

R. Paul Evans

Andrea Kokkonen

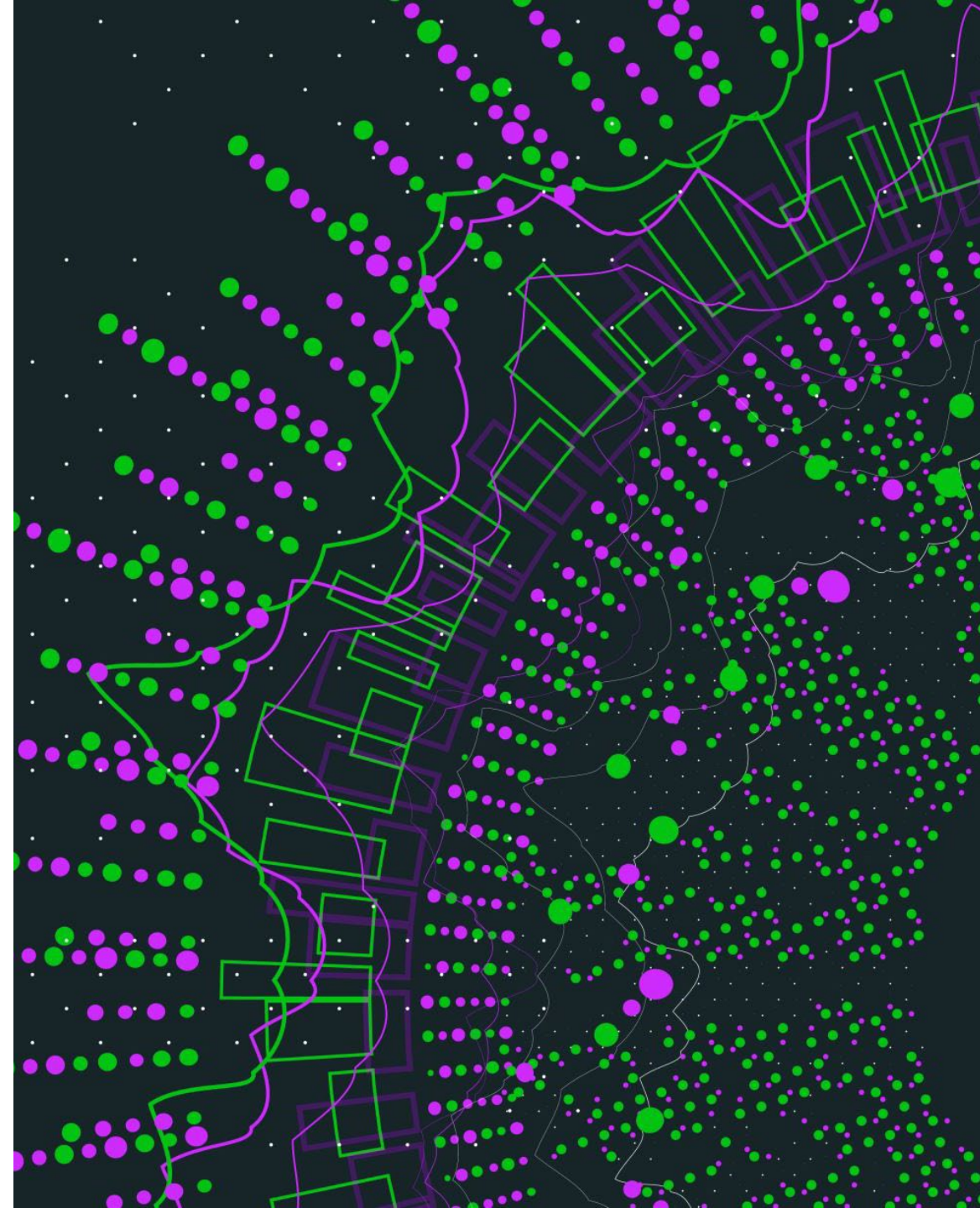
Peter Searle

Kevin Rogers

Dennis Shiozawa

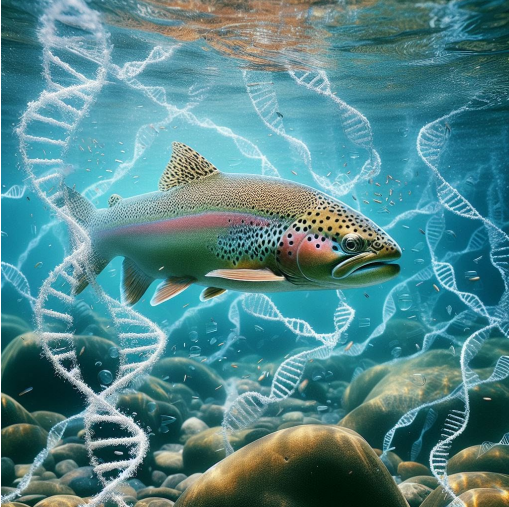
**TAXONOMIC
(R)EVOLUTIONS IN
ONCORHYNCHUS CLARKII
(CUTTHROAT TROUT):
THE FUTURE STARTS NOW**

BYU
Microbiology &
Molecular Biology
COLLEGE OF LIFE SCIENCES

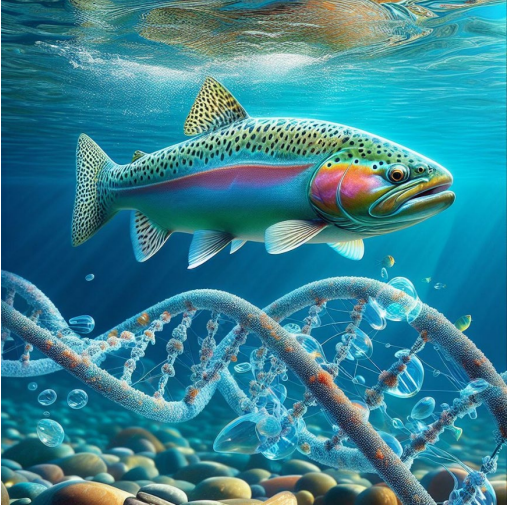


AI Prompt

“ *Cutthroat Trout DNA* ”



Coastal



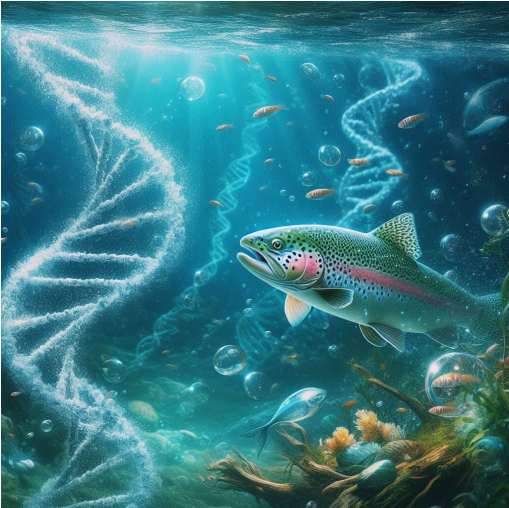
Lahontan



Westslope



Yellowstone



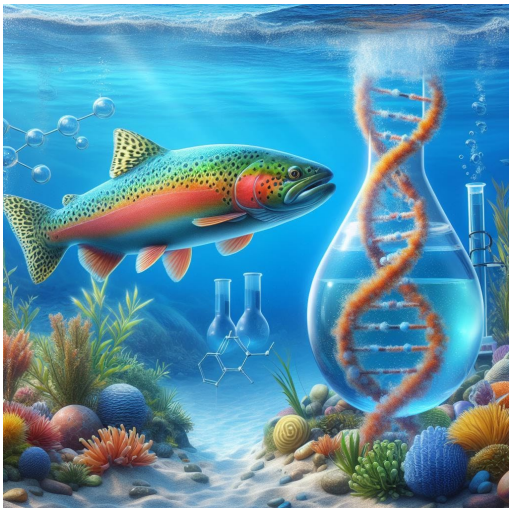
Greenback



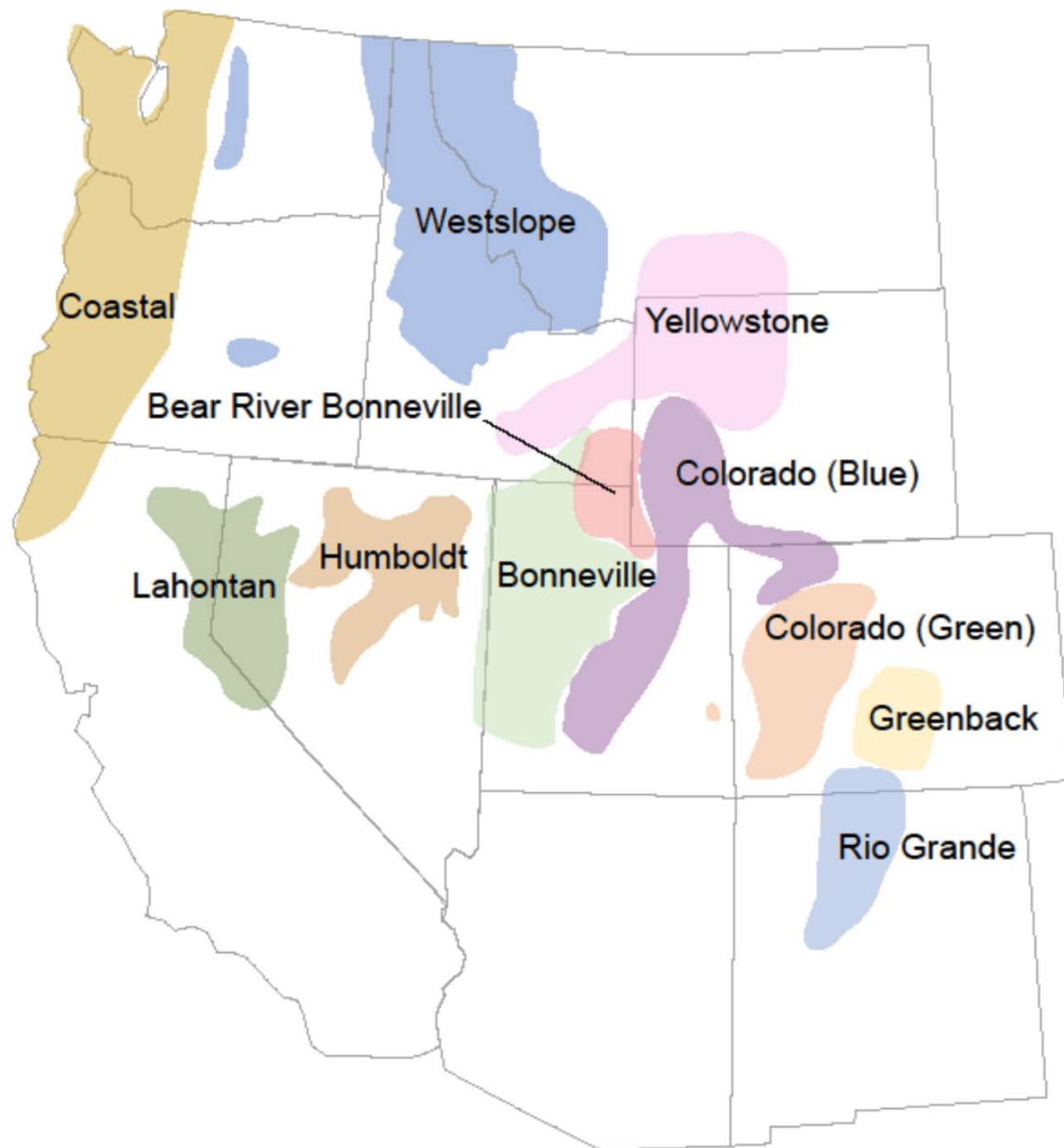
Bonneville



Colorado River “Blue” Lineage



Yellowfin



Transcriptome Sources

Common Name	Species	Year	Location
Bear River Bonneville form	<i>O. clarkii</i> utah	2012	Big Creek, UT
Bonneville	<i>O. clarkii</i> utah	2022	Big Wash Creek, NV
Bonneville	<i>O. clarkii</i> utah	2012	Diamond Fork River, UT
Coastal	<i>O. clarkii</i> clarkii	2019	Mack Creek, OR
Colorado R. Blue lineage	<i>O. clarkii</i> pleuriticus	2022	Little West Fork of Blacks Fork, UT
Colorado R. Blue lineage	<i>O. clarkii</i> pleuriticus	2022	Right Fork UM Creek, UT
Colorado R. Green lineage	<i>O. clarkii</i> pleuriticus	2022	Bobtail Creek, CO
Colorado R. Green lineage	<i>O. clarkii</i> pleuriticus	2022	Beaver Creek, UT
Greenback	<i>O. clarkii</i> stomias	2018	Bear Creek, CO
Humboldt	<i>O. clarkii</i> humboldtensis	2012	Mary's River, NV
Lahontan	<i>O. clarkii</i> henshawi	2016	Bettridge Creek, UT
Rio Grande	<i>O. clarkii</i> virginalis	2021	HayPress Lake, CO
Westslope	<i>O. clarkii</i> lewisi	2019	Middle Fork of Salmon River, ID
Yellowstone	<i>O. clarkii</i> bouvieri	2019	Soldier Creek, WY

In 2010, began whole genome and transcriptome assembly efforts using bits of funds

Isocitrate Dehydrogenase Transcripts

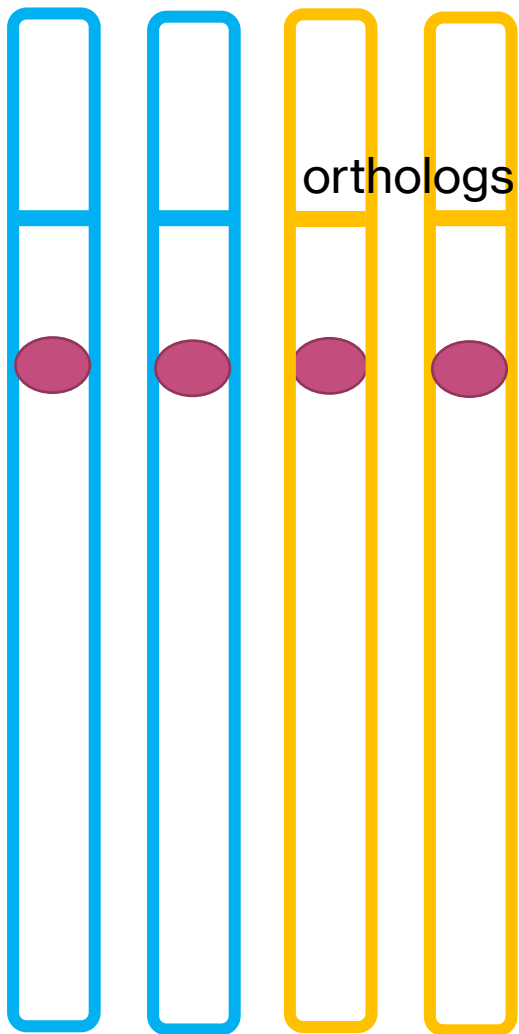
2 groups (paralogs)

30% sequence divergence

	Coastal	Humboldt	Lahontan	Westslope	Coastal	Lahontan	Westslope	Humboldt
Coastal		100	100	100	69	69	69	69
Humboldt	100		100	100	69	69	69	69
Lahontan	100	100		100	69	69	69	69
Westslope	100	100	100		68	68	69	69
Coastal	69	69	69	68		100	100	99
Lahontan	69	69	69	68	100		100	99
Westslope	69	69	69	69	100	100		99
Humboldt	69	69	69	69	99	99	99	

~40 million years since
Salmoninae autotetraploid
event

Subgenome 1 Subgenome 2



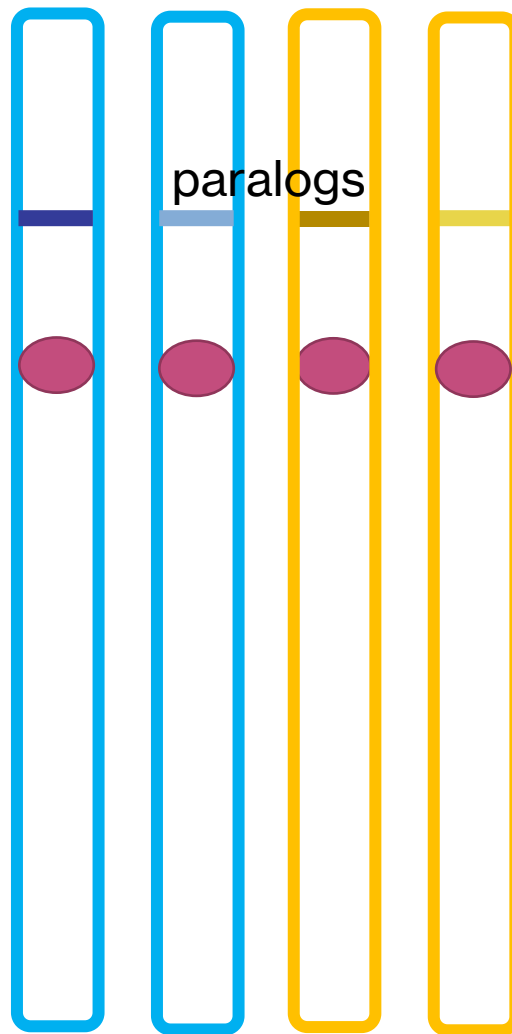
Salmoninae
~40 million years ago

Homeologs
Haplotypes
Subgenomes
Phases



Diploidization
Fusions
Fissions
Recombination

Subgenome 1 Subgenome 2



Oncorhynchus
~10 million years ago

Assumed Chromosome Number

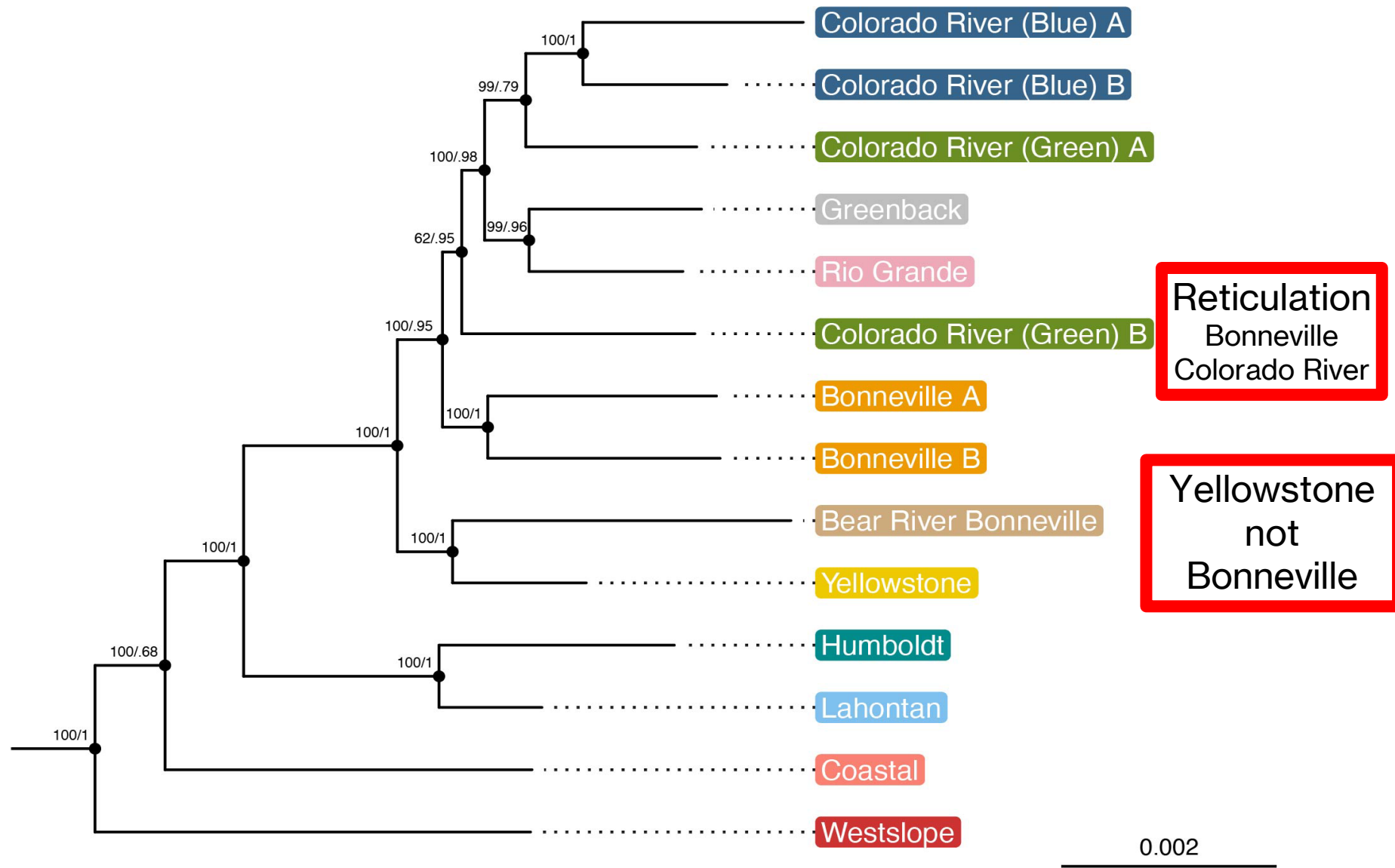
Rainbow	58-64
Coastal	68
Westslope	66
Lahontan	64
Bonneville	64
Colorado River	64
Rio Grande	64
Yellowstone	64
Bear River	64
Greenback	64 we show 68



Cutthroat Trout Phylogeny

1983 orthologous genes

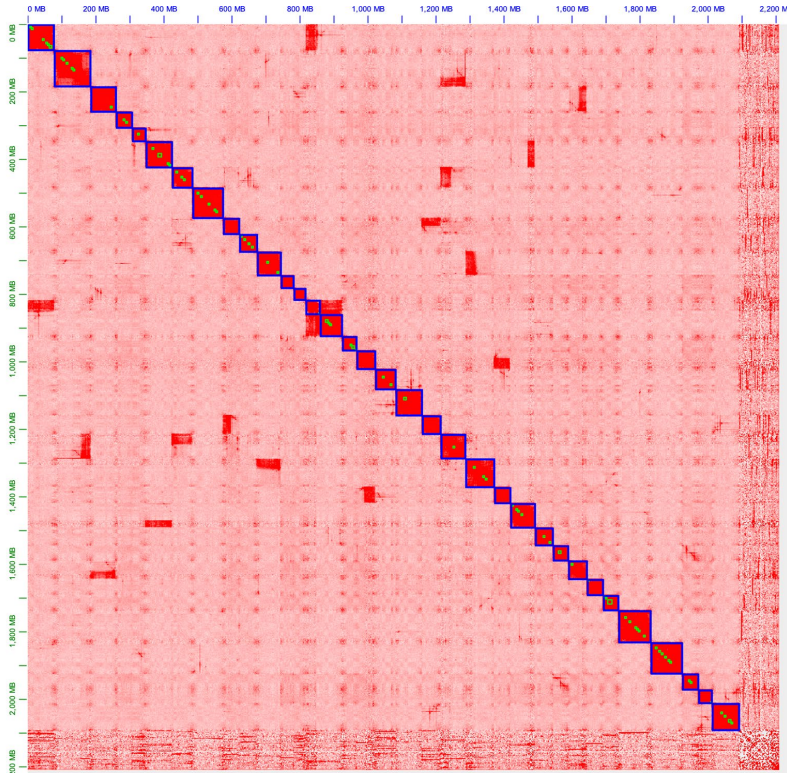
Transcriptome



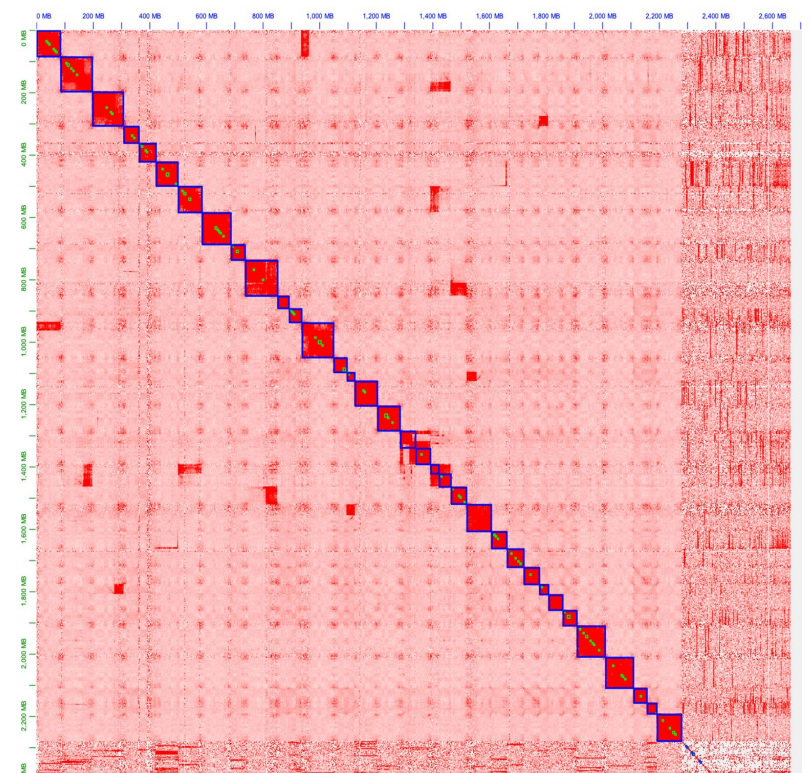
Concatenated maximum likelihood phylogeny from 1983 orthologous genes. A consensus phylogeny (not displayed) has the same topology. Support values represented are bootstrap values and local posterior probabilities for each branch. The scale bar represents the expected number of nucleotide substitutions for each site. The phylogeny was generated using three outgroups (Pink salmon, Coho salmon and Rainbow trout), but only the Cutthroat Trout are displayed.

Assemble genome by comparing physically cross-linked regions with sequence (PacBio, HiC, Juicer)

Cutthroat Trout Subgenome 1



Cutthroat Trout Subgenome 2



Autotetraploid



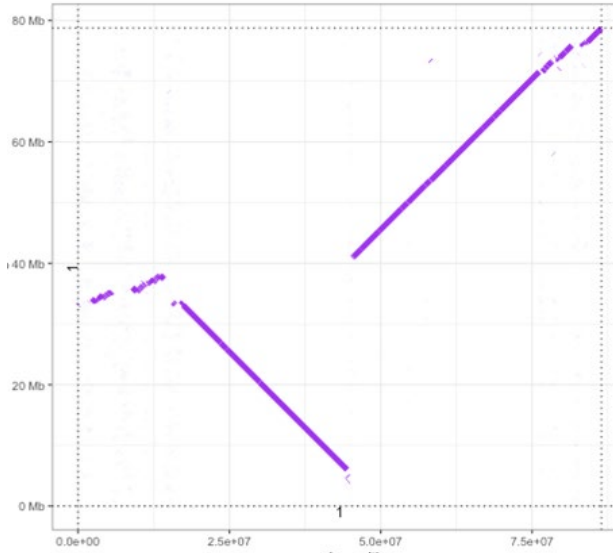
2

Homeologs
Haplotypes
Subgenomes
Phases

Assembly	Total Length	Num Contigs	N50	BUSCO Score
Hap1 Contigs	2.67 Gb	5,484	1.4 Mb	
Hap2 Contigs	2.21 Gb	4,614	1.35 Mb	
Hap1 Scaffolds	2.67 Gb	1,160	78.83 Mb	C:98.8%[S:45.5%,D:53.3%],F:0.8%,M:0.4%,n:255
Hap2 Scaffolds	2.21 Gb	572	65.09 Mb	C:93.7%[S:56.1%,D:37.6%],F:1.2%,M:5.1%,n:255

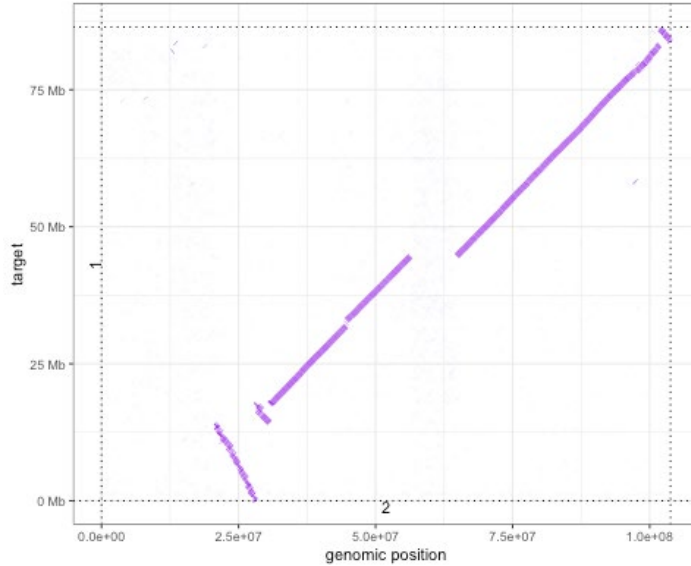
Align Chromosome 1
from subgenomes 1
and 2 with each other
and Rainbow Trout

Cutthroat Trout
Subgenome 2



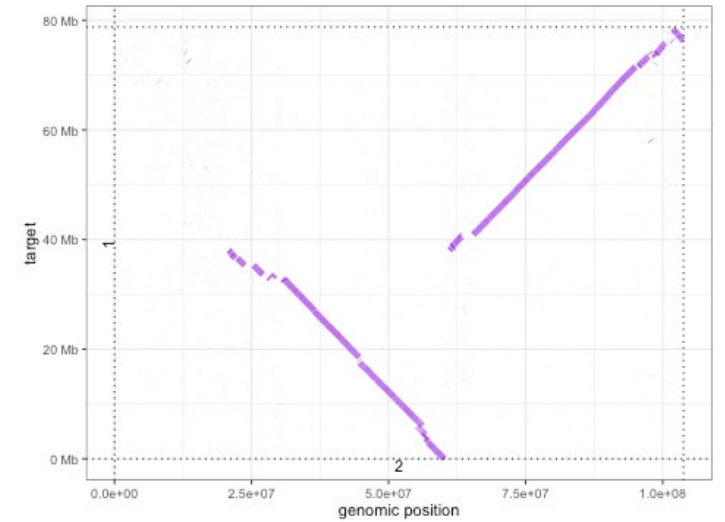
Cutthroat Trout
Subgenome 1

Cutthroat Trout
Subgenome 2



Rainbow Trout

Cutthroat Trout
Subgenome 1



Rainbow Trout

Isocitrate Dehydrogenase Transcripts

2 groups (paralogs)

30% sequence divergence

	Coastal	Humboldt	Lahontan	Westslope	Coastal	Lahontan	Westslope	Humboldt
Coastal		100	100	100	69	69	69	69
Humboldt	100		100	100	69	69	69	69
Lahontan	100	100		100	69	69	69	69
Westslope	100	100	100		68	68	69	69
Coastal	69	69	69	68		100	100	99
Lahontan	69	69	69	68	100		100	99
Westslope	69	69	69	69	100	100		99
Humboldt	69	69	69	69	99	99	99	

~40 million years since
Salmoninae autotetraploid
event

Current Salmonid Whole Genomes

Species	# Chromosomes in Genome	# Chromosomes in Karyotype
Atlantic salmon	29	58
Brown Trout	40	80
Lake Trout	42	84
Brook Trout	42	84
King Salmon	34	68
Coho Salmon	30	60
Sockeye Salmon	29	58
Chum Salmon	37	74
Pink Salmon	27	82-84
Masu Salmon	33	66
Lenok	40	90
Rainbow Trout	32	64

1983 Orthologous Genes Genetic Similarity Matrix

	CR Green	CR Blue	Greenback	Rio Grande	Bonneville	Bear River	Yellowstone	Humboldt	Lahontan	Coastal	Westslope	Rainbow	Pink
CR Green													
CR Blue	99.1												
Greenback	99.9	99.1											
Rio Grande	99.8	99.0	99.8										
Bonneville	99.4	98.6	99.4	99.4									
Bear River	99.9	99.1	99.9	99.8	99.4								
Yellowstone	99.9	99.1	99.9	99.8	99.4	99.9							
Humboldt	99.7	98.9	99.7	99.7	99.2	99.7	99.7						
Lahontan	99.8	98.9	99.8	99.7	99.2	99.7	99.7	100.0					
Coastal	99.8	98.9	99.8	99.7	99.2	99.7	99.7	99.7	99.7				
Westslope	99.6	98.8	99.6	99.5	99.1	99.6	99.6	99.6	99.6	99.6			
Rainbow*	98.4	97.5	98.4	98.3	97.9	98.4	98.4	98.4	98.4	98.4	98.4		97.7
Pink*	96.6	95.8	96.6	96.5	96.1	96.6	96.6	96.6	96.6	96.6	96.5	97.7	
Coho*	95.3	96.2	95.3	95.3	94.8	95.3	95.3	95.3	95.3	95.4	95.2	95.6	94.3

*homogenized genome – orthologs and paralogs are combined

Pairwise number of sequence differences

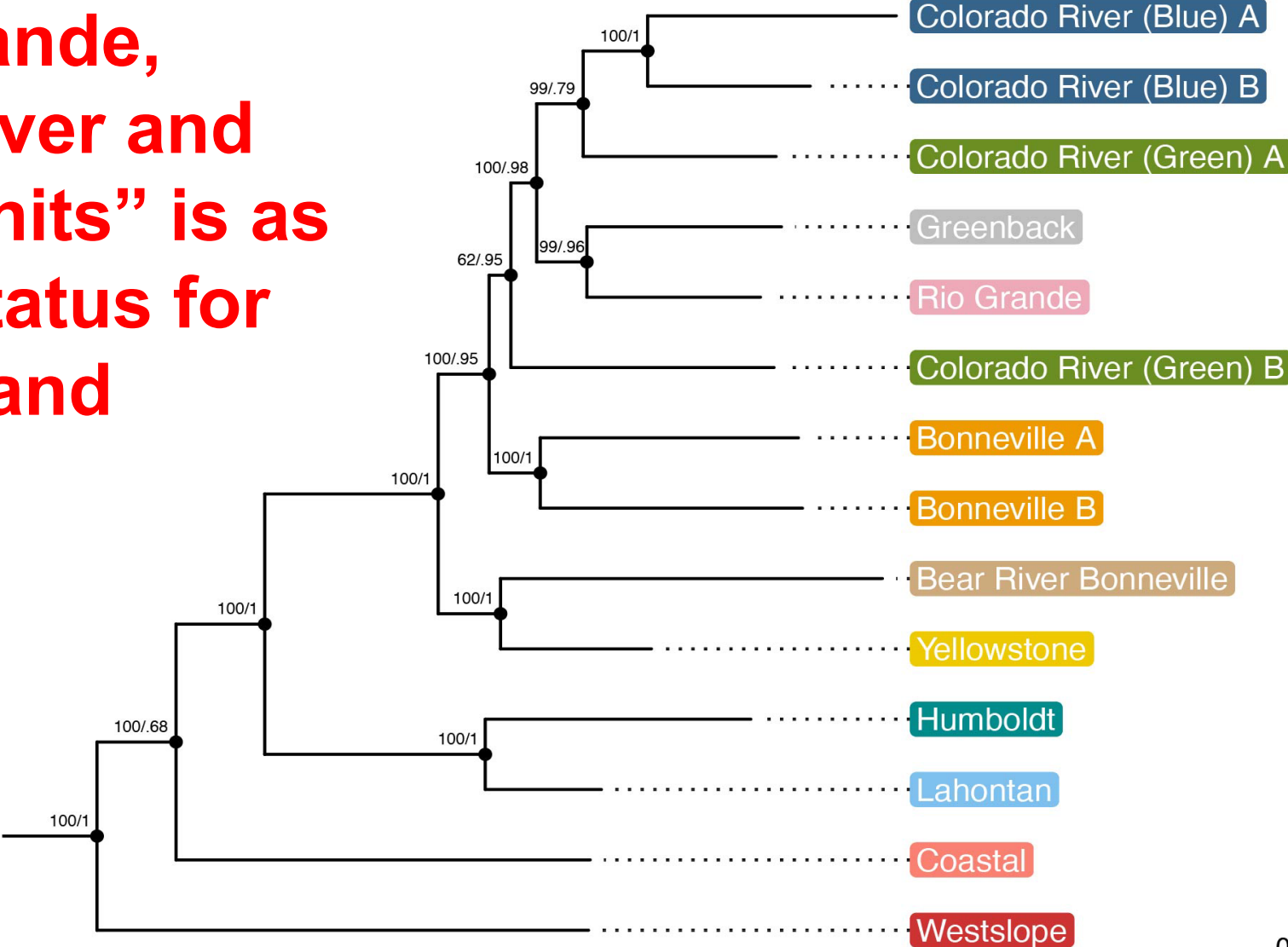
	CR Green	CR Blue	Greenback	Rio Grande	Bonneville	Bear River	Yellowstone	Humboldt	Lahontan	Coastal	Westslope	Rainbow	Pink	Coho
CR Blue	23													
Greenback	16	21												
Rio Grande	50	35	48											
Bonneville	162	164	160	118										
Bear River	30	19	28	44	94									
Yellowstone	33	22	33	47	98	15								
Humboldt	71	70	71	95	147	75	76							
Lahontan	69	68	69	93	145	73	74	4						
Coastal	69	70	69	95	149	75	76	76	74					
Westslope	107	102	105	129	181	103	108	120	118	104				
Rainbow*	451	443	449	469	523	446	449	458	456	449	457			
Pink*	945	945	944	972	875	948	952	956	954	938	973	638		1578
Coho*	1303	1300	1301	1313	1375	1302	1306	1309	1307	1294	1326	1223	1578	

28 orthologous genes
27,846 base pairs

Pairwise percent sequence divergence of mitochondrial ND2 gene

	Colorado	Rio Grande	Bonneville	Yellowstone	Lahontan	Coastal	Westslope
Rio Grande	1.8						
Bonneville	2.2	1.8					
Yellowstone	2.9	2.5	1.9				
Lahontan	1.9	2.2	3.2	2.7			
Coastal	2.2	2.4	3.0	2.7	2.0		
Westslope	2.5	2.6	3.1	2.7	1.9	2.3	
Rainbow	8.1	7.3	8.7	8.2	8.1	8.0	8.3

A unique taxonomic status for Colorado River, Greenback, Rio Grande, Bonneville, Bear River and Yellowstone “subunits” is as valid as a unique status for Lahontan, Coastal and Westslope



0.002

The joint AFS/ASIH Names of Fishes Committee action was both incomplete and premature

1. Ignored the “Interior Cutthroat” which remain without unique taxonomic identity lumped into the Rocky Mountain Cutthroat Trout clade. The status of these fish, some of which are federally listed and/or state species of concern, is not understood/accepted by fisheries professionals nor the public. There is no published basis for the action by the Committee.
2. Still waiting for a collaborative common study of all Cutthroat Trout “subunits”. With established chromosome-level Cutthroat Trout whole genomes, whole genomes of all 25 Cutthroat Trout “subunits” can be assembled with less coverage/cost.
3. The Names of Fishes Committee can rescind/alter naming recommendations. In the meantime, acknowledge the “recommendations” of the Committee as evidence of the need for further work, but, continue to use the established hierarchical and widely published species, subspecies, and lineage identifications.

