# Tools to Assess Hatchery Performance and Manage Conservation Based Hatchery Programs

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Tool Bag- Marking and Tagging

- **Adipose Fin Clip (AD-clip)**
  - Generic visual ID of hatchery origin
  - High mark rates
- **Coded Wire Tag (CWT)**
  - Group specific information
  - Electronic detection.
  - Lethal sampling to read tag
- **Passive Integrated Transponder (PIT)**
  - Individual specific information
  - Real time detection
  - Non-lethal sampling to read tag
  - Increasing number of remote detection sites
- **Genetic "Tags" (PBT and GSI)**
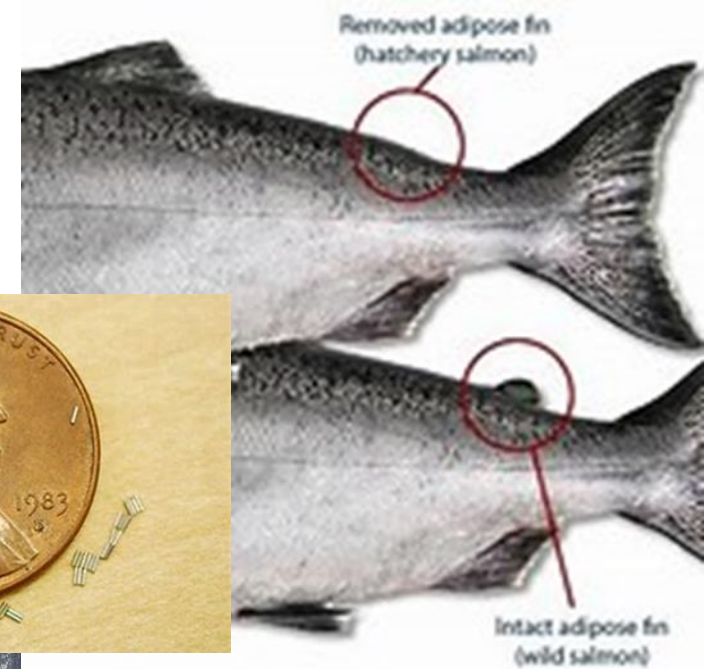
Assessing Risk Associated with Hatchery Programs

- **Hatchery adults on spawning grounds**
- **Genetic Diversity and Differentiation**
- **Hatchery Broodstock Management**
- **Reproductive Success**

Assessing Risk Associated with Hatchery Programs

Spring Chinook Salmon- (AD-clip CWT)

Percent of adults spawning in the wild that are hatchery origin 2005-2019

- Middle Fork managed as wild fish sanctuary

- Some areas managed for hatchery influence with supplementation as an objective

- To mitigate risk, some hatchery broodstocks are integrated with the natural population

Major Population Group	Population	Direct Hatchery Releases	Carcasses Recovered	Percent Hatchery Origin
Middle Fork Salmon River	Bear Valley Creek	No	2,393	0.4
	Big Creek	No	266	0.8
	Camas Creek	No	95	1.1
	Chamberlain Creek	No	450	0.7
	Loon Creek	No	82	2.4
	Marsh Creek	No	1,692	0.7
	MFSR below Indian Creek	No	18	11.1
	Sulphur Creek	No	273	0.7
Upper Salmon River	North Fork Salmon River	No	177	1.1
	Panther Creek	No	329	0.6
	Lemhi River	No	701	1.1
	Pahsimeroi River	Yes	512	25.2
	East Fork Salmon River	No	790	0.4
	Yankee Fork	Yes	759	71.3
	Valley Creek	No	339	4.7
	Salmon R below Redfish Lake	No	204	28.9
	Salmon R above Redfish Lake	Yes	4,911	45.0

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Assessing Risk Associated with Hatchery Programs

STRAYING- Summer Steelhead (PIT Tags)

- Spawning ground surveys are not feasible due to high flows and turbid water in the spring.

Juvenile Release Location	Number of PIT tags detected at LGD	Number of PITs Detected as a Stray	Percent of PITs Detected as Strays at Tributary Arrays
South Fork Clearwater River	1,275	1	**0.08%**
North Fork Clearwater	1,270	4	**0.31%**
Hells Canyon	768	0	**0.00%**
Little Salmon River	1,422	4	**0.28%**
Pahsimeroi Hatchery	1,440	11	**0.76%**
Sawtooth Hatchery	1,578	9	**0.57%**
East Fork Salmon River	312	2	**0.64%**
Yankee Fork	397	6	**1.51%**
Total	**8,462**	**37**	**0.44%**

Matt Campbell

Genetic Tools Used to Assess Hatchery Programs

Parentage-based genetic tagging - PBT
(Hatchery Fish)

- Genetic-based fish tagging method that involves genotyping hatchery broodstock

- By genetically sampling the parents, all offspring are genetically "tagged"

- 'Tag' recovery is non-lethal, and possible at all life stages
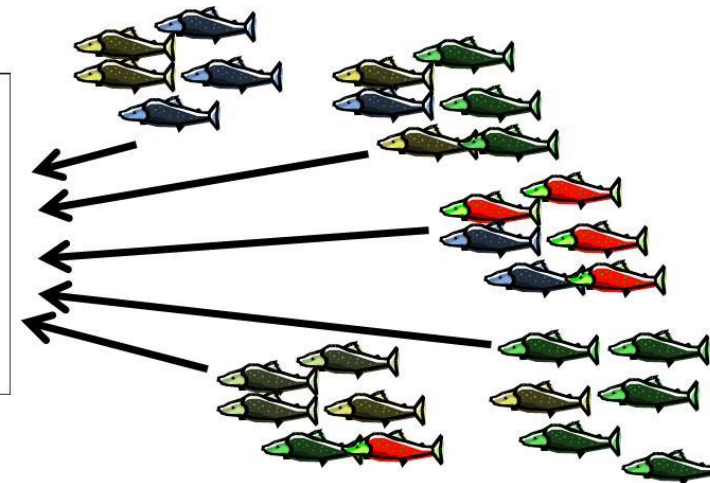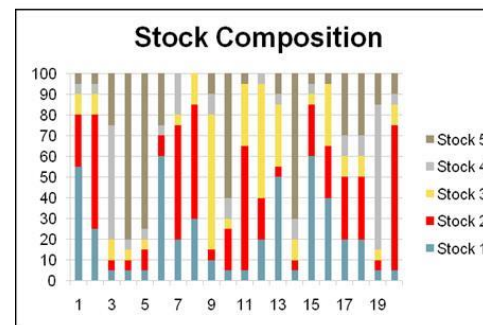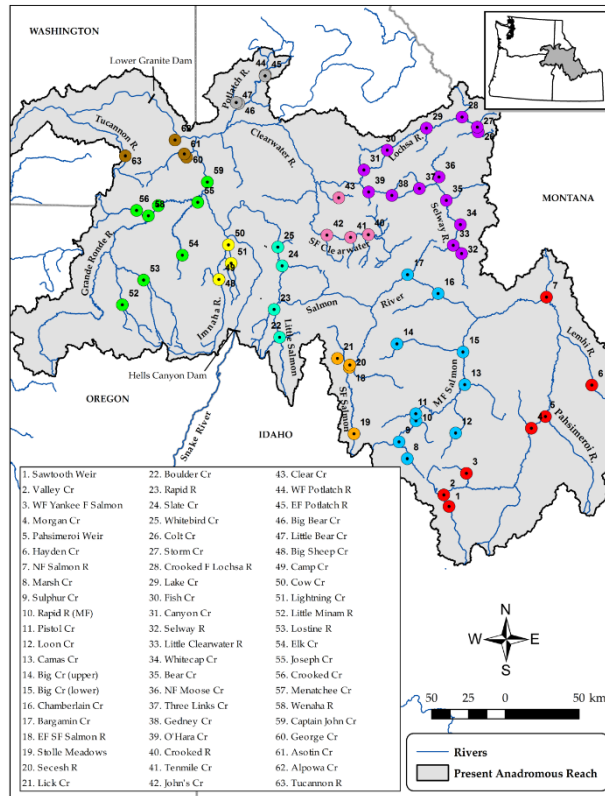
2 = 6,000!!!!

Genetic Tags

Genetic Stock Identification- GSI
(Wild fish)

- Uses genetic profiles from all contributing wild populations to identify the stock of origin of any unknown fish

1. Sawtooth Weir	22. Boulder Cr	43. Clear Cr
2. Valley Cr	23. Rapid R	44. WF Potlatch R
3. WF Yankee F Salmon	24. Slate Cr	45. EF Potlatch R
4. Morgan Cr	25. Whitebird Cr	46. Big Bear Cr
5. Pahsimeroi Weir	26. Colt Cr	47. Little Bear Cr
6. Hayden Cr	27. Storm Cr	48. Big Sheep Cr
7. NF Salmon R	28. Crooked F Lochsa R	49. Camp Cr
8. Marsh Cr	29. Lake Cr	50. Cow Cr
9. Sulphur Cr	30. Fish Cr	51. Lightning Cr
10. Rapid R (MF)	31. Canyon Cr	52. Little Minam R
11. Pistol Cr	32. Selway R	53. Lostine R
12. Loon Cr	33. Little Clearwater R	54. Elk Cr
13. Camas Cr	34. Whitecap R	55. Joseph Cr
14. Big Cr (upper)	35. Bear Cr	56. Crooked Cr
15. Big Cr (lower)	36. NF Moose Cr	57. Menatchee Cr
16. Chamberlain Cr	37. Three Links Cr	58. Wenaha R
17. Bargamin Cr	38. Gedney Cr	59. Captain John Cr
18. EF SF Salmon R	39. O'Hara Cr	60. George Cr
19. Stolle Meadows	40. Crooked R	61. Asotin Cr
20. Secesh R	41. Tenmile Cr	62. Alpowa Cr
21. Lick Cr	42. John's Cr	63. Tucannon R

Genetic Tags for assessing and reducing risk

Examples of information to guide conservation:

- Rangewide monitoring of genetic diversity and differentiation between hatchery and wild populations

- Hatchery Broodstock Management

- Reproductive Success

Types of information:

Wild Population	Reporting Group	Avg. Pairwise F_{ST} Pahsimeroi H.
1. Saw tooth Weir	UPSALM	0.004
5. Pahsimeroi Weir	UPSALM	0.005
7. NF Salmon R	UPSALM	0.005
3. WF Yankee F Salmon	UPSALM	0.005
2. Valley Cr	UPSALM	0.006
6. Hayden Cr	UPSALM	0.007
61. Asotin Cr	LSNAKE	0.007
60. George Cr	LSNAKE	0.007
62. Alpowa Cr	LSNAKE	0.008
63. Tucannon R	LSNAKE	0.009
25. Whitebird Cr	LOSALM	0.010
24. Slate Cr	LOSALM	0.010
57. Menatchee Cr	GRROND	0.010
53. Crooked Cr	GRROND	0.011
4. Morgan Cr	UPSALM	0.011
46. Big Bear Cr	PTLTCH	0.011
52. Joseph Cr	GRROND	0.011
47. Little Bear Cr	PTLTCH	0.011
58. Wenaha R	GRROND	0.011
23. Rapid R	LOSALM	0.012
22. Boulder Cr	LOSALM	0.012
48. Big Sheep Cr	IMNAHA	0.012
50. Cow Cr	IMNAHA	0.012
59. Captain John Cr	GRROND	0.014
44. WF Potlatch R	PTLTCH	0.015
45. EF Potlatch R	PTLTCH	0.015
51. Lightning Cr	IMNAHA	0.015
16. Chamberlain Cr	MFSALM	0.015
56. Lostine R	GRROND	0.015
17. Bargamin Cr	MFSALM	0.016
49. Camp Cr	IMNAHA	0.017
55. Little Minam R	GRROND	0.018
13. Loon Cr	MFSALM	0.020
54. Elk Cr	GRROND	0.021
12. Camas Cr	MFSALM	0.022
39. O'Hara Cr	UPCLWR	0.022
15. Big Cr (lower)	MFSALM	0.023
19. Secesh R	SFSALM	0.024
43. John's Cr	SFCLWR	0.024
20. Lick Cr	SFSALM	0.025
36. NF Moose Cr	UPCLWR	0.026
38. Gedney Cr	UPCLWR	0.026
10. Rapid R (MF)	MFSALM	0.026
41. Crooked R	SFCLWR	0.026
40. Clear Cr	SFCLWR	0.027
18. EF SF Salmon R	SFSALM	0.027
30. Fish Cr	UPCLWR	0.027
31. Canyon Cr	UPCLWR	0.027
28. Crooked F Lochsa R	UPCLWR	0.028
9. Sulphur Cr	MFSALM	0.028
33. Little Clearwater R	UPCLWR	0.029
21. Stolle Meadows	SFSALM	0.029
14. Big Cr (upper)	MFSALM	0.029
8. Marsh Cr	MFSALM	0.030
26. Colt Cr	UPCLWR	0.031
34. Whitecap Cr	UPCLWR	0.031
11. Pistol Cr	MFSALM	0.032
35. Bear Cr	UPCLWR	0.033
32. Selway R	UPCLWR	0.033
27. Storm Cr	UPCLWR	0.033
42. Tenmile Cr	SFCLWR	0.033
37. Three Links Cr	UPCLWR	0.034
29. Lake Cr	UPCLWR	0.034

Increasing genetic differentiation →

- Rangewide monitoring of genetic diversity and differentiation between hatchery and wild populations
- Because hatchery and wild populations are genotyped with the same subset of SNP markers we can measure pairwise genetic differentiation between every hatchery stock against every genotyped wild population.

- Green = lower differentiation;
- Red = higher differentiation.

- Despite offsite releases of hatchery steelhead in the upper Salmon, most S.F. Salmon and M.F. Salmon populations exhibit significant differentiation from **Pahsimeroi Hatchery stock**

Types of information: Diversity Monitoring

Intensive Broodstock Management

Redfish Lake Sockeye Salmon: Maintain genetic diversity of founding population, avoid inbreeding (mating among relatives)

	F-01	F-02	F-03	F-04	F-05	F-06
M-01	0.13	0.11	0.32	0.27	0.28	0.24
M-02	0.20	0.33	0.25	0.23	0.24	0.09
M-03	0.15	0.17	0.29	0.11	0.25	0.21
M-04	0.20	0.13	0.14	0.15	0.40	0.22
M-05	0.30	0.10	0.13	0.25	0.34	0.27
M-06	0.10	0.11	0.13	0.34	0.23	0.20

% genes shared

Good!   Not as good!

Solution
- **Results allow prioritization of crosses to maximize genetic diversity and minimize inbreeding (spawning matrices)**
- **This tool was used for many years as the population was growing**
- **~95% of the original founding diversity maintained.**

Types of information: Diversity Monitoring
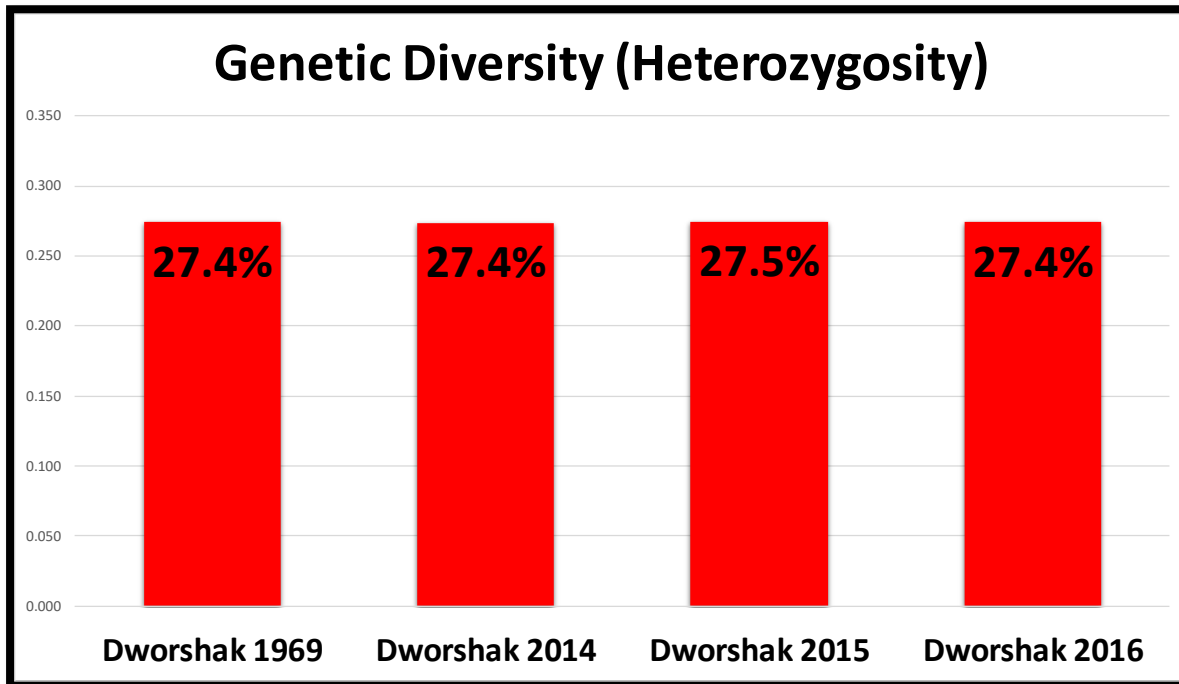
N.F. Clearwater

Dworshak B-Run Steelhead (1969 – Present)
Important hatchery stock:

B-run, contains diversity of wild N.F. Clearwater
1. Monitor genetic diversity over time
2. Demographic monitoring and heritability of traits

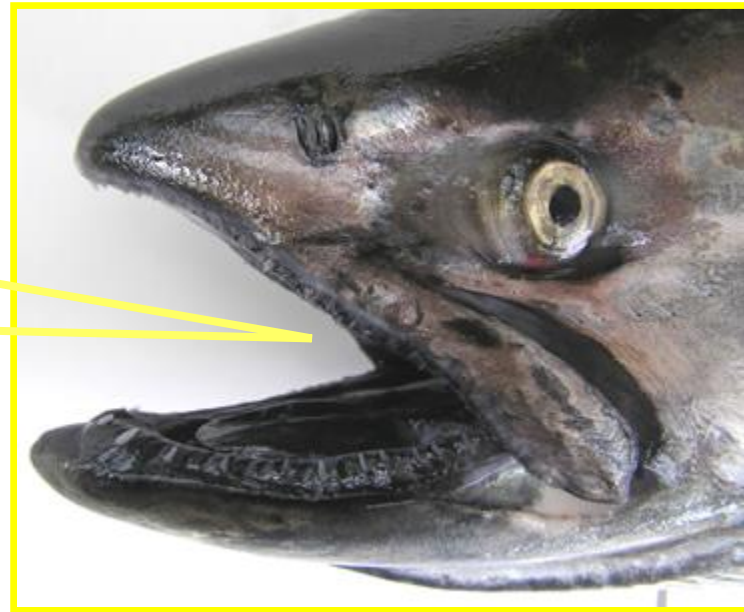**Genetic Diversity (Heterozygosity)**

	27.4%	27.4%	27.5%	27.4%
	Dworshak 1969	Dworshak 2014	Dworshak 2015	Dworshak 2016

No change in genetic diversity over time!!!-More intensive broodstock management may not be needed

Types of information:
Reproductive Success
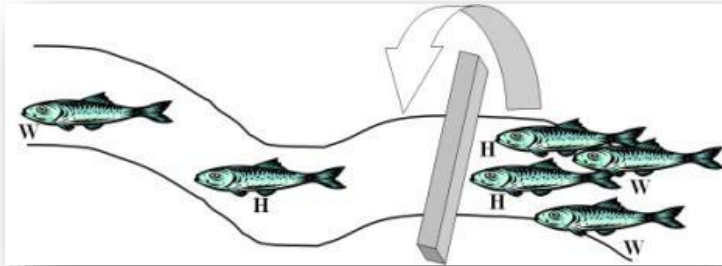
Hatchery versus Wild salmon

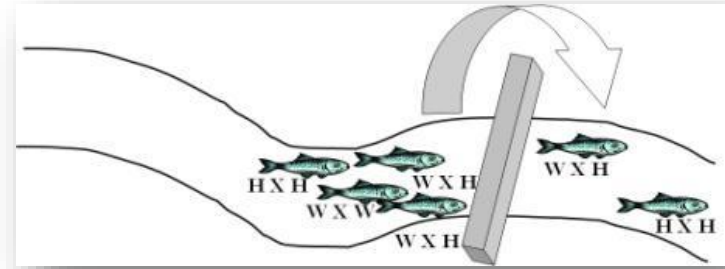**Who's your daddy?**

Problem

1. Concern that hatchery fish may not produce same number of offspring as wild fish

2. Difficult to measure relative contribution

Types of information:
Reproductive Success

Hatchery versus Wild salmon

Adults above

Juveniles below (or as adults on return)

Method

1. Genetically sample adult wild and hatchery fish released above a weir

2. Use parentage to evaluate reproductive success (juveniles and adult to adult)