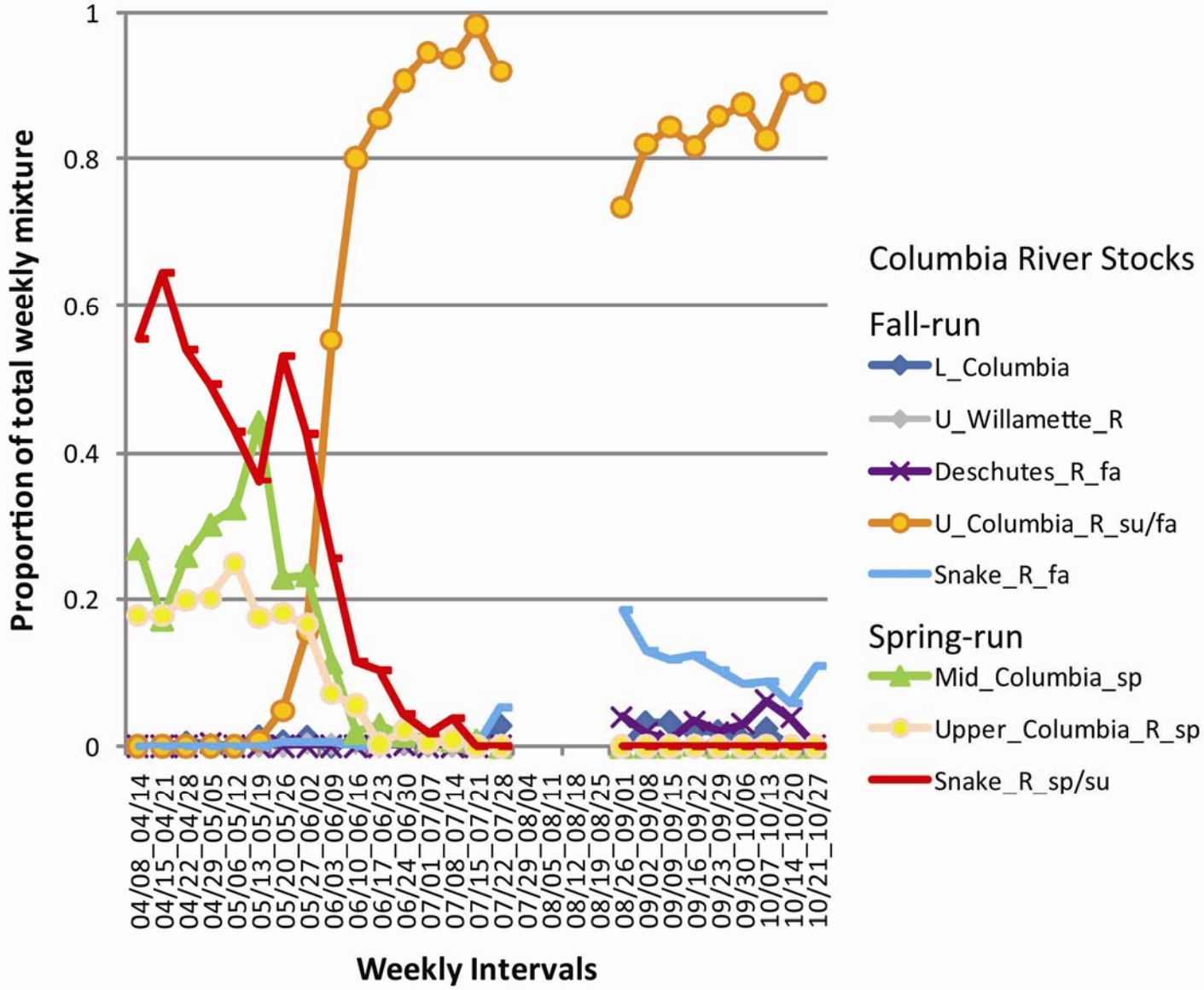
Fall-run

- L_Columbia
- U_Willamette_R
- Deschutes_R_fa
- U_Columbia_R_su/fa
- Snake_R_fa

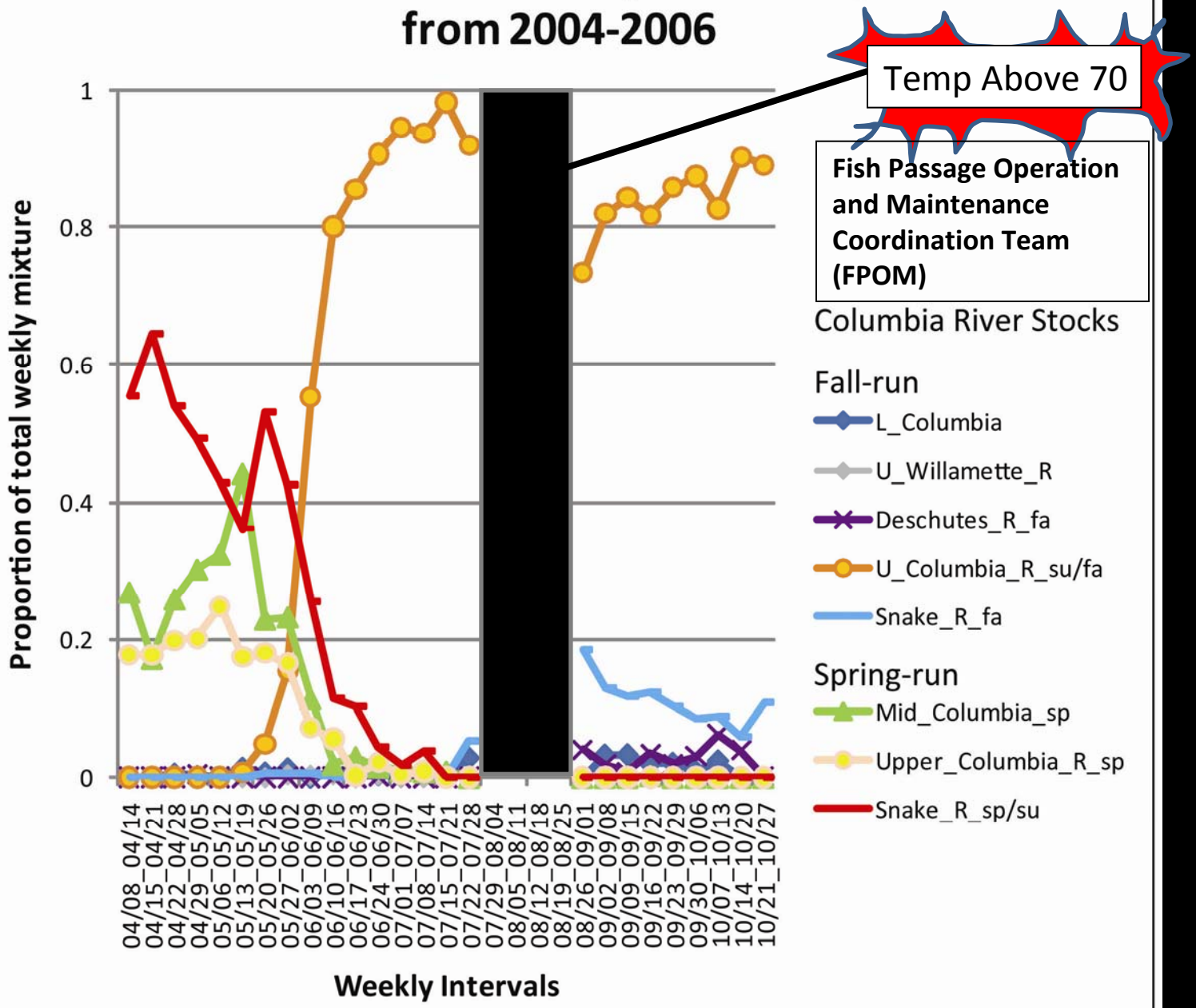
Spring-run

- Mid_Columbia_sp
- Upper_Columbia_R_sp
- Snake_R_sp/su

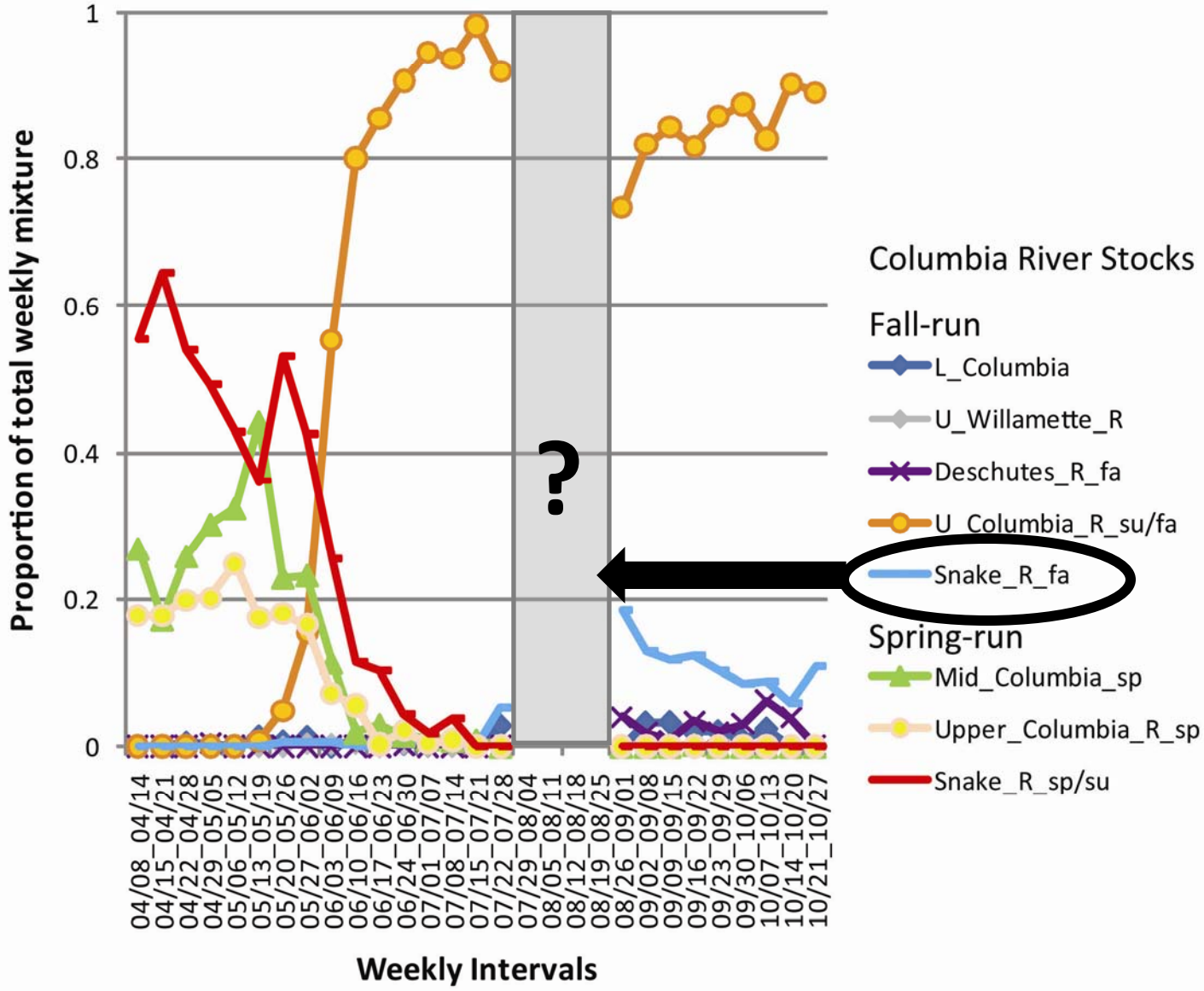
Bonneville Chinook weekly stock composition from 2004-2006



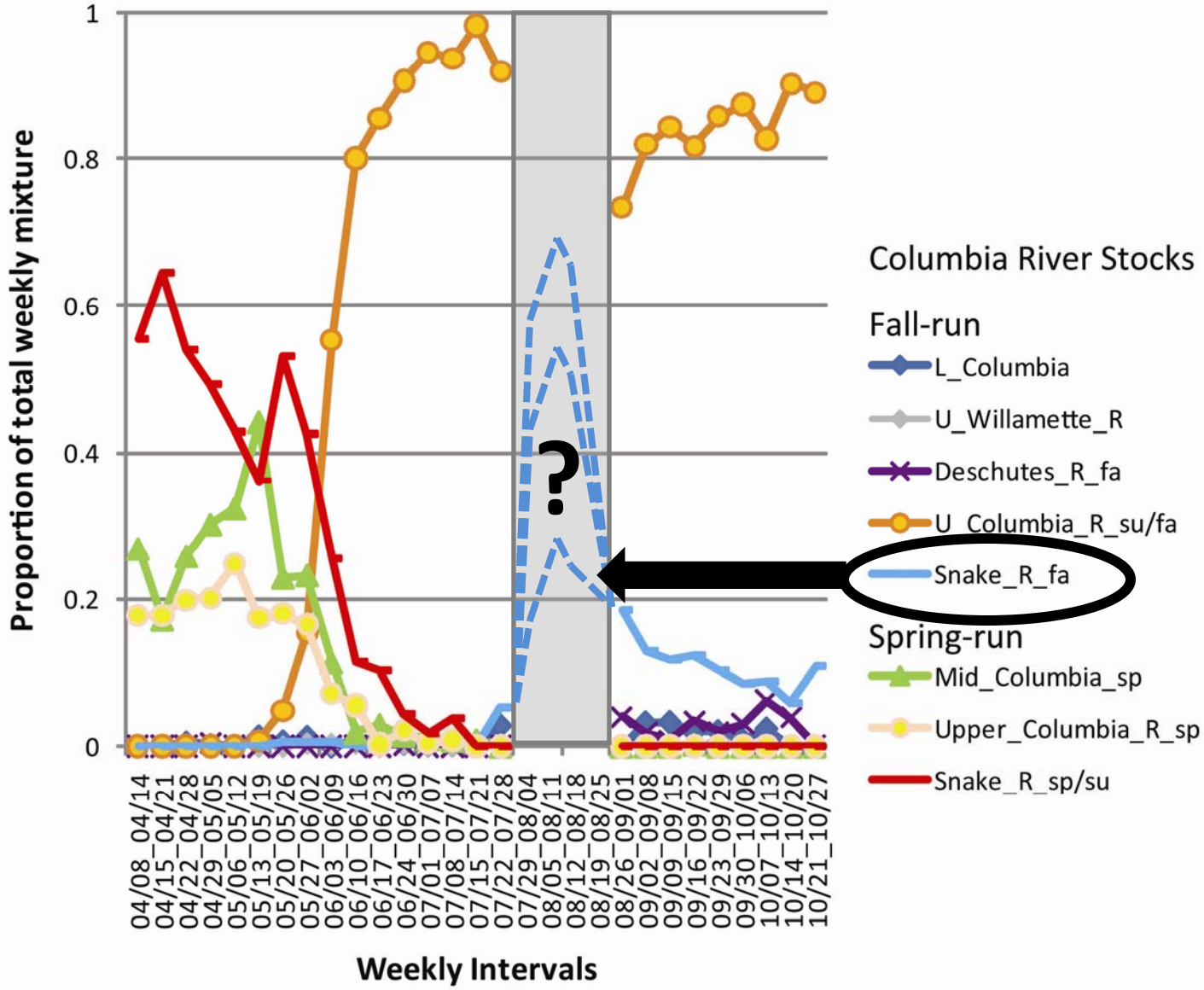
Bonneville Chinook weekly stock composition from 2004-2006



Bonneville Chinook weekly stock composition from 2004-2006



Bonneville Chinook weekly stock composition from 2004-2006



Acknowledgements

CRITFC Staff
Shawn Narum
Andrew Matala
Nate Campbell
Vanessa Jacobson
Amanda Matala
Lori Maxwell
Jeff Stephenson
Bobby Begay
John Whiteaker

Samplers
Yakama Nation
Oregon Department of Fish and Wildlife
Washington Department of Fish and Wildlife

Funding
Bonneville Power

Collaborative Center for Applied Fish Science
Hagerman, Idaho

Use of genetic data to estimate salmonid stock composition and migration patterns:

IDFG's goals and direction for Genetic Stock Identification and Parentage Based Tagging

Matthew Campbell
Idaho Department of Fish and Game, Eagle Fish Genetics Lab

NWPCC Committee and Council Meetings
October 7-8, 2009
Sun Valley, Idaho

Northwest Power and Conservation Council

IDFG is actively pursuing two different (but related) genetic technologies for managing and conserving wild and hatchery steelhead and salmon populations in the Snake River basin:

1. Genetic Stock Identification

2. Parentage Based Tagging

Department goals:

- Address genetic needs outlined in subbasin management plans and RPAs in the BiOp
- Ensure that our genetic programs are collaborative and 100% complimentary to existing/on-going genetic efforts in the Columbia River basin (CRITFC and NOAA)
- REQUIRES USING SAME GENETIC MARKERS!!!

Genetic Stock Identification

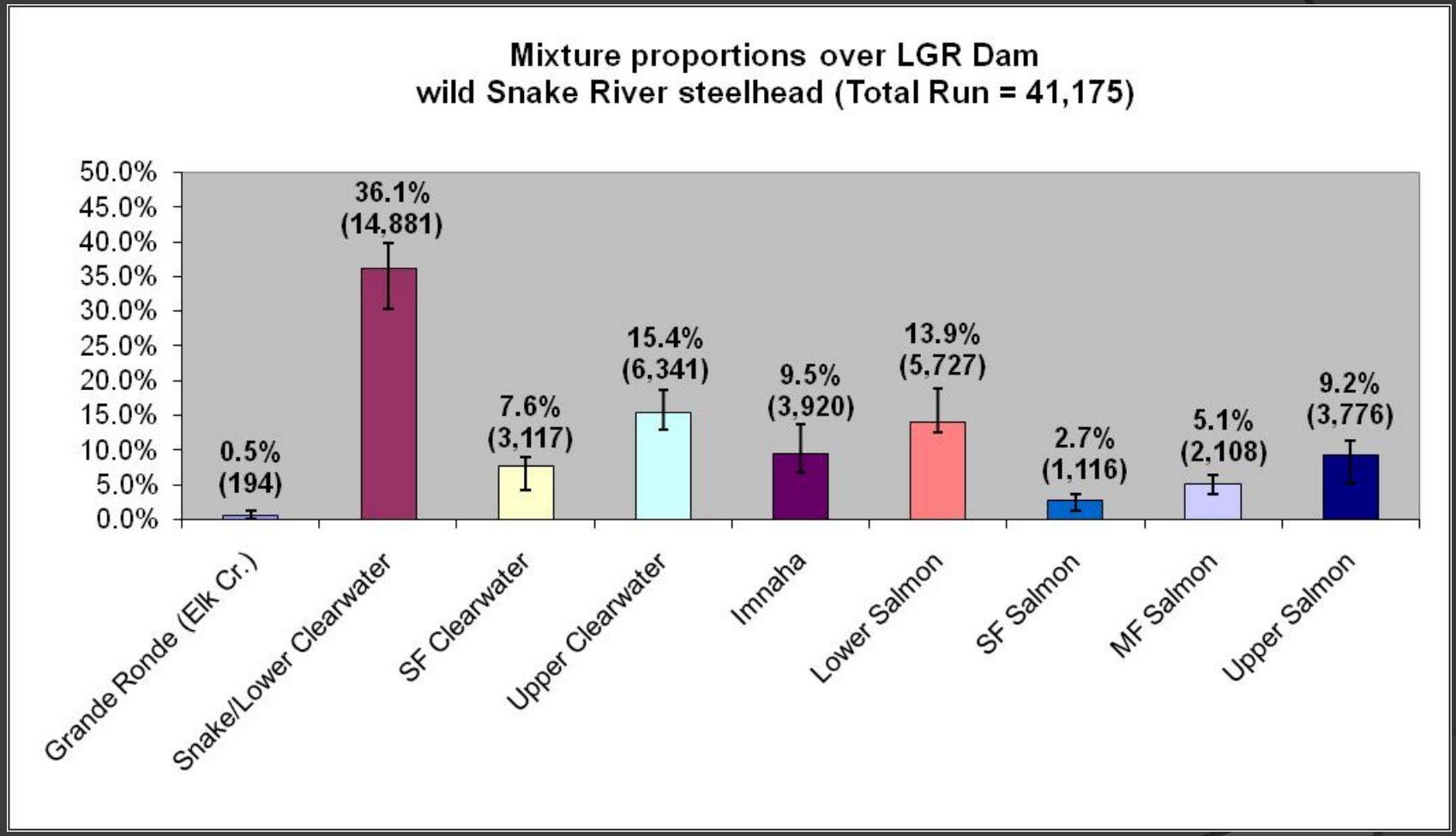
GSI

GSI

- 2008- collaborative project with CRITFC and NOAA using MICROSATELLITES
- IDFG used GSI procedures to identify the stock composition of wild adult steelhead passing Lower Granite Dam

Northwest Fisheries Science Center

Total Run



Number of adult steelhead returning over LGR Dam varies among stocks
Some basins are producing a lot of returning adults, others much less

GSI

- Why are we excited about these results?

- ✓ First time that wild Snake River steelhead abundance over LGR has been estimated at the stock/population level

- ✓ Estimates not previously available in Idaho for steelhead
  - ✓ Can't count redds
  - ✓ Can't operate weirs

- ✓ These results suggest that this approach could greatly assist managers in estimating stock specific Viable Salmonid Population parameters (Abundance, population productivity, spatial structure and diversity)

GSI

What's next???

•IDFG is seeking additional funds to transition from microsatellites to SNP markers and complete SNP baselines for Snake River steelhead and Chinook. Why?

✓Cheaper
✓More efficient
✓May provide better resolution
✓Allows collaboration with CRITFC on Columbia River basin GSI efforts

•Continue yearly GSI work at Lower Granite Dam for both adults and juveniles

✓For both steelhead and Chinook

•Maintain SNP baselines for both species in the future

Parentage Based Tagging

PBT

PBT

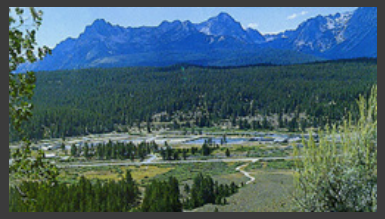
- Parentage-based genetic tagging, formerly called full parental genotyping, was proposed as a more powerful, more efficient, and cheaper method of mass marking hatchery steelhead and salmon (Anderson and Garza 2005)

PBT

Parentage-based tagging (PBT) involves the annual genotyping of all broodstock at each hatchery of interest, creating a parental genotype database

Lookinglass

Wallowa



Sawtooth

Oxbow

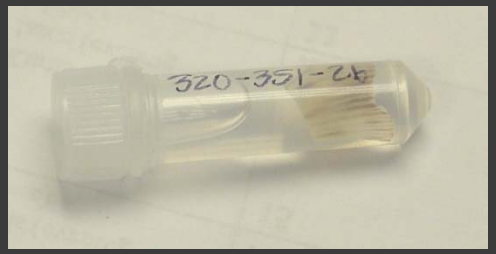
Pahsimeroi

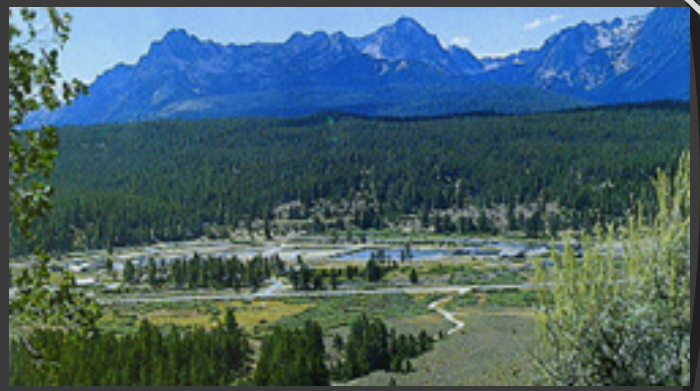
Dworshak/Clearwater

		PIT T	Other info	103-1	103-2	111-1	111-2	112-1	112-2	114-1	114-2	104-1	104-2	108-1	108-2	115-1	115-2
BY08	M	3D9.1BF11A9FCC	219-220-119	200	204	286	294	134	168	247	255	169	181	206	206	189	193
BY08	M	3D9.1BF11AA0B1	219-220-091	196	196	286	306	134	184	247	267	165	181	206	210	185	197
BY08	F	3D9.1BF11AA0D7	219-220-043	196	204	294	298	184	188	247	247	165	181	210	218	193	197
BY08	M	3D9.1BF11AA0F7	219-220-053	204	240	286	298	168	176	247	251	165	177	202	206	185	189
BY08	M	3D9.1BF11AA3F2	219-220-117	188	220	294	298	134	184	251	263	165	173	202	210	185	197
BY08	F	3D9.1BF11AA41C	219-220-284	224	312	234	234	134	184	255	267	165	165	194	210	185	193
BY08	M	3D9.1BF11AA68E	219-220-050	196	224	234	242	134	184	255	267	165	177	202	210	185	189
BY08	M	3D9.1BF11AA7B9	219-220-297	204	232	294	298	176	184	247	267	165	165	210	210	189	193
BY08	M	3D9.1BF11AABB9	219-220-270	220	224	234	294	184	188	247	255	177	181	210	210	189	193
BY08	M	3D9.1BF11AAC0E	219-220-200	196	216	234	294	134	168	255	255	165	165	206	206	193	201
BY08	M	3D9.1BF11AAC2F	219-220-138	188	196	242	298	134	134	255	255	234	294	202	202	234	294
BY08	F	3D9.1BF11AAC55	219-220-071	196	216	234	294	180	188	247	255	181	181	206	206	189	197
BY08	F	3D9.1BF11AAD25	219-220-067	192	312	230	298	134	176	251	255	181	181	202	210	197	197
BY08	M	3D9.1BF11AAD29	219-220-116	196	312	234	306	134	184	239	247	165	177	210	210	189	189
BY08	F	3D9.1BF11AAE26	219-220-333	196	220	242	294	184	184	251	267	165	165	210	210	189	197
BY08	M	3D9.1BF11AAEEC	219-220-314	220	236	298	298	134	134	247	267	165	181	202	210	189	201
BY08	M	3D9.1BF11AB010	219-220-190	196	312	234	294	134	184	255	255	165	177	210	210	189	193
BY08	M	3D9.1BF11AB223	219-220-278	200	204	286	294	134	184	247	251	165	169	202	206	185	193
BY08	F	3D9.1BF11AB341	219-220-185	196	200	234	294	134	134	255	255	165	177	206	206	185	189
BY08	M	3D9.1BF11AB3BE	219-220-229	204	212	294	294	176	180	255	255	177	181	206	210	189	201
BY08	F	3D9.1BF11AB537	219-220-017	220	232	234	298	134	184	234	294	173	181	202	210	185	197
BY08	F	3D9.1BF11AB62A	219-220-124	208	212	298	306	234	294	247	255	177	181	198	210	185	189
BY08	F	3D9.1BF11AB62D	219-220-318	196	224	234	306	234	294	255	271	165	185	210	210	234	294
BY08	M	3D9.1BF11AB631	219-220-224	188	312	234	298	134	188	255	255	165	173	202	206	189	197
BY08	M	3D9.1BF11ABA6B	219-220-259	220	312	234	298	134	134	251	255	165	165	202	210	189	189
BY08	M	3D9.1BF11ABB19	219-220-058	196	312	234	242	134	188	255	263	177	177	206	206	193	197
BY08	M	3D9.1BF11AC253	219-220-120	212	232	294	306	134	134	247	251	165	165	210	210	189	201
BY08	M	3D9.1BF11AC255	219-220-052	196	196	286	294	134	180	251	255	165	197	210	210	189	197
BY08	M	3D9.1BF11AC295	219-220-261	196	204	294	298	134	188	247	255	165	181	194	210	197	197
BY08	F	3D9.1BF11AC2E9	219-220-300	196	204	298	306	134	184	267	267	165	177	202	206	189	201
BY08	F	3D9.1BF11AC31B	219-220-042	204	220	294	298	134	180	234	234	294	181	206	210	197	197
BY08	M	3D9.1BF11AC323	219-220-004	196	204	234	298	134	134	255	263	165	181	206	210	189	197
BY08	F	3D9.1BF11AC32F	219-220-165	224	228	226	234	188	188	251	255	177	181	194	214	193	197
BY08	M	3D9.1BF11AC345	219-220-219	204	232	226	298	176	188	255	255	181	185	210	210	189	197
BY08	F	3D9.1BF11AC428	219-220-294	204	232	226	298	176	188	255	255	181	185	210	210	189	197
BY08	M	3D9.1BF11AC4A0	219-220-204	204	220	298	298	134	134	255	255	165	181	210	210	189	189
BY08	F	3D9.1BF11AC4CF	219-220-287	204	232	226	298	176	188	255	255	181	185	210	210	189	197

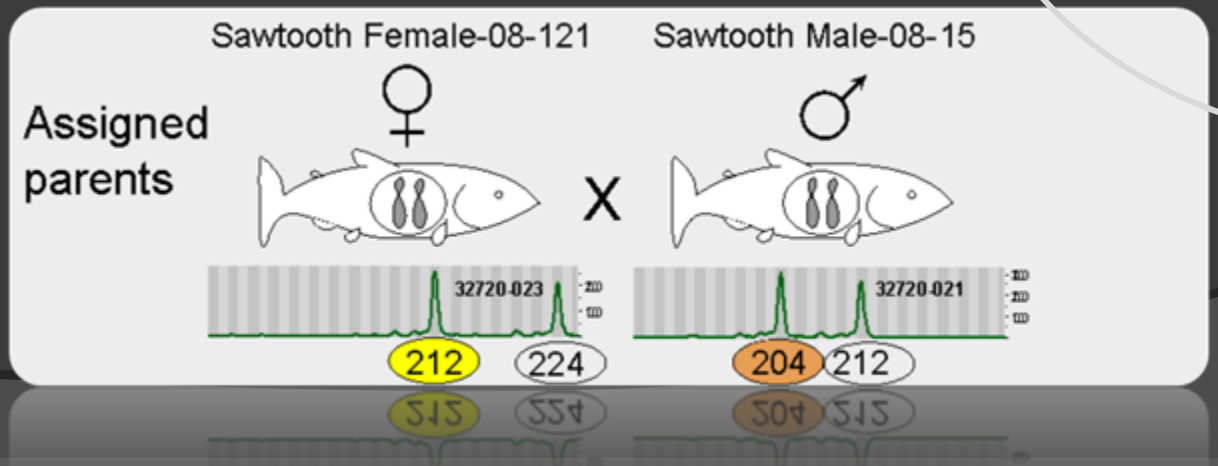
PBT

Progeny from any of these parents (either collected as juveniles or returning adults), if genotyped, could be assigned back to their parents, thus identifying the hatchery they originated from and exact brood year they were produced in





Sawtooth BY2008

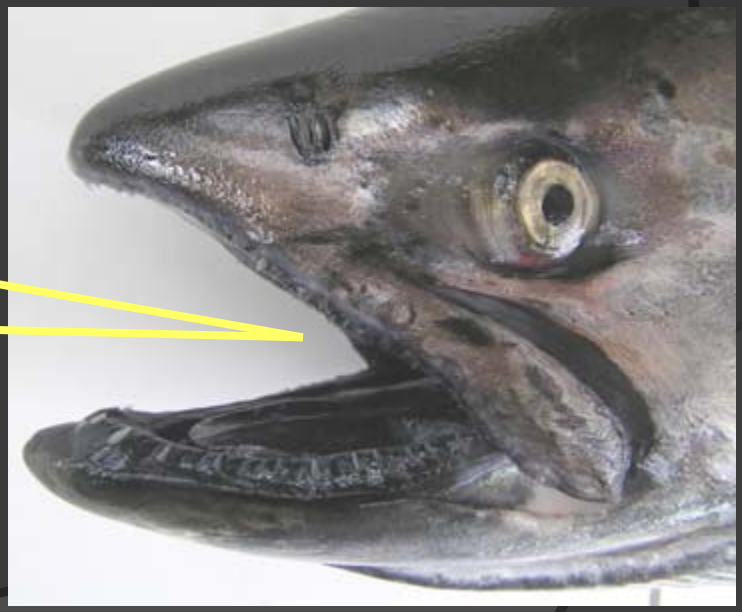


PBT

•Essentially this technology is very similar to human parentage analyses (i.e. “who’s the father?”)

•The exceptional advantage PBT has over other tagging technologies is increased sample size. By genotyping all parental broodstock, every juvenile is “tagged”

Who’s your daddy?



•*Any* hatchery steelhead encountered in the Snake River basin (juvenile or adult) could be sampled, genotyped and its sex, exact age, and stock of origin could be determined

•If you followed parental groups to release site then you would also know exactly when and where fish were released

PBT

Why are we excited about this technology?

•Could be a much more efficient and cost-effective tool than CWTs in Idaho's fisheries to know when and where specific hatchery stocks are being caught (everything is marked)

•Could be used to address needs in multiple "Reasonable and Prudent Alternatives" (RPA) in the BiOp:

- ✓RPA No. 41, Preserve genetic resources
- ✓RPA No. 50, Fish population status monitoring
- ✓RPA No. 53, Monitor adult salmonids passing through FCRPS
- ✓RPA No. 62, Fund selected harvest investigations
- ✓RPA No. 63, Monitor hatchery effectiveness
- ✓RPA no. 64, Investigate hatchery critical uncertainties (i.e., Estimate relative reproductive success with genetic markers)

PBT

Will it work? Anderson and Garza (2005) was theoretical modeling

In 2008, a collaborative pilot study by IDFG and CRITFC demonstrated that both microsatellite markers (17) and SNP markers (96) could accurately assign known juveniles from 5 Snake River hatchery stocks back to their stock of origin

Hatchery Stock	Juveniles Genotyped	Juveniles Assigned	# assigned correctly to stock	% assigned correctly to stock	# matching cross spawn records	% matching spawn cross records
Squaw	92	92	92	100.0%	N/A	N/A
Sawtooth	93	91	91	100.0%	85	93.4%
Dworshak	93	93	93	100.0%	93	100.0%
EF Salmon	93	85	85	100.0%	N/A	N/A
Pahsimeroi	93	93	93	100.0%	N/A	N/A

1 rearing hatchery: Magic Valley

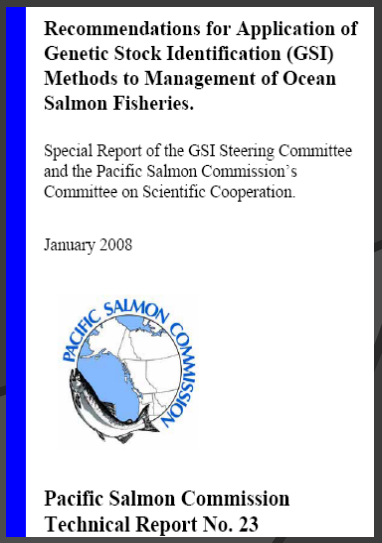
PBT

What is needed next?

- While a potentially powerful tool for marking hatchery stocks, conducting hatchery evaluations and reform, and enforcing salmonid fishery management measures, it still needs to be empirically tested and validated on a large-scale (Includes evaluations of costs and sampling requirements)

- These types of evaluations have been directly called for by:
- ISRP
- ISAB
- Pacific Salmon Commission

Recommendation 11:
Two or more independent assessments of the (large scale) application of Parentage-Based Tagging (PBT) should be undertaken….



PBT

The plan:

State, tribal and federal agencies in the Snake River basin are uniquely positioned to perform proof of concept PBT studies for both steelhead and Chinook:

•All hatchery steelhead and Chinook broodstock spawned in the Snake River for the past two years have been sampled (WA, OR, and ID)

•Sets of 96 SNPs have been recently development for both species

•There are sampling programs in place at Bonneville Dam, at Lower Granite Dam, in tribal and non-tribal fisheries in the mainstem Columbia River and in the Snake River basin, to sample returning hatchery adults (CRITFC and IDFG)

PBT

The plan:

IDFG is seeking funding to create the first PBT parental genetic baselines for Snake River hatchery steelhead and Chinook salmon

•This project would effectively, permanently genetically mark ~12 million smolts, per species, per year

•Any Snake River hatchery adults sampled and genotyped by CRITFC at Bonneville Dam and in main-stem fisheries could be assigned to the parental baseline identifying their stock of origin and age

GSI and PBT

Conclusion:

Continued collaborative projects between IDFG and CRITFC (and other NW agencies/labs), using a standardized set of genetic markers (SNPs), will provide unprecedented tools for managing wild and hatchery stocks in the Columbia River basin

- GSI will segregate adult wild runs by stock
- PBT will be used to identify stock and age of sampled hatchery fish

Questions???

Acknowledgements:

Lab:
- Christine Kozfkay
- Amanda Boone
- Kelly Heindel
- Eric Tretter
- Lynn Schrader

Field:
- IDFG hatchery staff
- ODFW
- WDFW
- NPT
- SBT

Funding:
- BPA
- LSRCP/BPA
- Idaho Power