Geographic Variation in Genetic and Meristic Characters of Coastal Cutthroat Trout

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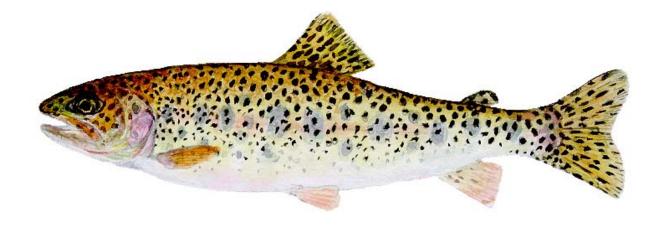
Funding:

• US Forest Service – Region 6, Region 10, and the Pacific Northwest Research Station

Laboratory facilities:

 Genetic and meristic work conducted in the laboratories of the Oregon Cooperative Fishery Research Unit "In this day of detailed research, surprisingly little is known of the cutthroat, especially in his sea-running phase. Life history, migration stages, feeding habitats, stream preferences, all are matters of vague surmise and angler's observation. Even his peak spawning time remains a matter for debate, although it probably varies a good deal from one watershed to another."

R. Haig-Brown 1964 – Fisherman's Fall

















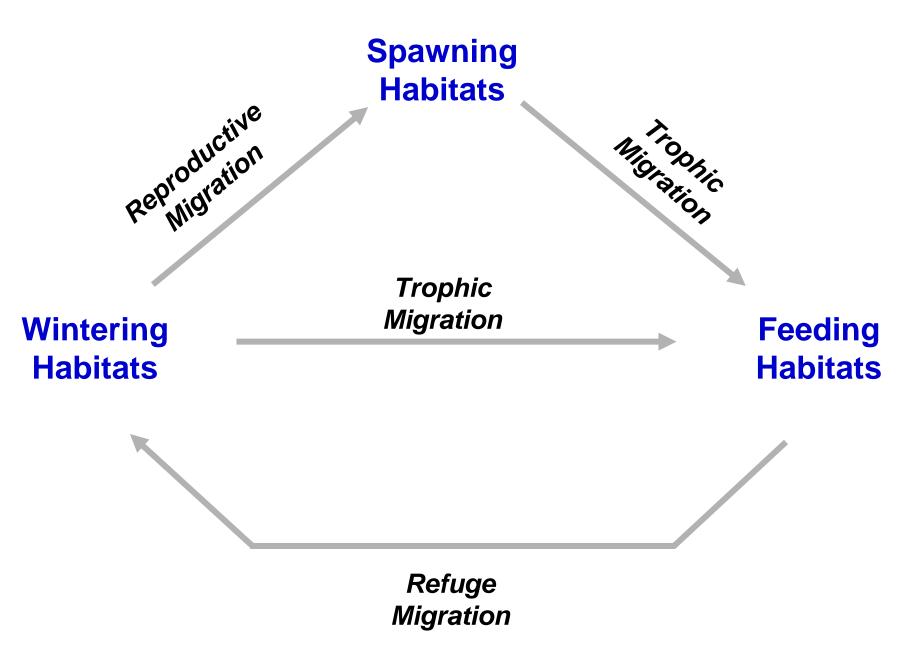












From: Northcote 1997



Fish No. 920055 Bakewell Creek, AK

Fish No. 930155 Thorne River, AK

Fish No. 953513 Survey Creek – Queen Charlotte Islands, B.C.

Fish No. 953292 Wheeler Creek, OR Present data concerning the geographic variation in population structure of coastal cutthroat trout from across their distributional range.

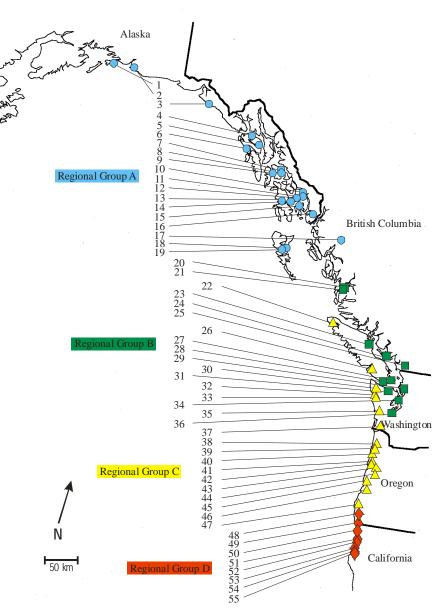
Describe population structure with two "tools":

- meristics
- allozymes



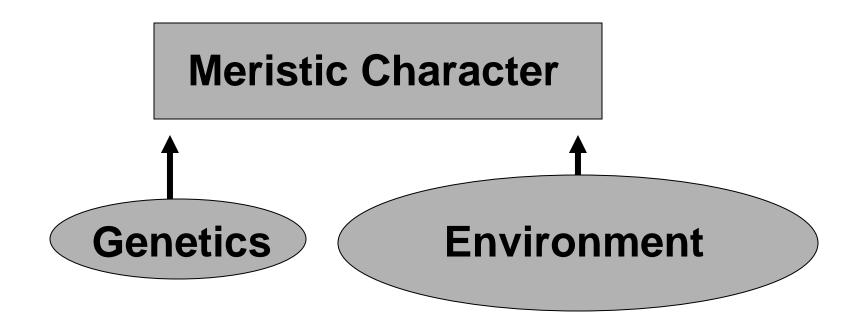
- Samples from across distributional range
- 55 locations sampled
- 4 regional groups
- Sites located downstream of barriers
- Multiple size (age) classes





Meristic characters are body segments and other features, primarily fin rays and scales, that at one time in the evolutionary past corresponded to body segmentation; other characters that can be counted are sometimes referred to as meristic even though they have no correspondence with the myomeres.



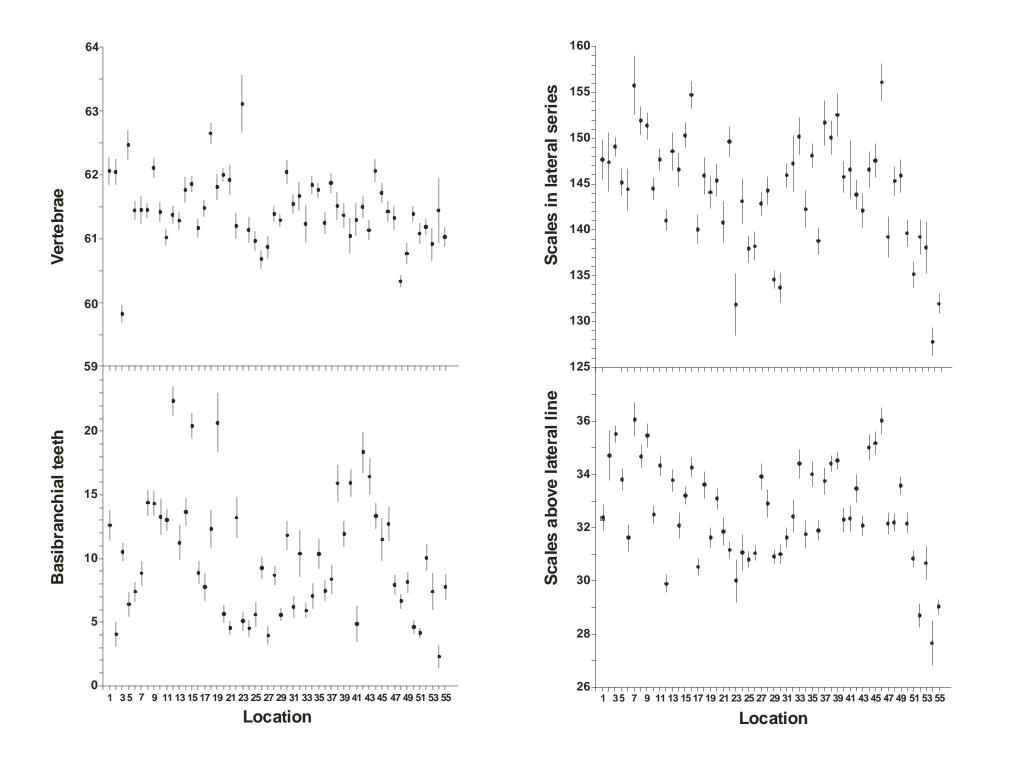


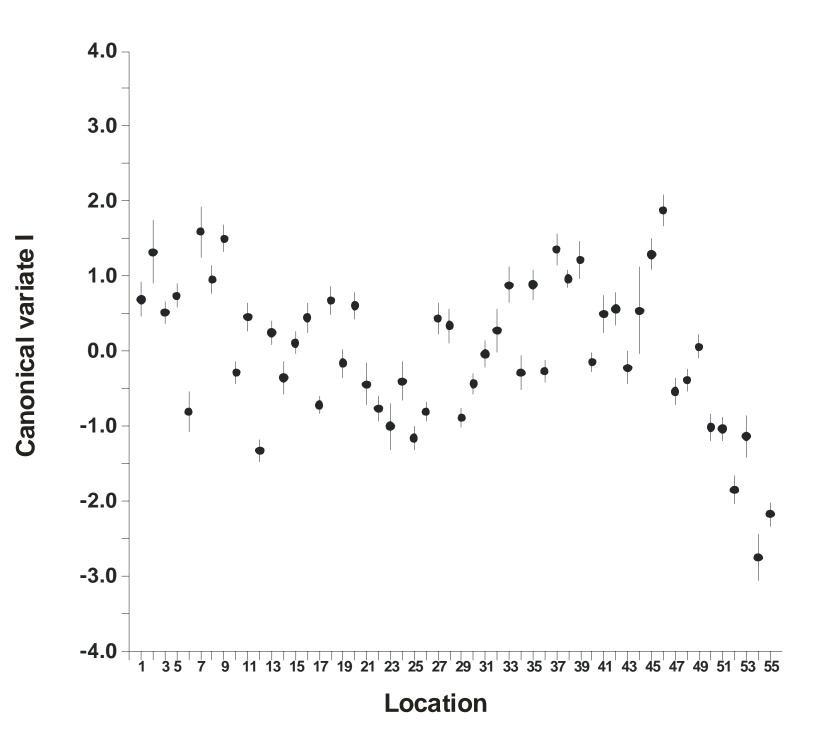
- Meristic characters in fish are generally considered to have a genetic basis
- Environmental factors can have substantial influence on meristic characters and may modify an individual's phenotype
- Minor changes in environment during ontogeny can result in significant intra-specific differences

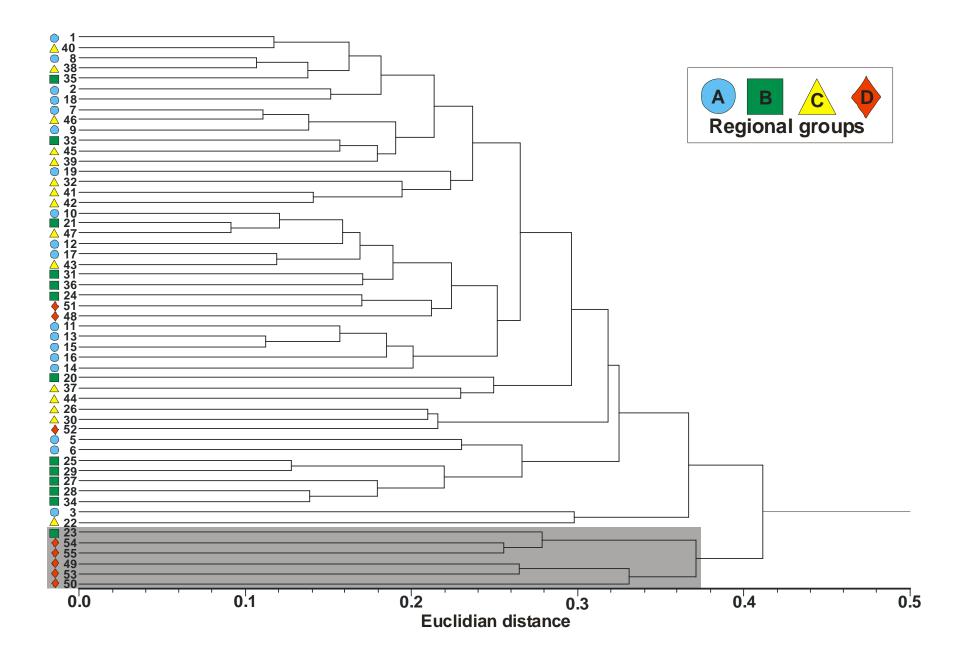
- Meristic characters are phenotypic expressions of environmental conditions during egg and larval development, adequate temporal and spatial heterogeneity form the basis of population differentiation using these characters (Sheppard 1991)
- Even with environmental influence, if differences among populations are significant, these measures may be meaningful for understanding population structure

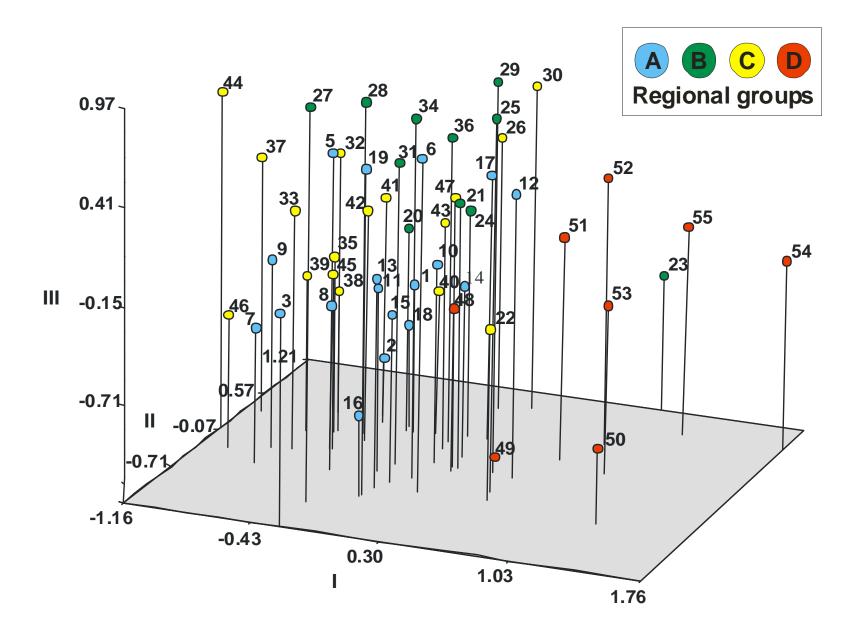
	Ν	Mean	SD	Min	Max
Fork length (mm)	1400	171.4	81.0	52	468
Weight (g)	1238	112.2	210.0	2	2505
Meristic character					
Anal pterygiophores	1430	11.2	0.6	9	13
Dorsal pterygiophores	1429	11.5	0.7	10	13
Vertebrae	1421	61.4	1.0	56	66
Scales in lateral series	1429	144.9	10.9	114	187
Scales above lateral line	1427	32.7	2.9	20	42
Pelvic fin rays	1422	9.1	0.4	8	10
Pectoral fin rays	1419	13.6	0.7	7	15
Gill rakers - lower arch	1425	11.5	0.8	8	14
Gill rakers - upper arch	1426	6.7	0.8	3	12
Gill rakers - total	1425	18.2	1.2	13	23
Branchiostegal rays	1417	11.0	0.7	9	13
Pyloric caeca	1345	43.3	6.9	19	74
Basibranchial teeth	1431	10.8	7.5	0	48

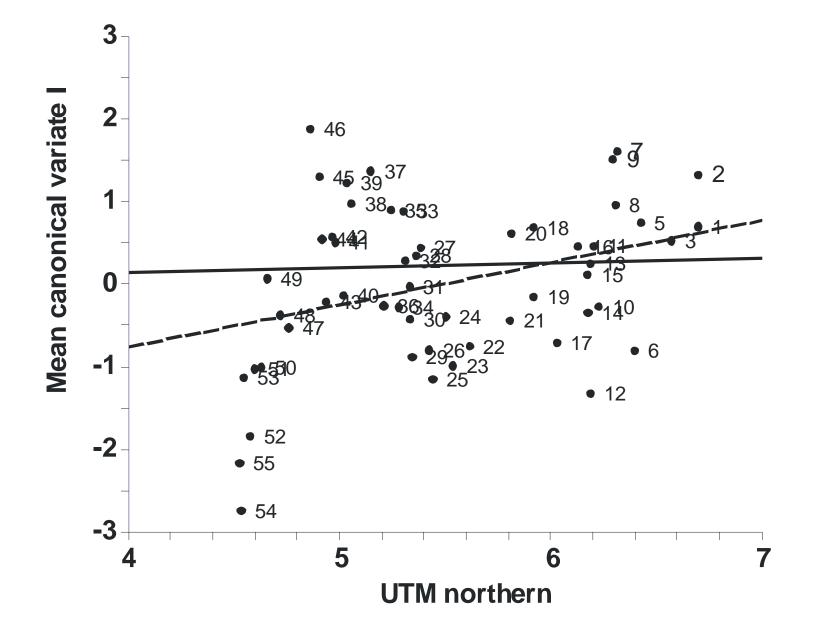
- No differences between males and females pooled for analysis
- No differences between size classes pooled for analysis
- Significant differences among all locations at each of the 11 meristic characters examined (ANOVA, P<0.001)
- Significant differences in meristic counts among all sites (MANOVA, Wilkes' 8 = 0.0695, P<0.001)

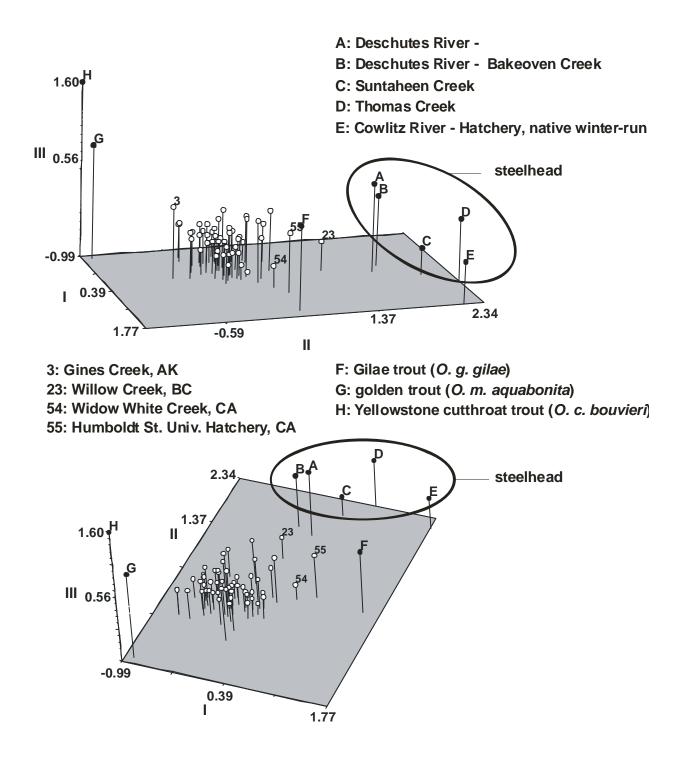












Meristics

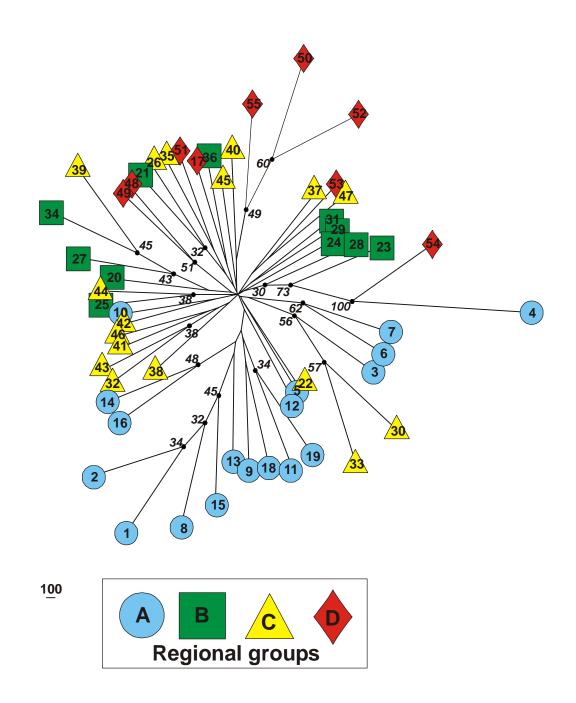
- coastal cutthroat trout exhibited extensive variation in meristic characters across their distributional range
- populations at the southern end of the range exhibited phenetic affinity, significant meristic differences within southern regional area

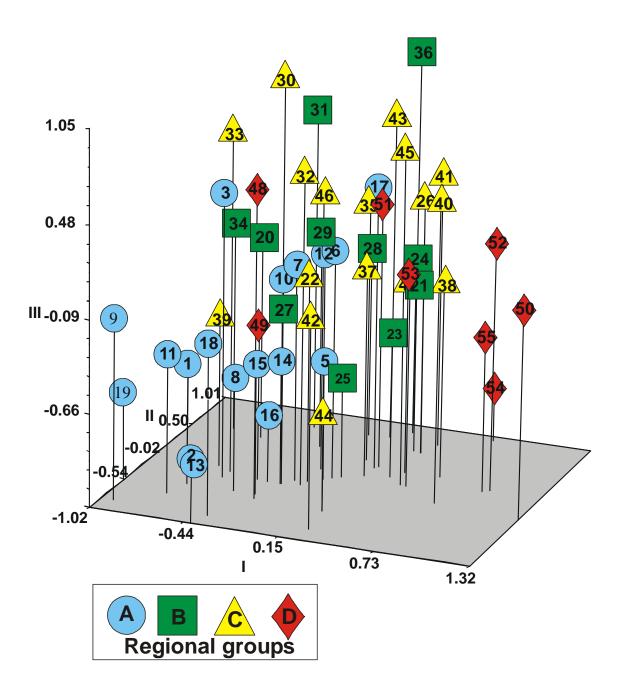
Genetics - allozymes

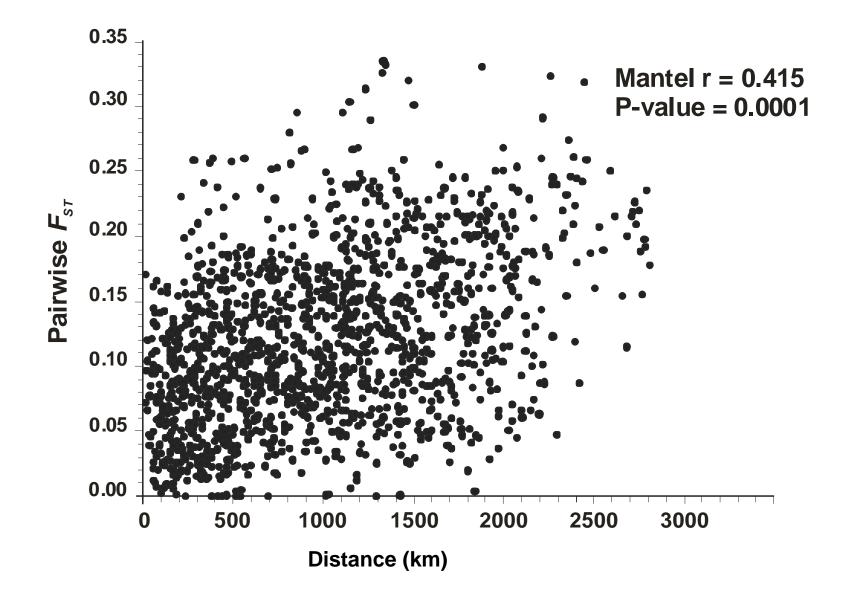
Examine the geographic distribution of genetic variation of coastal cutthroat trout across distributional range

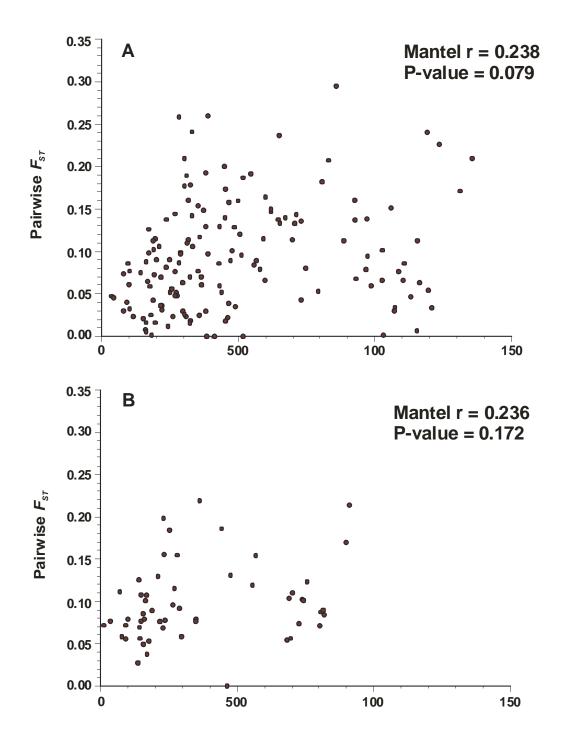
- to determine if genetic diversity among populations differs regionally, perhaps reflecting historical landscape/environmental features
- to determine the spatial distribution of genetic diversity across the range

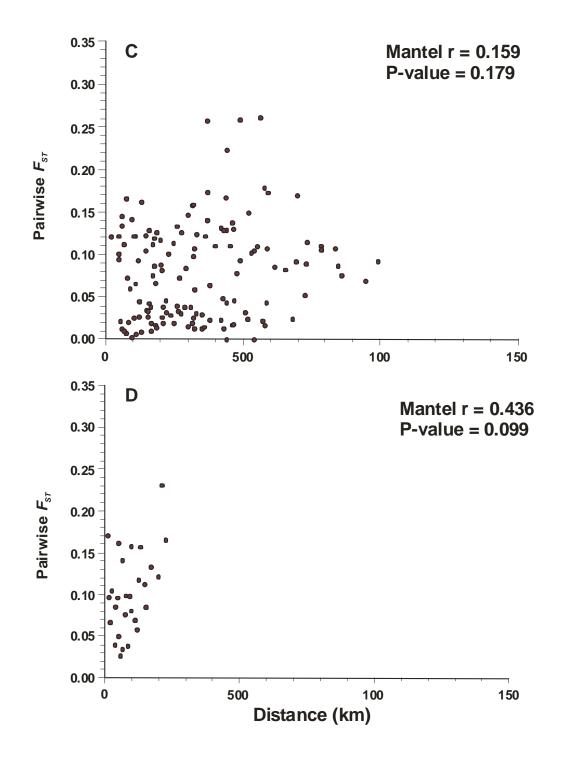
- 54 populations of coastal cutthroat trout (1,414 fish) sampled
- 30 loci (95 alleles)
- 17 polymorphic loci (P_{0.95})
- average heterozygosity 0.062 (0.036 0.101)
- % polymorphic loci ranged from 7.4 25.9% (mean = 17.4%)
- genetic differentiation among the 54 samples was significant (*P*<0.05) for 16 of the 17 loci; global significance over all loci was significant (*P*<0.05)
- significant heterogeneity in allele frequency found in all pair-wise comparisons (i.e., coastal cutthroat trout sampled from across the range were composed of genetically distinct populations)

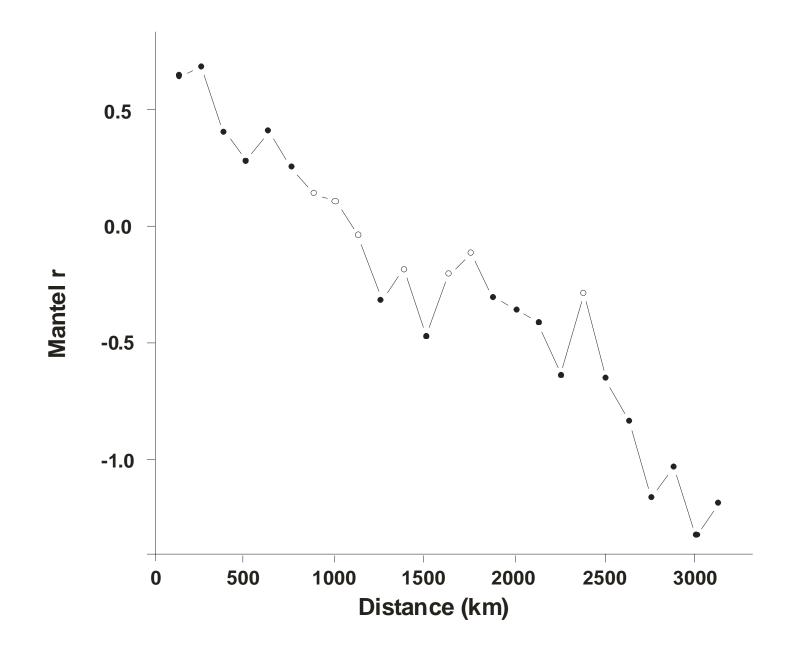












Grouping	<i>F</i> -statistics		Isolati dista	
	2	95% confidence interval	Mantelr	p-value
Region A	0.095	0.125 - 0.059	0.238	0.079
Region B	0.101	0.165 - 0.059	0.236	0.172
Region C	0.084	0.125 - 0.040	0.159	0.179
Region D	0.100	0.185 - 0.050	0.436	0.099
Overall	0.131	0.176 - 0.086	0.415	0.0001

Allozymes

- genetic population structure was primarily at the individual stream level
- the amount of genetic diversity attributed to differences among populations was high
- consistent with other studies at smaller spatial scales and suggest a range-wide consistency in the population structure of coastal cutthroat trout

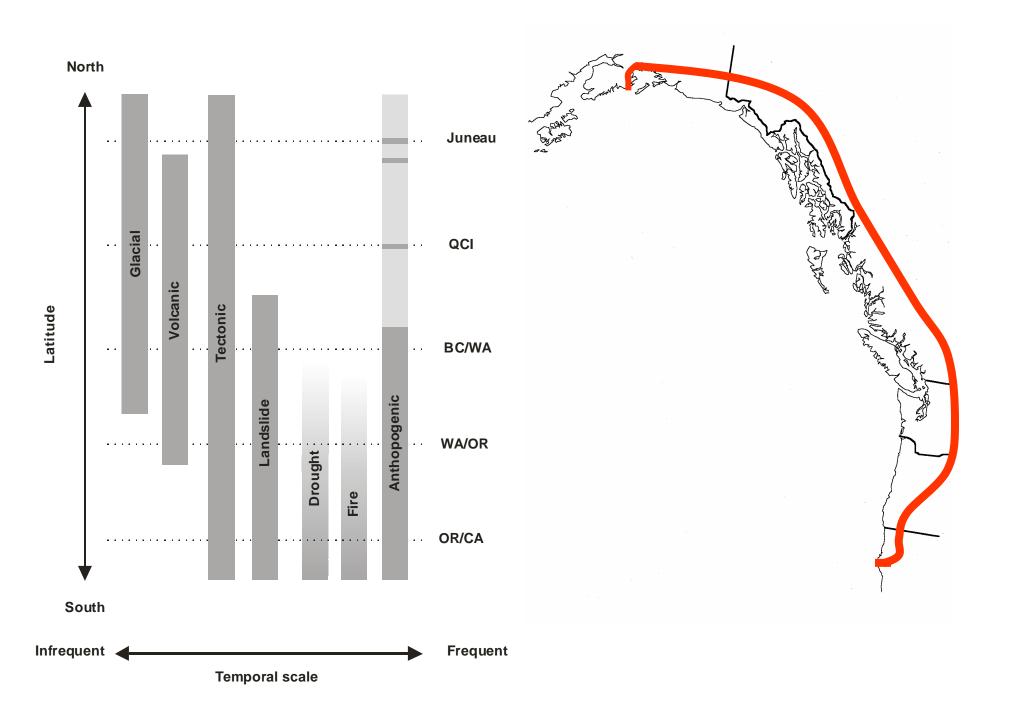
Meristics

- extensive variation in meristic characters across their distributional range
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Allozymes

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- Population structure was primarily at the individual stream level
- The northern populations did not show a strong phenetic affinity with meristics, but there was geographic structuring detected in this region with allozymes
- The southern populations were distinct with both meristics and allozymes
- The intra-regional differences were greatest in the southern region with both meristics and allozymes







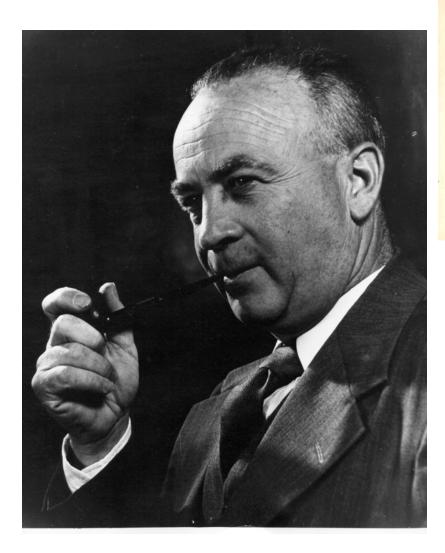






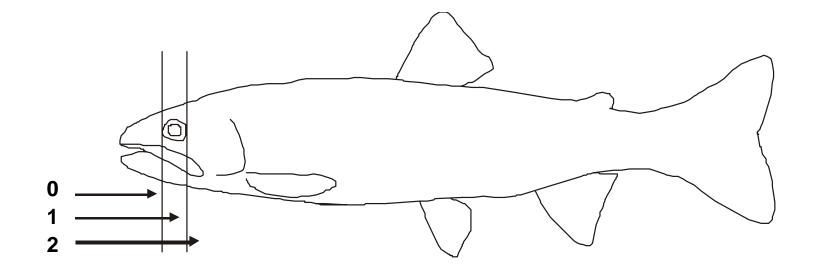


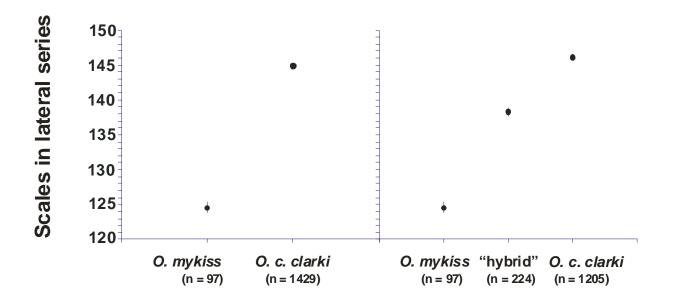
Looking south, Lost Coast, southern extent of O. c. clarki distribution

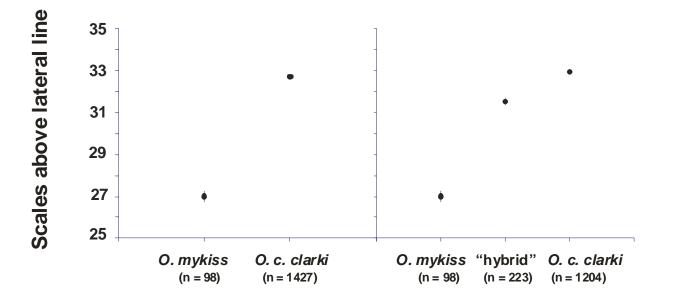


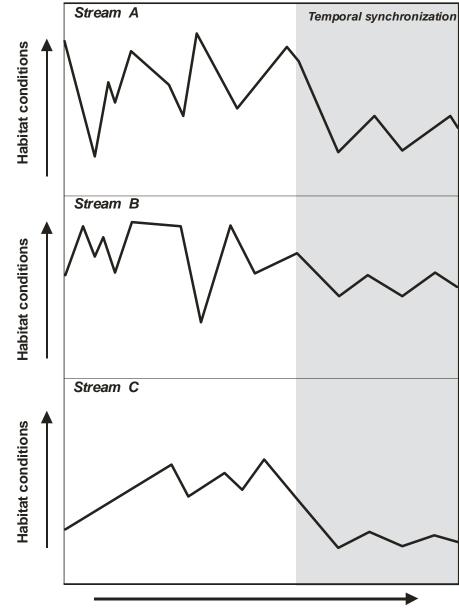
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	Character Quantities and Their Values
1 Hyprid Teeth Pre	
3 Max. Ext. Presen	t. = 9
4 20 primore diss, be scales in lateral lin	$e \neq = 5$
Scale pateral lin	
6 Apal Rays 10 or 11	
2 Dorsal Rays 10 or 11 8 Scales above later	2/ 1/2 = 2
9 Joaks below laten	1 10 = 3 50 = True cutthroat









Time

Peripheral / Marginal Populations

- Populations at northern and southern extent of range are both geographically marginal based on spatial distance
- Southern region populations are also ecologically marginal (e.g., Klamath Province, etc.); they experience very different abiotic and biotic conditions compared with adjacent populations along the Oregon coast

Peripheral populations tend to be genetically and morphologically divergent from central populations and morphological characters are expected to diverge more rapidly in isolated populations than gene frequencies.

Lesica and Allendorf 1995

In contrast to conventional thinking that predicts core populations persisting and range contraction as a species becomes endangered, most species (of 245 examined) persist in the periphery of their historical geographic range.

Channell and Lomolino 2000