

Applied Conservation Genetics At The Lahontan National Fish Hatchery Complex

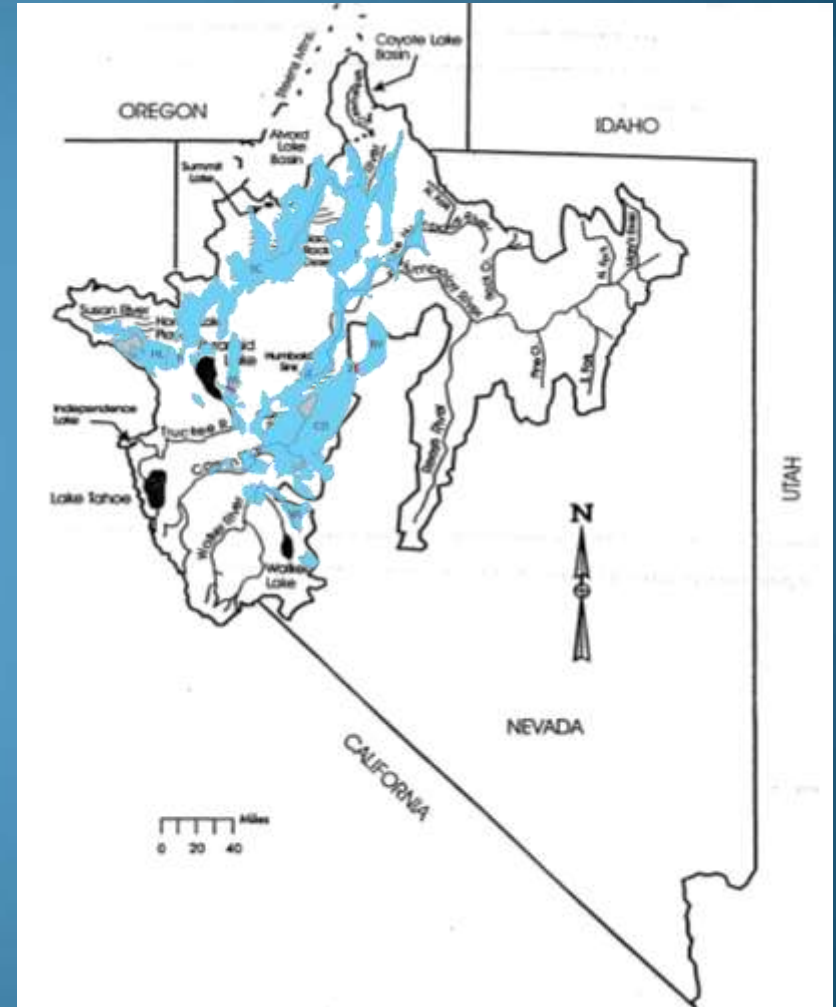


Corene Jones

Fish Biologist/Broodstock Coordinator, Lahontan National Fish Hatchery Complex

Lahontan Cutthroat Trout

- Evolved in Pleistocene Lake Lahontan
- Northwest, Humbolt and Western GMUs
- Pilot Peak strain = Lake Tahoe/Truckee River/Pyramid Lake Basin



Tahoe/Truckee/Pyramid LCT

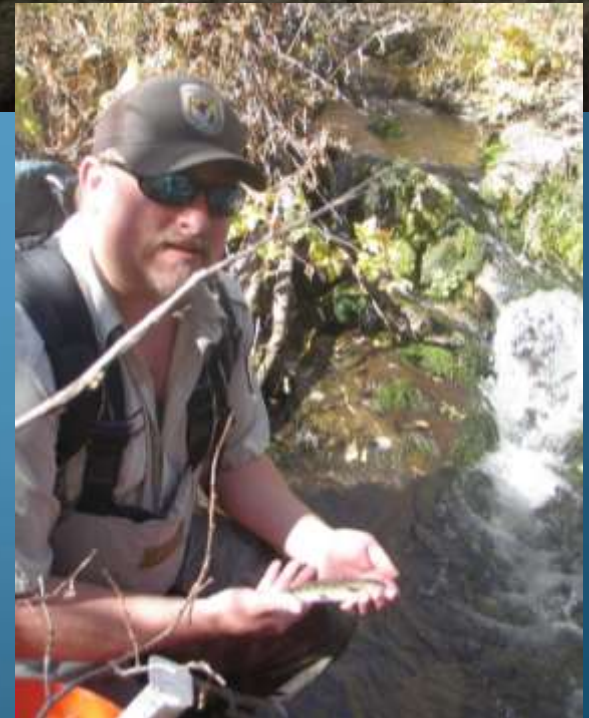
- Large, highly piscivorous
- Extirpated from native range by 1940's
- Rediscovered at Pilot Peak, NV in late 1970's
- Confirmed through genetic testing to be direct descendants



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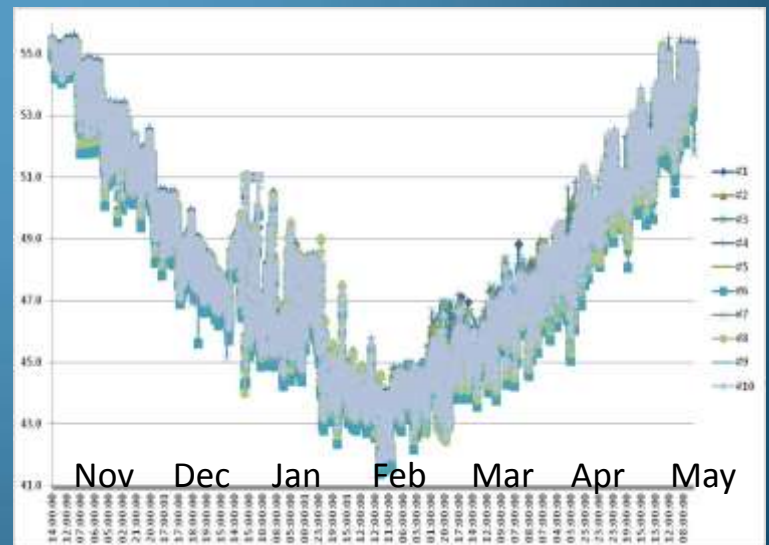
Pilot Peak Lahontan Cutthroat Trout

- Complex began propagating Pilot Peak strain in 1996
- Purpose: use native strain for recovery activities in high priority waters
- AND: provide native fish for recreational opportunities



Genetic Management

- Developed captive broodstock and genetic management techniques over 15 year period
- 2010 restructuring
- In partnership with UNR, developed intensive genetic management protocol



Broodstock Tracking with PIT Tags

- All broodstock on station at LNFH are PIT tagged
- Individual genetic profiles generated by UNR
- 14 nuclear microsatellite loci, 8-30 alleles



Optimizing Genetics During Spawning

- Genetic profiles used to pair individuals
- Pairwise mating matrix

Goal: maintain high levels of genetic variation in production fish as well as future broodstock



2017Matrix: Database (Access 2007 - 2010) - Microsoft Access

File Home Create External Data Database Tools Fields Table

View Paste Cut Copy Format Painter Filter Ascending Descending Selection Advanced Refresh All New Save Totals Spelling Find Replace Go To Select Text Formatting

All Tables

tblSimilarity_Matrix

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Datasheet View

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Spawning Protocol

- P4 tag entry/tracking software
- Sort, scan and record spawning condition
- Pair ripe individuals according to genetic criteria



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tblSimilarity_Matrix

tblSimilarity_Matrix : Table

NoMAmeetingCriteriaPerFE

qry1FindMatches2016

qry4DefineGroups2016

qryFindSimValue

qryNumberMAperFE

tblHeterozygosity

tblHeterozygosity : Table

qry1FindMatches2016

qry4DefineGroups2016

Female Sorting

Female Sorting : Table

qry1FindMatches2016

qry2MatchCount2016

qry4DefineGroups2016

Male Sorting

Male Sorting : Table

qry1FindMatches2016

tbl3matchcount

tbl3matchcount : Table

qry4DefineGroups2016

CrossesTake4and5

CrossesTake4and5 : Table

qryFindSimValue

Table1

Table1 : Table

tbl_PIT_tag_broodstock_all

tbl_PIT_tag_broodstock_all : T...

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first clear contents then copy and paste the results of qry2Match count into this table

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2017Matrix: Database (Access 2007 - 2010) - Microsoft Access

File Home Create External Data Database Tools

View Paste Copy Cut Filter Ascending Selection Descending Advanced Refresh New Save Totals Spelling Find Replace Go To Select Text Formatting

All Tables

- tblSimilarity_Matrix
- tblSimilarity_Matrix : Table
- NoMAmeetingCriteriaPerFE
- qry1FindMatches2016
- qry4DefineGroups2016
- qryFindSimValue
- qryNumberMAperFE
- tblHeterozygosity
- tblHeterozygosity : Table
- qry1FindMatches2016
- qry4DefineGroups2016
- Female Sorting
- Female Sorting : Table
- qry1FindMatches2016
- qry2MatchCount2016
- qry4DefineGroups2016
- Male Sorting
- Male Sorting : Table
- qry1FindMatches2016
- tbl3matchcount
- tbl3matchcount : Table
- qry4DefineGroups2016
- CrossesTake4and5
- CrossesTake4and5 : Table
- qryFindSimValue
- Table1
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- tbl_PIT_tag_broodstock_all
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qry4DefineGroups2016

ID	PIT Code	tblHeterozygosity.Hete	tblHeterozygos	maPIT	qry1FindMatches2016.f	qry1FindMa	simValue
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61	3D9.239F892609	0.615384615384615		3D6.000B96F5EE	0.615384615384615		0.384615385
62	3D9.239F88A986	0.666666666666667		3D9.239F88D02	0.769230769230769		0.375
63	3D9.1C2DB94FCB	0.538461538461538		3D9.239F8924C8	0.923076923076923		0.384615385
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68	3D6.000B969CFC	0.769230769230769		3D9.239F88A6C7	0.461538461538462		0.384615385
69	3D6.000B96F11B	0.846153846153846		384.1B796D8496	0.384615384615385		0.346153846
69	3D6.000B96F11B	0.846153846153846		3D9.1C2DB8D9C7	0.692307692307692		0.384615385
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70	3D9.1C2DB8CA61	0.461538461538462		3D9.239F88ACAC	0.8		0.4
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72	3D6.000B96F6A1	0.615384615384615		3D9.239F88ACAC	0.8		0.4
73	3D6.000B96F68A	0.615384615384615		384.1B796D8496	0.384615384615385		0.346153846
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73	3D6.000B96F68A	0.615384615384615		3D6.000B969C0C	0.615384615384615		0.384615385
74	384.1B796D82AF	0.692307692307692		3D6.000B969948	0.615384615384615		0.346153846
74	384.1B796D82AF	0.692307692307692		3D9.239F88ACC3	0.538461538461538		0.384615385
74	384.1B796D82AF	0.692307692307692		3D9.239F88A6C7	0.461538461538462		0.384615385

Record: 1 of 533 No Filter Search

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Spawning Protocol

- Upload tag lists
- Re-sort males, collect milt into vials
- Spawn females, add milt from matching male
- 700-1000 crosses per year



Tracking Crosses

Data on individual crosses:

- egg and milt condition
- # of eggs
- percent eye-up
- survival to swim-up
- parentage



Future Broodstock

- all crosses genetically analyzed
- rare alleles, high heterozygosity
- individuals from 150 crosses
- housed separately until taggable size (60-100mm)



Average heterozygosity of Broodstock



Marlette Lake Offsite Broodstock

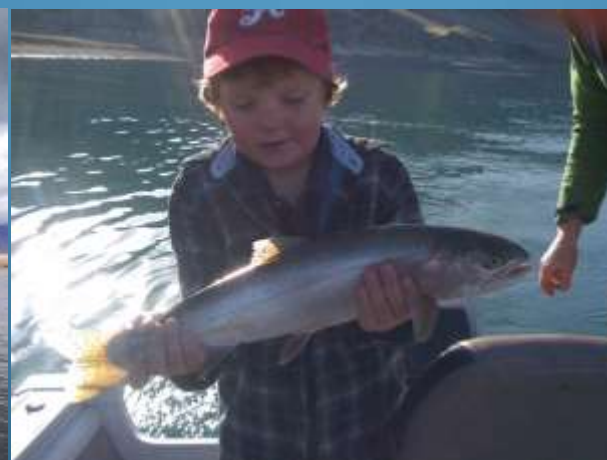
- offsite replicate broodstock
- In partnership with NDOW
- Returning fish PIT tagged and genetic clipped



Pyramid Lake Potential Broodstock

- Possible egg/milt source
- 6,000+ eggs per female





Questions?

