CALIFORNIA FISH AND GAME
Calif. Fish and Game 78(3):88-104 1992

POPULATION GENETIC STRUCTURE OF COHO SALMON *(ONCORHYNCHUS KISUTCH)* IN CALIFORNIA

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We used allozymes to examine the genetic structure of 27 populations of coho salmon from northern and central California. Genetic variability was low throughout the study area. Although 23 of 45 loci were variable, much of the observed variation was due to rare and uncommon alleles (frequency < 10%). Average heterozygosity estimates ranged from 0.000 to 0.050 with a mean of 0.027. We found little pattern in the distribution of variant alleles or genetic variation; we observed only weak associations between genetic identity and geographic location. Substantial transfers of coho salmon have taken place in California, and stocks of coho from Oregon have been introduced into the State. It is difficult to assess the relative influence of these stocking practices, selection, and random processes on the genetic structure of California coho salmon populations. The genetic structure of coho salmon in California, as well as current stocking practices, indicate that genetic stock identification of California coho salmon from individual streams or localized areas may be difficult with isozyme technology. Differences among coho salmon populations from the Pacific Northwest and California may allow genetic identification of stocks from broad geographic areas.

INTRODUCTION

Coho salmon are native to the west coast of North America from Monterey, California to Point Hope, Alaska (Scott and Crossman 1973). California populations of coho salmon have declined due primarily to habitat degradation associated with water diversions, mining, and deforestation (Netboy 1974). In order to manage and preserve California's coho salmon populations, basic information on genetic variability and gene flow in subpopulations and stocks will be essential (Allendorf and Utter 1979, Allendorf and Phelps 1981, Ihssen et al. 1981). As in other species of Pacific salmon, coho salmon make spawning migrations to their natal streams (Ricker 1972). The resulting restriction of gene flow among subpopulations spawning in different streams creates the potential for genetic differences to accumulate due to natural selection, genetic drift, and mutation (Wright 1943).

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Allozyme analyses have been used in research on salmonids of the Pacific Northwest to identify subpopulation structure (Utter, Allendorf, and Hodgins 1973, Kristianson and McIntyre 1976, Carl and Healy 1984, Wilmot and Burger 1985, Utter et al. 1989), to estimate levels of gene flow (Wehrhahn and Powell 1987, Berg and Gall 1988, Bartley and Gall 1990), to assess hatchery enhancement programs (Seeb, Seeb, and Utter 1986), to document interspecific hybridization (Bartley, Gall, and Bentley 1990), and to determine the composition of mixed fisheries (Pella and Milner 1987). However, coho salmon display the lowest level of allozyme variation of the five species of Pacific salmon (Allendorf and Utter 1979).

Here we report on the genetic structure of California populations of coho salmon. We sampled wild and hatchery stocks of fish, and analyzed their allozymes using standard laboratory techniques. Our main objective was to assess the use of allozymes of California coho salmon for stock identification purposes.

METHODS

Coho salmon were collected during the spring and summer of 1983-1985 and 1986 (Table 1, Fig. 1). Emigrating juvenile salmon were captured by standard backpack electro-shocking and fyke-netting. Salmon were either frozen on dry ice in the field or transported live to the laboratory. Samples of liver, muscle, blood, and eye were removed and frozen at -20°C.

Standard horizontal starch-gel electrophoresis and histo-chemical staining procedures were followed (Harris and Hopkinson 1976, Aebersold et al. 1987) to analyze 45 loci from 23 enzyme systems (Table 2). Allele nomenclature followed Allendorf and Utter (1979); a locus was considered polymorphic if we observed more than one allele in any collection. Loci that could not be scored in all samples were still included in the analyses.

Average heterozygosity, H, was calculated from the allele frequencies according to Nei (1973). Total gene diversity, H_T, was partitioned into within-sample, H_S, and between-sample, D_{ST}, components and the relative gene diversity, G_{ST}, was estimated (Nei 1973, Chakraborty and Leimar 1987). Deviations from Hardy-Weinberg proportions and gametic phase disequilibrium were assessed by the goodness-of-fit G-statistic (Sokal and Rohlf 1981) and Burrows' composite D (Weir 1979, Campton 1987), respectively. Duplicated loci, IDH-3,4, IDDH-1,2 and MDH-3,4 were omitted from the analyses of disequilibrium because variation could not be assigned to a particular locus. Homogeneity of allele frequencies among samples was tested by the G-test (Sokal and Rohlf 1981) after adjusting the significance level of $\alpha = 0.05$ for the number of simultaneous tests performed (Cooper 1968). The allele frequencies for samples from six geographic areas were pooled and again tested for homogeneity. The areas were (see Fig. 1 for sample number locations): 1) South Coast (sample numbers 1-2), 2) Russian River (3-5), 3) Mendocino Coast (6-18), 4) Eel River (19-21), 5) North Coast (22,23,27), and 6) Trinity River (24-26).

Genetic identities, I, based on allele frequencies of all 45 loci were calculated for each pair of samples (Nei 1978) and used to construct an unweighted pair-group

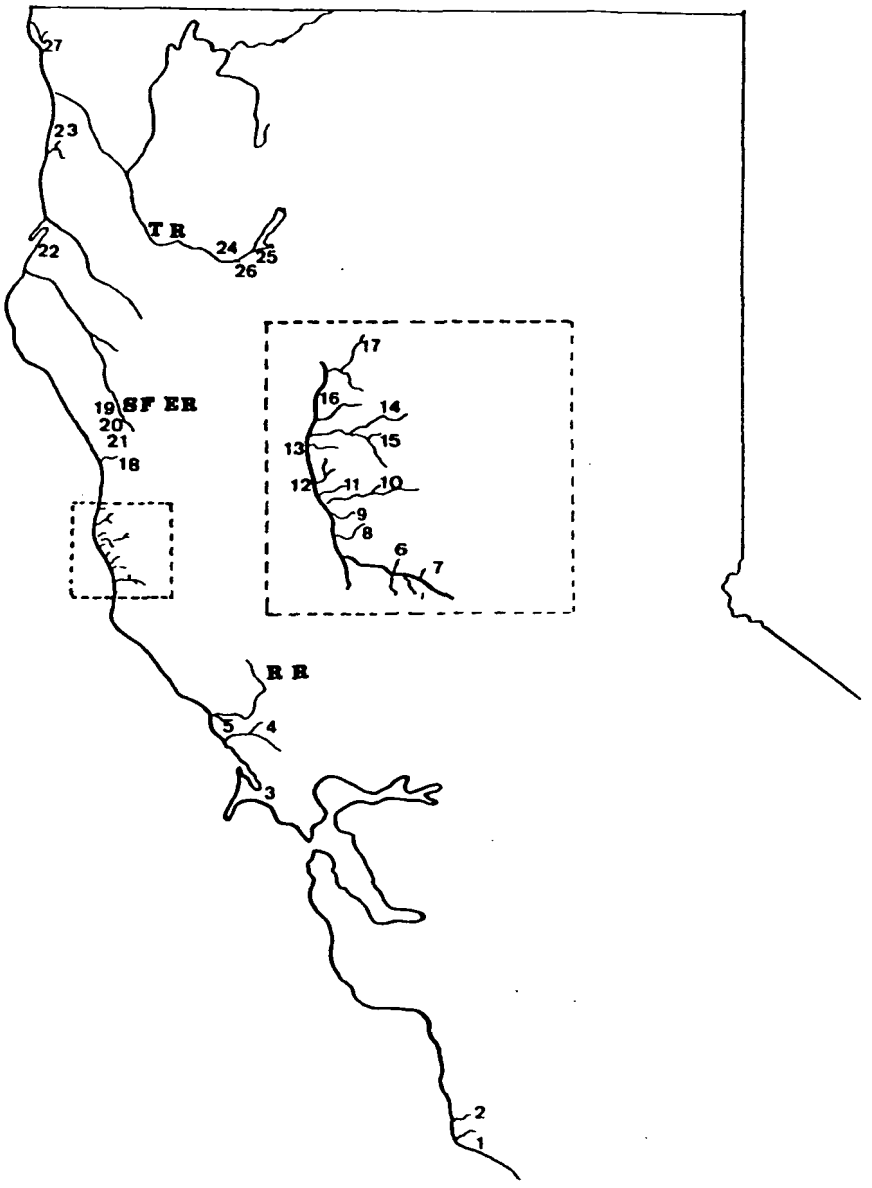

Figure 1. Collection sites for 27 populations of coho salmon in California. Numbers are identified in Table 1. TR = Trinity River, SF ER = South Fork Eel River, RR = Russian River.

Table 1. Collection sites for 27 populations of coho salmon from California. See Figure 1 for site locations. No. loci = number of loci analyzed. Heterozygosity is defined by Nei (1973).

Location (Site No.)	Number of fish	No. loci	Hetero-zygosity
Scott Creek (1)	39	35	0.000
Waddell Creek (2)	10	40	0.050
Lagunitas Creek (3)	32	35	0.024
Tanner Creek, Salmon Creek (4)	62	43	0.020
Willow Creek, Russian River (5)	38	33	0.014
Flynn Creek, Navarro River (6)	23	44	0.035
John Smith Creek, Navarro River (7)	15	42	0.034
Albion River (8)	30	45	0.038
Little River (9)	51	42	0.031
Twolog Creek, Big River (10)	23	44	0.042
Russian Gulch (11)	31	41	0.022
Caspar Creek (12)	82	45	0.034
Hare Creek (13)	28	44	0.033
Little North Fork Noyo River (14)	20	42	0.026
Kass Creek, Noyo River (15)	17	44	0.039
Pudding Creek (16)	47	44	0.032
Little N. Fk. Ten Mile R. (17)	22	45	0.026
Cottoneva Creek (18)	28	44	0.009
Huckleberry Cr., S.F. Eel R. (19)	52	44	0.042
Butler Creek, S.F. Eel R. (20)	30	44	0.026
Redwood Creek, S.F. Eel R. (21)	29	44	0.027
Elk River (22)	30	34	0.008
Prairie Creek (23)	3	43	0.042
Rush Creek, Trinity River (24)	7	32	0.014
Trinity River Hatchery (25)	111	44	0.039
Deadwood Creek, Trinity River (26)	26	40	0.008
West Branch Mill Cr., Smith R. (27)	30	39	0.016

dendrogram (Sneath and Sokal 1973). Gene diversity analysis followed Nei (1973).

A quantitative estimate of gene flow, the numbers of individuals exchanging genes between populations, was calculated from Wright's (1943) fixation index:

$$F_{ST} = 1/(4Nm+1)$$

where Nm is the average number of migrants per generation. This equation was solved for Nm by setting F_{ST} equal to the relative gene diversity G_{ST} (Nei 1977).

RESULTS

We observed allozyme variation at 23 of 45 (51%) isozyme loci studied (Appendices A-1 and A-2). Much of the variation was due to alleles with low frequencies. For example, 39% of the polymorphism observed at all loci over all samples involved variant alleles at frequencies of less than 5%. Also, of the 39 variant alleles identified, 27 (69%) occurred in three or fewer samples.

Table 2. Enzyme systems, abbreviations, number of loci scored, and tissue expression used in the analysis of 27 samples of coho salmon from northern and central California. M = muscle, E = eye, L = liver, B = blood.

Enzyme System	Abbreviation	No. of loci	Tissue
Aspartate aminotransferase	AAT	3	M,L
Aconitate hydratase	AH	1	L
Alcohol dehydrogenase	ADH	1	L
Adenylate kinase	AK	2	M,E
Fructose biphosphate aldolase	FBA	1	E
Creatine kinase	CK	5	M,E
ß-N-acetyl-D-galactosaminidase	ßGALA	1	L
Glycerol-3-phosphate dehydrogenase	GPDH	2	M
Glucose phosphate isomerase	GPI	3	M
L-iditol dehydrogenase	IDDH	2	L
Isocitrate dehydrogenase	IDH	4	M,E,L
Lactate dehydrogenase	LDH	5	M,E,L
Malate dehydrogenase	MDH	4	M,L
Mannose-6-phosphate isomerase	MPI	1	M,E,L
Phosphogluconate dehydrogenase	PGDH	1	M,L
Phosphoglycerate kinase	PGK	1	M,L
Phosphoglucomutase	PGM	2	M,L
Superoxide dismutase	SOD	1	L
Transferrin	TFN	1	B
Peptidase Substrates			
Glycyl-leucine	PEPA	1	M
	PEPC	1	E
Leucyl-glycyl-glycine	PEPB	1	M
Phenylalanyl-L-proline	PEPD	1	M

Genotypic frequencies conformed to Hardy-Weinberg proportions for all loci analyzed in all samples except for the PEPC locus in Flynn Creek (G = 4.60). Estimates of linkage disequilibrium revealed that 20 out of 299 (6.7%) comparisons significantly (P >.05) deviated from equilibrium values. No pattern of significant deviations was apparent: a pair of loci would be in disequilibrium in only one group and no more. The samples of coho salmon can be assumed to be in Hardy-Weinberg and linkage equilibrium, as the number of significant deviations was approximately what one would expect allowing for a 5% chance of a Type I statistical error.

Low levels of genetic variability were observed throughout the study area and only loose associations of alleles with geographic area were found. For example, the CK-2(85) allele was present at frequencies of 0.356 and 0.138 in two tributaries to the South Fork Eel River, Huckleberry Creek (19) and Redwood Creek (21), respectively, but the allele was absent from Butler Creek (20), which is also a tributary to the South Fork Eel River. The IDDH-1(150) allele was present in the three South Fork Eel River samples— Huckleberry Creek (19), Butler Creek (20), and Redwood Creek (21)— but was also found in Kass Creek (15) and Pudding Creek (16).

The GPI-3(85) allele was found exclusively in samples from the Trinity River system. The frequencies of this allele in Rush Creek (24), the Trinity River Salmon

Table 3. Summary of tests for homogeneity (G statistic, Sokal and Rohlf 1981) of allele frequencies for six geographic groups of California coho salmon (degrees of freedom in parentheses). Loci listed are those for which significant heterogeneity was observed before partitioning the data set into six geographic subgroups. N.V. and I.D. indicate no variation and insufficient data for comparisons, respectively.

Locus	South Coast	Russian River	Mendocino Coast	Eel River	North Coast	Trinity River
AAT-2	N.V.	N.V.	N.V.	N.V.	N.V.	0.98 (1)
CK-2	N.V.	N.V.	N.V.	30.68* (4)	N.V.	N.V.
BGALA	I.D.	N.V.	N.V.	2.17 (1)	2.49 (1)	N.V.
GPI-3	N.V.	N.V.	N.V.	N.V.	N.V.	5.14 (3)
IDDH-1	I.D.	I.D.	19.33 (12)	7.84	N.V.	I.D.
IDH-1	15.09* (1)	N.V.	N.V.	N.V.	N.V.	N.V.
IDH-2	27.90* (1)	N.V.	46.98* (9)	N.V.	5.67 (2)	N.V.
LDG-4	N.V.	8.33* (2)	N.V.	N.V.	10.38* (2)	N.V.
PGM-1	I.D.	4.28 (2)	84.06* (12)	1.40 (1)	4.61* (1)	N.V.
TFN	I.D	I.D.	76.95* (24)	9.53 (4)	I.D.	I.D.
PEPC	I.D.	I.D.	128.12* (13)	7.13* (2)	I.D.	0.98* (1)
PWPD	I.D.	I.D.	34.16* (14)	I.D.	I.D.	I.D.
TOTALS	42.99** (2)	12.62** (4)	389.60** (84)	58.75** (14)	23.15** (6)	12.11 (5)

* = $P < 0.05$.
** = significant G statistic after adjustment of α for multiple comparisons (Cooper 1968).

and Steelhead Hatchery (25), and Deadwood Creek (26) were 0.357, 0.126, and 0.135, respectively.

Heterozygosities ranged from 0.000 for Scott Creek (1) to 0.050 for Waddell Creek (2) (Table 1). The average heterozygosity of the 27 samples was 0.027. Geographic patterns or associations of heterozygosity estimates were not obvious; the two samples with the extreme values, Scott and Waddell creeks, were located adjacent to each other.

Total gene heterozygosity, H_T, and within-sample heterozygosity, H_S, of the 27 samples were 0.038 and 0.032, respectively. Genetic diversity among samples, D_{ST}, was 0.006. Thus, 84.2% of the total genetic variation (H_S/H_T) was due to variability within individual samples, whereas differences among samples ($G_{ST}=D_{ST}/H_T$) accounted for 15.8% of the variation. An estimate of 0.158 for G_{ST} yielded an estimate of 1.3 for Nm.

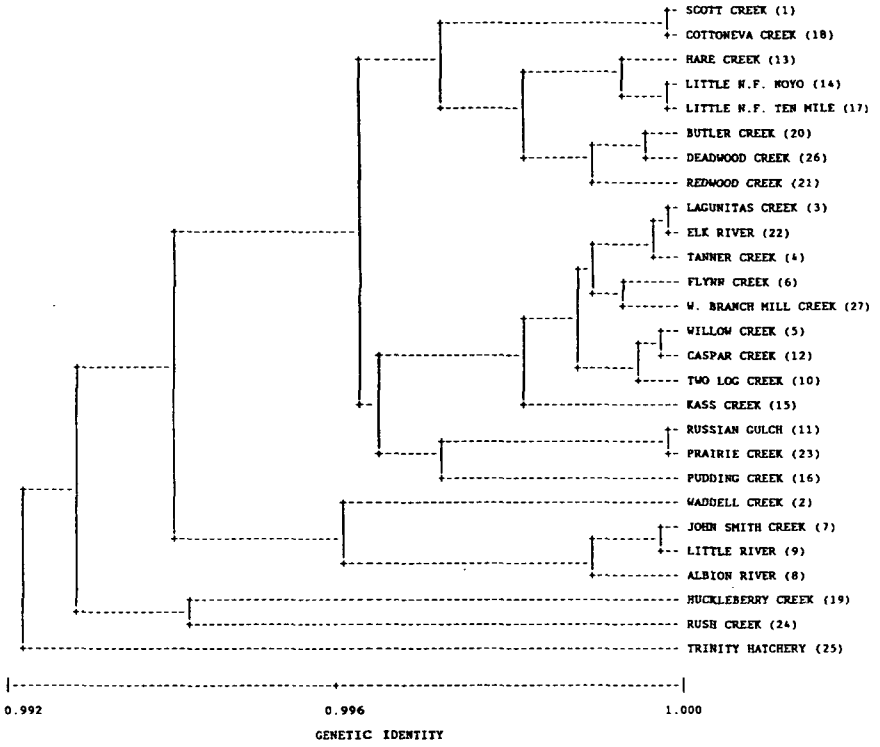

Figure 2. Dendrogram produced from unweighted pair group clustering of Nei's (1978) genetic identities between 27 populations of coho salmon from California.

Significant heterogeneity of allele frequencies was observed at 12 loci (Table 3) before partitioning the 27 samples into six geographic areas. After partitioning, heterogeneity still existed in all areas except for the Trinity River.

Average genetic identity between samples was 0.996. Various clusters of samples may appear in the dendrogram based on Nei's (1978) genetic identity values (Fig. 2). The clustering does not appear to reflect the geographic association of the samples.

DISCUSSION

The low level of genetic variability of California coho salmon (average heterozygosity value of 0.027) is characteristic of coho salmon from other areas of the Pacific Northwest. Allendorf and Utter (1979) reported an average heterozygosity of 0.015 for coho from Oregon and Washington; Olin (1984) found values of 0.026 to 0.052 (average 0.04) for populations from Oregon. Wehrhahn and Powell (1987) reported an average heterozygosity value of 0.0025 for Canadian populations of coho salmon, but they omitted the polymorphic transferrin locus.

Although 51% of the loci were polymorphic in this study, most of the variation was due to rare alleles that occurred in only a few samples. Wehrhahn and Powell (1987) found no loci that were polymorphic in more than one-fifth of 96 Canadian coho salmon populations. Olin (1984) found 31 of 53 (58%) loci to be polymorphic in 23 samples of Oregon coho salmon. In Olin's samples, 78% of the variant allele frequencies were less than 0.10. For coho populations from northwestern Washington, Reisenbichler and Phelps (1987) found only 2 of 54 loci (4%) with a common allele frequency of < 0.95.

The excessive and often undocumented transplants of coho salmon throughout the Pacific Northwest may obscure natural patterns of genetic variability and make geographical identification of stocks difficult. In the 1950s and 1960s the California Department of Fish and Game (CDFG) imported coho salmon eggs from Oregon to start most of California's hatchery stocks. During this same period, an extensive coho salmon stocking effort was undertaken in coastal streams using yearling fish produced from Pudding Creek and Noyo River egg sources. About 500,000 yearling coho salmon were stocked annually into watersheds of the north and central coastal regions. The Trinity River Salmon and Steelhead Hatchery coho program was started with eggs from native fish, as well as those from the Eel River, the Cascade and Alsea hatcheries in Oregon and the Noyo River Egg Taking Station. Currently, the Mad River and Warm Springs hatcheries provide fish and eggs for some coastal waters, as well as for the State's cooperative rearing programs. Eggs from the Noyo River Egg Taking Station are still taken for distribution of yearling coho salmon to other coastal waters, and State facilities routinely exchange coho eggs, unless there is a concern for disease transmission (L. Boydstun, Calif. Dept. Fish and Game, pers. comm.).

The coho population in Waddell Creek, Santa Cruz County, has apparently received eggs and transplants from hatcheries in northern California and Oregon and from private aquaculturists that did not keep records of their egg sources (D. Streig, Monterey Bay Salmon and Trout Project, pers. comm.). Thus, the varied origin of coho salmon in Waddell Creek may explain its high level of heterozygosity.

It is interesting that Scott Creek, which is about 6 km from Waddell Creek, showed no genetic variation. This suggests that coho salmon populations from the two creeks are maintaining some degree of reproductive isolation. Shapovalov and Taft (1954) observed that about 15% of the salmon tagged from the wild run of coho salmon in Waddell Creek strayed into Scott Creek, whereas about 27% of the fish marked in Scott Creek strayed into Waddell Creek. This amount of straying should be sufficient to homogenize the gene pools between the two creeks, if the straying salmon are actually contributing to the spawn (Allendorf and Phelps 1981), and unless Waddell Creek is currently being infused with new genes.

Although we could define very little in the way of a geographic pattern to the distribution of variant alleles, we did observe significant allele frequency differences among the 27 samples, which suggests that the coho salmon gene pool is not homogeneous throughout California. Given past and present stocking practices, this result is somewhat surprising. The causes of this heterogeneity are at present unclear. We do not know the relative influences of selection, drift, sampling error and human

activities on the genetic structure of California coho.

Some allele frequency differences may be maintained by selection. Certain transferrin genotypes have been shown to have increased resistance to bacterial kidney disease in specific stocks of coho salmon (Suzumoto et al. 1977, Winter, Schreck, and McIntyre 1980, Withler and Evelyn 1990). These same genotypes were also shown to be associated with poor growth and survival in one hatchery (McIntyre and Johnson 1977).

The frequency of transferrin alleles has been shown to vary significantly within the range of coho salmon (Utter, Ames, and Hodgins 1970). A north-south cline in the frequency of the TFN-(103) allele exists between samples from California and Oregon (Fig. 3); average frequencies of the allele in Olin's (1984) collections and ours were 0.34 and 0.80, respectively. Oregon also has had an extensive program of stock transfers within the State (Olin 1984). The fact that this cline exists, in spite of the homogenizing effects of stock transfers, may indicate a selective advantage for certain transferrin genotypes in California.

Transferrin expression on starch gels requires that the plasma be extracted from fresh blood and frozen prior to electrophoresis. Unfortunately, we were unable to score this locus for many of our collections because whole blood was frozen. With incomplete allele frequency data and vague stocking records, it is difficult to

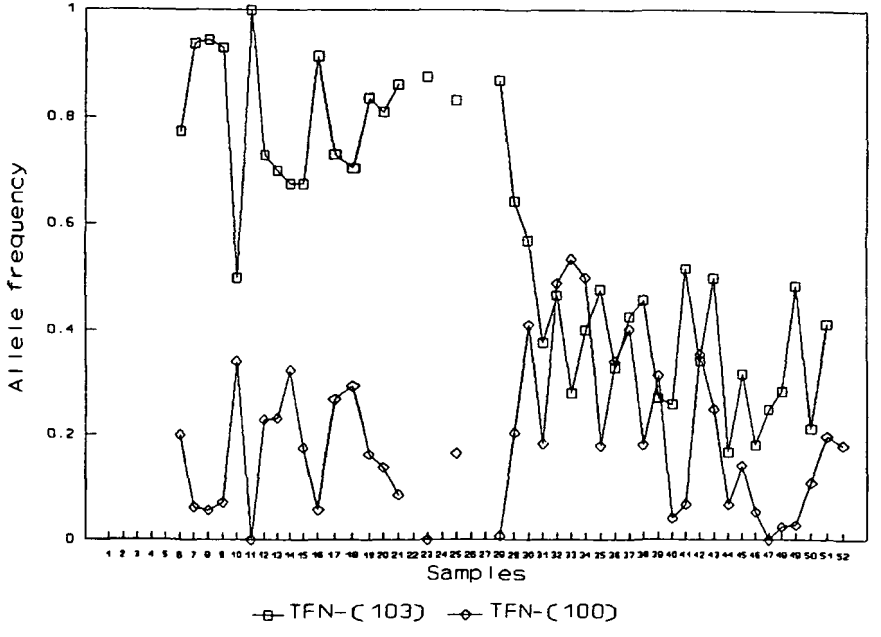

Figure 3. Frequencies of the TFN-(103) (squares) and TFN-(100) (diamonds) alleles in 27 samples of California coho salmon and 25 samples of Oregon coho salmon. Sample numbers 1-27 are from present study and numbers 26-52 are from Olin (1984). Sample numbers arranged from south to north with number 1 the most southern sample and number 52 the most northern. Gaps in line drawing indicate no data.

determine accurately the causes of the distribution of this allele.

Coho salmon may not be genetically differentiated on a geographic basis within their range in California, but may show differentiation when examined on a coast-wide basis. For example, Olin (1984) observed variant alleles at AAT-2, AH, CK-2, CK-3, PEPC and GPI-2, that were either extremely rare or not present in our California collections. The north-south cline in TFN-(103) may also serve to delineate broad areas of coho salmon. In addition, a GPI-3 variant we found in the Trinity River was only observed in one Oregon sample. Wehrhahn and Powell (1987) found geographical differences among populations of coho salmon from Vancouver Island, British Columbia, and Oregon. They felt that genetic differentiation may have resulted from bottlenecks and founder effects associated with glaciation in the late Pleistocene.

The natural genetic structure of coho salmon populations is assumed to be maintained by a balance between selection and gene flow. The level of gene flow will depend on the salmon's homing ability and the tendency to stray into non-natal streams. In coastal streams, high levels of straying and gene flow are expected as salmon from small unstable streams were shown to home less precisely than salmon from large stable streams (Quinn 1982). In our study, the average level of gene flow among coho salmon samples was considered high ($Nm = 1.3$), from an evolutionary standpoint (Slatkin 1981), but low from a population genetic standpoint (Allendorf and Phelps 1981).

Because coho salmon in California are restricted to the smaller, unstable coastal streams (Moyle 1976), straying may play a large role in influencing genetic variation within our study area. Berg and Gall (1988) also reported a lack of a genetic/geographic association among collections of coastal rainbow trout, *O. mykiss*, from northern California. Whereas, others (Utter et al. 1989, Bartley and Gall 1990) observed a strong geographic component to the genetic structure of chinook salmon, *O. tshawytscha*, a species that does inhabit large rivers in California and elsewhere.

An important application of allozyme analysis of salmonids has been in providing a means for stock identification to fishery scientists and managers (Pella and Miller 1987, Brodziak et al. in press). The application of these techniques to differentiate coho salmon populations within California appears problematic given the nature of the allozyme variation observed here. The usefulness of genetic stock identification for fishery management depends on the level of genetic divergence of populations, as well as on a fairly constant genetic structure of baseline populations: past and present transfers of coho salmon in California may have rendered the technique inappropriate for identifying stocks from localized areas in California. Significant allele frequency heterogeneity exists within the larger geographic areas except for the Trinity River area, and these geographic areas are not reflected in the dendrogram of genetic similarities.

We recommend continued study of California coho salmon populations. Genetic analyses could be greatly improved by increasing the samples sizes; only the sample from the Trinity River Salmon and Steelhead Hatchery contained the recommended number of 100 fish currently used by laboratories involved with salmon genetic stock

identification. Thorough examination of CDFG stocking records would also be beneficial in determining the possible existence of native gene pools or evaluating the effects of selection and random processes on coho salmon genetic structure. Improvements in estimation procedures, the increased number of isozyme loci being analyzed, and new techniques for DNA-level analyses (Hallerman and Beckman 1988) may also increase the usefulness of genetic analyses in stock identification of California coho salmon.

ACKNOWLEDGMENTS

We gratefully acknowledge the support of the California Department of Fish and Game and especially R. Painter for field collections of coho salmon. We are grateful to L. Boydstun for providing information on the stocking history of coho salmon. The manuscript benefitted from reviews and suggestions by W. Berg, L. Boydstun, and D. Campton. The San Diego State University Joint-Doctoral Program in Ecology provided partial funding for this research. This work is a result of research sponsored in part by the National Sea Grant College Program, NOAA, Department of Commerce, under grant number NA80AA-D-00120, project number 12/F-87, through the California College Sea Grant Program; and in part by the California Department of Fish and Game. The U.S. Government is authorized to reproduce and distribute reports for governmental purposes.

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Received: 23 October 1990
Accepted: 3 September 1991

Appendix A-1. Allele frequencies at the AAT-2 through IDH-3 loci from 27 populations of California coho salmon. See Figure 1 for stream locations by sample site number (shown under each stream name).

Locus (allele)	Scott Creek 1	Waddell Creek 2	Lagunitas Creek 3	Tanner Creek 4	Willow Creek 5	Flynn Creek 6	John Smith Creek 7	Albion River 8	Little River 9	Twolog Creek 10	Russian Gulch 11	Caspar Creek 12	Hare Creek 13	Little N.F. Noyo River 14
AAT-2 (100)		1.000		1.000		1.000	1.000	1.000	1.000	1.000	1.000	0.994	1.000	1.000
AAT-2 (110)												0.006		
AAT-3 (100)		1.000		1.000		1.000	1.000	1.000		0.977		1.000	1.000	1.000
AAT-3 (120)										0.023				
AM (100)	1.000		0.969	1.000	1.000	1.000		1.000	1.000	1.000	1.000	1.000	1.000	1.000
AM (125)			0.016											
AM (112)			0.016											
CK-2 (100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
CK-2 (85)														
CK-3 (100)	1.000	0.800	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.994	1.000	1.000
CK-3 (110)		0.200										0.006		
RGALA (100)		1.000		1.000	1.000	1.000	1.000	1.000	1.000	1.000		1.000	1.000	1.000
RGALA (90)														
GPI-2 (100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
GPI-2 (150)														
GPI-2 (50)														
GPI-3 (100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.967	0.980	1.000	1.000	0.988	1.000	1.000
GPI-3 (115)								0.033	0.020			0.012		
GPI-3 (85)														
GPI-3 (NULL)														
IDDH-1 (100)		1.000		1.000		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
IDDH-1 (150)														
IDH-1 (100)	1.000	0.750	1.000	1.000		1.000		1.000		1.000		0.992	1.000	1.000
IDH-1 (120)		0.250										0.008		
IDH-2 (100)	1.000	0.563	1.000	1.000		0.913		0.591		0.913		0.873	0.850	1.000
IDH-2 (80)		0.438				0.087		0.409		0.087		0.127	0.150	
IDH-3 (100)	1.000	1.000	1.000	1.000	1.000	0.978	1.000	1.000	1.000	0.957	1.000	0.988	1.000	1.000
IDH-3 (150)						0.022				0.022				
IDH-3 (130)												0.013		
IDH-3 (120)										0.022				

Appendix A-1. (Continued)

Locus	(allele)	Kass Creek 15	Pudding Creek 16	Little N.F. Ten Mile R. 17	Cottoneva Creek 18	Huckleberry Creek 19	Butler Creek 20	Redwood Creek 21	Elk River 22	Prairie Creek 23	Rush Creek 24	Trinity Hatchery 25	Deadwood Creek 26	West Branch Mill Creek 27
AAT-2	(100)	1.000	1.000	1.000	1.000	1.000	1.000	0.983		1.000		0.865	1.000	
	(110)							0.017				0.135		
AAT-3	(100)	0.912	0.978	1.000	1.000	1.000	1.000	1.000		1.000		1.000	1.000	
	(120)	0.088	0.022											
AH	(100)	1.000	0.826	1.000	1.000	1.000	1.000	1.000	1.000		1.000	1.000	1.000	1.000
	(125)		0.174											
	(112)													
CK-2	(100)	1.000	1.000	1.000	1.000	0.644	1.000	0.862	1.000	1.000		1.000	1.000	1.000
	(85)					0.356		0.138						
CK-3	(100)	1.000	1.000	1.000	1.000	1.000	1.000	0.983	1.000	1.000		1.000	1.000	1.000
	(110)							0.017						
βGALA	(100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000		0.625		1.000	1.000	0.867
	(90)									0.375				0.133
GPI-2	(100)	1.000	1.000	1.000	1.000	0.981	0.983	1.000	0.967	0.875	1.000	0.991	1.000	1.000
	(150)					0.019	0.017		0.033	0.125				
	(50)											0.009		
GPI-3	(100)	1.000	1.000	1.000	1.000	1.000	1.000	0.983	1.000	1.000	0.643	0.874	0.865	1.000
	(115)							0.017						
	(85)										0.357	0.126	0.135	
	(NULL)													
IDDH-1	(100)	0.912	0.989	1.000	1.000	0.940	0.948	0.931	1.000	1.000		1.000		1.000
	(150)	0.088	0.011			0.060	0.052	0.069						
IDH-1	(100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000		1.000	1.000	1.000
	(120)													
IDH-2	(100)	0.971	0.913	1.000	1.000	1.000	1.000	1.000	1.000	0.875		1.000	1.000	1.000
	(80)	0.029	0.087							0.125				
IDH-3	(100)	0.941	1.000	1.000	1.000	0.952	0.983	1.000	1.000	1.000	1.000	0.621	0.981	1.000
	(150)	0.029										0.379		
	(130)	0.029				0.048	0.017						0.019	
	(120)													

Appendix A-2. Allele frequencies at the IDH-4 through PEPD loci from 27 populations of California coho salmon. See Figure 1 for stream locations by sample site number (shown under each stream name).

Locus	(allele)	Scott Creek 1	Waddell Creek 2	Lagunitas Creek 3	Tanner Creek 4	Willow Creek 5	Flynn Creek 6	John Smith Creek 7	Albion River 8	Little River 9	Twolog Creek 10	Russian Gulch 11	Caspar Creek 12	Hare Creek 13	Little N.F. Noyo River 14
IDH-4	(100)	1.000	0.750	0.968	0.984	0.961	1.000	1.000	1.000	1.000	0.978	1.000	1.000	1.000	1.000
	(120)					0.039									
	(90)										0.022				
	(70)		0.250	0.032	0.016										
LDH-3	(100)		1.000		1.000		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	(125)														
LDH-4	(100)	1.000	1.000	0.871	0.893	0.987	1.000	1.000	1.000	1.000	1.000	1.000	0.994	1.000	1.000
	(115)			0.129	0.105	0.013							0.006		
MDH-3	(100)	1.000	0.700	0.922	0.893	0.986	0.978	0.714	0.983	0.902	0.957	0.952	0.982	1.000	1.000
	(110)														
	(120)		0.300	0.078	0.107	0.014	0.022	0.286	0.017	0.098	0.043	0.048	0.018		
MPI	(100)		1.000		1.000		1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	(110)														
	(80)														
PGDH	(100)		1.000	1.000	1.000		1.000	1.000	1.000	0.949	1.000	1.000	1.000	1.000	
	(120)									0.051					
PGM-1	(100)	1.000		0.760	0.871	0.892	0.682	0.700	0.767	0.630	0.804	0.887	0.846	0.786	0.950
	(120)			0.240	0.129	0.108	0.318	0.300	0.233	0.370	0.196	0.113	0.156	0.214	0.050
TFN	(103)						0.775	0.938	0.944	0.929	0.500	1.000	0.730	0.700	0.676
	(100)						0.200	0.063	0.056	0.071	0.341		0.230	0.233	0.324
	(97)						0.025				0.159		0.041	0.067	
	(106)														
PEPA	(100)	1.000		1.000	1.000	0.917	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.925
	(120)					0.083									
	(110)														0.075
	(89)														
PEPC	(100)	1.000					0.455	0.615	0.667	0.720	0.523	0.758	0.513	0.768	0.700
	(80)						0.545	0.346	0.300	0.280	0.477	0.242	0.487	0.232	0.275
	(120)							0.038	0.033						0.025
PEPD	(100)		1.000		1.000			1.000	0.900	1.000		0.850	0.991	0.981	
	(120)											0.150	0.009	0.019	
	(90)								0.100						

Appendix A-2. (Continued)

Locus (allele)	Kass Creek 15	Pudding Creek 16	Little N.F. Ten Mile R. 17	Cottonevn Creek 18	Huckleberry Creek 19	Butler Creek 20	Redwood Creek 21	Elk River 22	Prairie Creek 23	Rush Creek 24	Trinity Hatchery 25	Deadwood Creek 26	West Branch Mill Creek 27
LDH-4 (100)	1.000	0.967	1.000	1.000	0.962	1.000	1.000	1.000	0.875	1.000	1.000	1.000	1.000
(120)					0.019								
(90)					0.019								
(70)		0.033							0.125				
LDH-3 (100)	0.971	0.989	1.000	1.000	1.000	1.000	0.966		1.000	1.000	1.000	1.000	1.000
(125)	0.029	0.011					0.034						
LDH-4 (100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.883	1.000	1.000	0.970	1.000	1.000
(115)													
MDH-3 (100)	0.912	1.000	1.000	1.000	0.923	0.900	0.966	1.000	1.000	1.000	1.000		1.000
(110)							0.034						
(120)	0.088				0.077	0.100							
MPI (100)	1.000	1.000	1.000	1.000	1.000	1.000	1.000		1.000		0.924	1.000	1.000
(110)											0.061		
(80)											0.015		
PGDH (100)	1.000	0.964	1.000		1.000	1.000	1.000	1.000	1.000		1.000	1.000	1.000
(120)		0.036											
PGM-1 (100)	0.941	0.968	0.841	1.000	0.990	0.983	1.000		1.000		1.000	1.000	0.732
(120)	0.059	0.032	0.159		0.010	0.017							0.268
TPI (103)	0.676	0.914	0.731	0.706	0.837	0.810	0.862		0.875		0.832		
(100)	0.176	0.057	0.269	0.294	0.163	0.138	0.086				0.164		
(97)	0.147	0.029				0.052	0.052		0.125				
(106)											0.005		
PEPA (100)	1.000	0.989	0.864	1.000	0.952	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
(120)					0.019								
(110)					0.029								
(89)		0.011	0.136										
PEPC (100)	0.265	0.500	0.841	1.000	0.827	0.638	0.776		0.625	1.000	0.832		
(80)	0.735	0.500	0.159		0.173	0.362	0.224		0.375		0.168		
(120)													
PEPD (100)			1.000	1.000						1.000		0.978	
(120)												0.022	
(90)													

Calif. Fish and Game 78(3):105-115 1992

CULTURE OF SPOTTED SEATROUT, ORANGEMOUTH CORVINA, AND THEIR HYBRIDS

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Artificial propagation research with spotted seatrout (*Cynoscion nebulosus*) and orangemouth corvina (*Cynoscion xanthulus*) prompted interest in intrageneric hybrids between the two species. Spotted seatrout and hybrid fry were produced utilizing strip-spawning procedures following injection with human chorionic gonadotropin. Orangemouth corvina fry were obtained from use of a combination of hormone (des-Gly$_{10}$ [D-Ala^6]-luteinizing hormone-releasing hormone [1-9] ethylamide [LHRHa] and pimozide) and photoperiod-temperature manipulation to induce spawns. Twenty-two pond culture trials ranging from 18 to 40 days were conducted from 1984 to 1986. Fingerling survival for spotted seatrout, orangemouth corvina, spotted seatrout female X orangemouth corvina male, and reciprocal hybrids averaged (± SD) 51 ± 25.1% (*n*=7), 44 ± 39.7% (*n*=8), 36 ± 7.0% (*n*=5), and 76 ± 33.9% (*n*=2), respectively. Respective average production for the four fishes was 1.1, 2.9, 1.1, and 0.7 kg/ha/day. Average total lengths and weights were 44 mm and 0.74 g for spotted seatrout; 36 mm and 0.41 g for orangemouth corvina; 50 mm and 1.03 g for spotted seatrout X orangemouth corvina hybrids; and 48 mm and 1.43 g for reciprocal hybrids. Numbers of fingerlings reared were: spotted seatrout - 68,000; orangemouth corvina - 835,900; spotted seatrout female X orangemouth corvina male hybrids - 42,400; and reciprocal hybrids - 25,600. These successful initial attempts at pond culture of orangemouth corvina and the two hybrids indicate the fish can be produced in large numbers to satisfy requirements of a management or population enhancement stocking program.

INTRODUCTION

Spotted seatrout (*Cynoscion nebulosus*) support important recreational fisheries along the southeastern Atlantic and Gulf coasts (Perret et al. 1980, Collins 1981). Similarly, the orangemouth corvina (*Cynoscion xanthulus*) is a valued game fish in the Gulf of California and the Salton Sea (Whitney 1961, Black 1974). Both species are predatory (Whitney 1961, Perret et al. 1980) and therefore candidates for stocking in inland reservoirs overpopulated with forage species. Orangemouth corvina readily adapt to freshwater (Prentice 1985) but die at temperatures below 12°C in freshwater.

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Received: 18 June 1992
Accepted: 29 September 1992

Calif. Fish and Game 78(4):145-152

CRITICAL THERMAL MAXIMA AND OXYGEN MINIMA OF FIVE FISHES FROM THE UPPER KLAMATH BASIN

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We measured the critical thermal maxima and critical oxygen minima of five fishes from the Upper Klamath basin to determine their relative vulnerability to high temperatures and low dissolved oxygen. Species examined were shortnose sucker (*Chasmistes brevirostris*) speckled dace (*Rhinichthys osculus*) fathead minnow (*Pimephales promelas*) blue chub (*Gila coerulea*) and tui chub (*Gila bicolor*). Three Klamath largescale sucker (*Catostomus snyderi*) were also examined. Species ranked from greatest to lowest thermal maxima as follows: tui chub and fathead minnow similar to shortnose sucker and speckled dace, but greater than blue chub. Shortnose sucker and speckled dace were similar to blue chub. Species ranked from lowest to highest oxygen minima as follows: fathead minnow similar to tui chub and shortnose sucker, but greater than speckled dace and blue chub. Tui chub, shortnose sucker and speckled dace were not significantly different. This information suggests that fathead minnow and tui chub would be most likely to survive, shortnose sucker and speckled dace intermediate, and blue chub least likely to survive high temperature and low dissolved oxygen conditions. Limited information on Klamath largescale sucker suggests they are similar to shortnose sucker and speckled dace. Our observations support the hypothesis that increased temperatures and decreased dissolved oxygen levels have contributed to the decline of fishes in the Upper Klamath basin.

INTRODUCTION

Lost River sucker (*Deltistes luxatus*), shortnose sucker (*Chasmistes brevirostris*), Klamath largescale sucker (*Catostomus snyderi*), and blue chub (*Gila coerulea*) have suffered declines in population numbers in the Upper Klamath basin, Oregon, while tui chub (*Gila bicolor*) and introduced fathead minnow (*Pimephales promelas*) have not.

Blue chubs were once the numerically dominant fish in Upper Klamath Lake (Vincent 1968). Blue chub are no longer dominant (Beinz and Ziller 1987; Jeff Ziller, Oregon Dep. of Fish and Wildlife, unpubl. data) and recent studies suggest blue chub populations are reduced from historic levels, but data necessary to document this decline have not been collected (Jeff Ziller, pers. comm.). Reductions in Lost River and shortnose sucker populations lead to their being listed as endangered (USFWS 1988).

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Mortality of large numbers of Lost River sucker and smaller numbers of shortnose and Klamath largescale sucker and chubs coincided with high water temperatures, low dissolved oxygen levels, and high pH levels during 1986 in Upper Klamath Lake (Scoppettone 1986). Temperatures in Upper Klamath Lake can approach 30°C, dissolved oxygen levels can drop below 4 mg/l, and pH can rise above 10.5 (Coleman et al. 1988). Limnological data suggests these conditions occur more often and last longer today than they did in the past (Coleman et al. 1988). These observations led Scoppettone (1986) and others to hypothesize that poor water quality caused the mortalities.

If deteriorating water conditions were causing reductions in fish populations, then we would expect sucker and blue chub to be less tolerant of these conditions than relatively unaffected species, like tui chub and fathead minnow. Our objective was to measure and compare critical thermal maxima and critical oxygen minima of several fishes from the Upper Klamath basin to predict which would be likely to survive high temperature and/or low dissolved oxygen events.

We looked at temperature and dissolved oxygen tolerances because high temperatures and low dissolved oxygen levels may limit survival and distribution of fish in these systems (Vincent 1968, Scoppettone 1986, Coleman, Kann and Scoppettone 1988, Buettner and Scoppettone 1990). Correlations between tolerance ranges and the range of conditions fish encounter in nature are common (see review in Matthews 1987, Cech et al. 1990), suggesting tolerance is an important determinant of species distribution. We used critical maxima and minima because these methods are an efficient means for comparing the tolerance of fish to environmental stress (Becker and Genoway 1979, Kilgour and McCauley 1986). Matthews and Maness (1979) demonstrated that relative success of four species in thermally stressful environments was directly related to their comparative thermal maxima, suggesting tolerance determines a species' ability to thrive in variable environments.

Species examined in this study were shortnose sucker, speckled dace (*Rhinichthys osculus*) fathead minnow, blue chub, tui chub and Klamath largescale sucker. These species include fishes with declining, stable or increasing populations in the Upper Klamath basin. Only speckled dace inhabit streams their entire life cycle (Moyle 1976). All other species spend significant portions of their lives in lakes (Moyle 1976, Buettner and Scoppetone 1990). We collected no data on Lost River sucker and little data on Klamath largescale sucker because no Lost River sucker and only three Klamath largescale sucker were available.

METHODS

Fishes were collected by seining or electrofishing from the Upper Klamath basin. Shortnose sucker were provided by the Klamath Tribe's Braymill Hatchery. Fish were acclimated to 20°C and fed cladocerans, mosquito larvae, tubificid worms, frozen brine shrimp, and flake food for at least 6 weeks prior to experiments. Several shortnose sucker had incomplete opercular covers and curved spines, possibly indicating an unbalanced diet (lack of vitamin C, Stickney 1979) during early development. We did not test fish with visible abnormalities.

We followed Becker and Genoway's (1979) guidelines for determination of critical maxima of fishes. Fish were weighed, placed in individual plexiglass tubes (6 cm long, 1.5 cm diameter), acclimatized to the tubes for 2 h, and exposed to increasing temperature (0.3°C per min) or decreasing dissolved oxygen (1.25 torr partial pressure of oxygen [PO_2] per min [1 torr = 133.3 Pa]) to determine their critical thermal maxima and critical dissolved oxygen minima. Five fish were run simultaneously. Care was taken to make sure results for fish run simultaneously were independent (i.e., no visual or chemosensory interaction among fish) and that runs contained fish selected randomly from the six species tested. End-point reported is permanent loss of equilibrium (defined as the temperature or dissolved oxygen level at which a fish could no longer right itself despite prodding with a nylon filament).

Temperature was manipulated by regularly adjusting a mercury thermostat/relay which controlled a pump that mixed hot water (>40°C) with 20° water to achieve the desired temperature (± 0.5°) in a mixing tank. Hot water, 20° water and mixed water were aerated to maintain dissolved oxygen levels at air saturation. Mixed water then flowed through fish enclosures exposing fish to manipulated temperature conditions. Temperature in each enclosure was continuously monitored with temperature probes (YSI Model 401).

Dissolved oxygen concentrations were changed by adjusting an electronic, gas-mixing flowmeter to proportionally mix nitrogen and oxygen. The mixed gas was equilibrated with 20° water in a multi-chambered gas stripping column to achieve the desired dissolved oxygen tension (± 5 torr PO_2). Water from the column flowed through fish enclosures exposing fish to manipulated oxygen levels. Dissolved oxygen tension in the water flowing into the fish enclosures was continuously monitored with an electrometric oxygen analyzer system (Radiometer Model PHM 71/D616/E5046). The plexiglass enclosures denied fish access to the surface where they might respire oxygen-rich water.

Fish weights were compared using ANOVA. Critical minima and maxima values were log-transformed and interspecies differences were compared using a blocked ANOVA with fish weight as a factor. Specific differences were identified using appropriate hypothesis tests (Wilkinson 1988) with sequential Bonferroni adjustments (Rice 1989).

RESULTS

Fish used for each maxima or minima determination were small (between 0.88 g and 3.65 g) and the mean weights for each species were not significantly different (Table 1).

Tui chub and fathead minnow had significantly greater critical thermal maxima than blue chub (Table 2). Shortnose sucker and speckled dace were not significantly different from tui chub and fathead minnow or from blue chub. Datum on one Klamath largescale sucker fell within the ranges for all other species tested.

Fathead minnow had a significantly lower critical oxygen minimum than speckled

Table 1. Means (± SE)[1,2] and ranges for weights (g) of fishes used for critical thermal maxima and critical oxygen minima measurements.

	Weight (g)			
	Thermal maxima		O_2 minima	
Species	Mean	Range	Mean	Range
Fathead minnow	1.82±0.14	1.27-2.72	1.66±0.16	1.07-2.64
Tui chub	1.72±0.16	0.93-2.80	1.73±0.20	0.88-3.02
Shortnose sucker	2.10±0.25	1.16-3.24	1.96±0.22	1.11-3.32
Klamath largescale sucker	2.94*	--*	2.78±0.43*	2.29-3.63
Speckled dace	2.12±0.25	1.53-3.65	2.06±0.11	1.63-2.60
Blue chub	1.62±0.14	0.90-2.16	1.46±0.13	1.19-2.63

[1] 10 replicates for each species except for critical oxygen minima measurements for fathead minnow (9 replicates) and critical thermal maxima (1 individual), and critical oxygen minima (3 replicates) for Klamath largescale sucker.
[2] Weights are not significantly different between species ($P > 0.05$).
* Not enough data for Klamath largescale sucker to warrant statistical comparison with other fishes or a range entry for critical thermal maxima.

dace and blue chub (Table 2). Tui chub and shortnose sucker were similar to both fathead minnow and speckled dace. Although speckled dace had a significantly higher minimum than fathead minnow, they were not significantly different from tui chub and shortnose sucker. Blue chub had the highest minimum. Data on three Klamath largescale sucker suggest they were similar to shortnose sucker and speckled dace.

DISCUSSION

Temperature Tolerance

Our data suggest that fathead minnow and tui chub would be most tolerant, speckled dace and shortnose sucker intermediate, and blue chub least tolerant of high temperatures (Table 2). Possible declines in blue chub populations could be due to increased temperatures. Shortnose sucker were not significantly different from blue chub and have declined in numbers. Speckled dace were also not significantly different from blue chub in their tolerance to high temperatures, but we could not find information on the status of speckled dace populations. Because speckled dace are primarily inhabitants of cool, flowing streams (Moyle 1976), they may find refuge from high temperatures by remaining upstream of warmer reaches of rivers and lakes in the Upper Klamath basin.

The highest temperatures recorded in Upper Klamath Lake did not exceed 30°C (Coleman et al. 1988), and these were recorded only in dense algal scum. Coleman and his coworkers rarely recorded temperatures greater than 25°C in their limnological surveys of Upper Klamath Lake, Agency Lake, and Sprague and Williamson rivers. Even if we consider that critical thermal maxima may overestimate the upper limit of a fishes tolerance range by 2-6°C (Kilgour and McCauley 1986, Becker and Genoway 1979), temperatures rarely reach lethal levels in Upper Klamath Lake for any of the

Table 2. Means (± SE)[1] and ranges for critical thermal maxima and critical oxygen minima of six species of fishes from the Upper Klamath basin.

	Thermal maxima (°C)		O_2 minima (torr)	
Species	*Mean*	*Range*	*Mean*	*Range*
Fathead minnow	33.1±0.2[a]	31.8-33.1	8.4±0.5[a]	6.7-11.3
Tui chub	33.2±0.2[a]	32.3-34.1	9.8±0.7[a,b]	6.7-14.2
Shortnose sucker	32.7±0.1[a,b]	32.1-33.3	11.8±1.0[a,b]	7.5-16.7
Klamath largescale sucker	32.6*	--*	12.7±3.1*	7.9-18.6
Speckled dace	32.4±0.6[a,b]	27.8-33.7	13.4±1.0[b]	8.0-17.9
Blue chub	31.5±0.4[b]	28.3-32.8	18.2±1.4[c]	11.8-25.5

[1] Sample sizes same as for Table 1.
[a,b,c] *Means for maxima or minima with similar superscripted letters are not significantly different ($P > 0.05$).*
* Not enough data for Klamath largescale sucker to warrant comparison with other fishes or a range entry for critical thermal maxima.

fishes we considered in this study. This does not mean that high temperatures are not affecting the viability of fish populations in the Upper Klamath basin. Earlier life history (egg to juvenile) stages of fish may be more vulnerable to high temperatures, and the ability to reproduce may be more sensitive to environmental stress than any other aspect of a fishes' life history (Gerking 1980). The fact that species ranked in order of increasing tolerance to high temperatures matched their rank in order of declining to increasing populations suggests that high temperatures may play a role in the decline of populations of fishes in the Upper Klamath basin.

The critical thermal maxima of species studied here fall within a 1.7°C range (Table 2) This narrow range suggests that if less tolerant fishes are being adversely affected and environmental conditions continue to decline, all species will soon be affected.

Dissolved Oxygen Tolerance

Critical oxygen minima for the species studied here also fall into a small range, with one exception. Blue chub were less tolerant of low dissolved oxygen than all other species (Table 2), suggesting blue chub would be the first species affected by critically low dissolved oxygen events. Fathead minnow were more tolerant than speckled dace, but were similar to tui chub and shortnose sucker, suggesting these species would be adversely impacted by similarly low levels of dissolved oxygen.

The ability to survive low dissolved oxygen conditions may be important for fish living in Upper Klamath Lake. Dissolved oxygen levels as low as 0.3 mg/l (5 torr) have been measured in Upper Klamath Lake (Scoppettone 1986, Coleman et al. 1988). Vincent (1968) observed that dissolved oxygen levels showed an inverse correlation with tui chub and especially blue chub distributions. Dissolved oxygen levels are lowest near the bottom, exposing bottom dwelling suckers to critically low levels of dissolved oxygen (Buettner and Scoppettone 1990). Scoppettone (1986)

reported that substantial numbers of blue chubs that were trapped live died in the traps and attributed this to the traps confining fish in an area of the lake with low dissolved oxygen. Scoppettone (1986) also reported that both suckers and chubs appeared to be distressed and lethargic during poor water quality events in Upper Klamath Lake.

In Upper Klamath Lake, high temperatures promote algal blooms and these algal blooms result in low dissolved oxygen and high pH conditions (Hazel 1969) such that stressful temperature, dissolved oxygen, and pH conditions occur simultaneously. We have demonstrated low tolerance to high temperature and low dissolved oxygen concentrations in fishes with declining populations in the Upper Klamath basin. Falter and Cech (1991) demonstrated low tolerance to high pH conditions in the endangered shortnose sucker. Unfavorable temperature, dissolved oxygen, and pH conditions probably have synergistic effects on fish survival, such that stressful levels of one variable lowers tolerance of another variable (Wedemeyer, McLeay, and Goodyear 1984). For example, high temperatures reduce the ability of fish to survive low dissolved oxygen events because high temperatures increase metabolic oxygen demand while decreasing hemoglobin-oxygen affinity.

CONCLUSIONS

Our objective was to obtain comparative values for the species we considered. In general, species experiencing population declines were less tolerant of high temperatures and low dissolved oxygen levels than species with relatively stable or increasing populations. This observation supports the hypothesis that increased temperatures and decreased dissolved oxygen levels have contributed to the decline of fishes in the Upper Klamath basin.

Workers in the Upper Klamath basin have observed an increase in fathead minnow populations coincident with a decline in blue chub and have speculated that fathead minnow are replacing blue chub (Jack Williams, Bureau of Land Management, pers. comm.). Our data suggest that blue chub are less well-suited than fathead minnow to changing conditions in the Upper Klamath basin. It is likely that possible declines in blue chub populations are due to degraded environmental conditions, while the increase in fathead minnow populations is due to their recent introduction to the system (Andreason 1975) and their ability to thrive in warmer, less oxygenated waters.

The strength of any conclusion concerning effects of environmental variables on status of fish populations in the Upper Klamath basin is impaired by the lack of published data on these species. In addition, other factors (e.g., environmental contaminants, disease, introduced predators and competitors, dam construction, diversion of water, temporary dewatering of spawning streams, and overfishing) have changed along with changes in temperature and dissolved oxygen levels. Although we can not conclude that increasing temperature and decreasing dissolved oxygen conditions have caused reductions in fish populations, our data suggest that these factors may have played a role in these reductions and/or could prevent the recovery of fish populations.

ACKNOWLEDGMENTS

The California Department of Fish and Game, United States Fish and Wildlife Service, Oregon Department of Fish and Wildlife, and especially Klamath Tribe Fish and Wildlife contributed to our efforts. Comments from C. Bond, P. Moyle, G. Scoppettone and C.R. Feldmeth improved the manuscript.

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Received: 8 June 1992
Accepted: 15 October 1992

Calif. Fish and Game 78(4):153-159

ILLEGAL HARVEST OF SPIKE BUCKS DURING A REGULATED MULE DEER HUNT

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The illegal harvest of deer (*Odocoileus* spp.) removes a component of the population that is difficult to assess. This creates an error factor that can be important when developing management plans based on density-dependent harvest rates related to age and sex class. We designed a study to measure the number of spike mule deer illegally killed by licensed hunters and examined how to consider these data in our management plan. We found that spike bucks comprised 3.8% to 11.5% of the total deer kill and their harvest was not correlated to tag type. This percentage represents the minimum number of bucks illegally harvested because hunters did not recognize spikes which were illegal under their respective tags. We recommend that managers regulating land holdings with restricted access consider harvesting spike bucks and manage the total harvest of bucks in accordance with age and sex class.

INTRODUCTION

An accurate estimate of total harvest is important when developing effective management plans for big game. Contemporary plans may incorporate a Linked Sex Harvest Strategy to manage herds in a density-dependent manner where harvest levels of each sex are related to age class and minimum population size (McCullough et al. 1990). These plans are greatly strengthened by knowing the age class of males that are harvested or removed from the herd by hunters. Determining the number of males removed is particularly important in Southern California where mule deer populations are small, non-migratory and in many cases, occupy fragmented habitats. Here, knowing the number of deer killed in each sex and age class is important for developing management plans that avoid over-exploitation.

One of the most difficult components of total harvest to ascertain is illegal kill because of the secretive nature of people that violate laws. Thus, most estimates of illegal kill have large confidence intervals, and often are derived by the indiscriminate use of data collected as part of normal operating procedures, ignoring necessary assumptions required by the statistical analysis used (Cowles et al. 1979). Beattie et al. (1980), in an effort to improve confidence intervals to reliable and meaningful levels, recommended using two or more estimating techniques. Although this may

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Calif. Fish and Game 78(4):174-176

CALIFORNIA FISH AND GAME, CALIFORNIA'S LONGEST CONTINUOUSLY PUBLISHED JOURNAL

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While a graduate student at the University of California in the 1980s, I frequently sat in the library flipping through volumes of *California Fish and Game* looking for articles on deer (there have been more than 100 published on deer in California). What I usually ended up doing was getting side-tracked by the wealth of non-technical articles, stories, editorials, color plates, and photographs that comprised the bulk of the journal from its first issue in 1914 until the 1930s. I "wasted" many hours reading stories, life history notes, about wildlife species and their conservation in California and other states. Since the late 1940s, the journal has been a technical journal publishing peer-reviewed articles related to fish and wildlife.

The journal, (early editors called it a "magazine" or "quarterly") has been a State of California publication for 78 continuous and uninterrupted years. The journal has always been produced and printed at the Office of State Printing in Sacramento. The last page typically provided the job number and the number of copies printed, although recently, only the job number has been printed.

Editorship of the journal has rotated among the "fact-finding" programs within the Department of Fish and Game (currently Inland Fisheries, Marine Resources, Bay-Delta, and Wildlife Management). Each program finds a willing participant when its their turn to serve as lead editor. This task comes in addition to the individual's regular duties. One obvious benefit for each of the programs while they have editorship is that the journal tends to emphasize the editors program area (e.g., wildlife) because of the greater familiarity with potential authors, reviewers, and subject matter (i.e., wildlife papers tend to go through the system faster with a wildlife editor than do fisheries papers). Each program assigns "volunteers" to serve as Associate Editors to handle the review process for articles in their area of expertise.

California Fish and Game has had the same cover since its first issue, right? Well, almost. The very first issue in October 1914 (1:1) (Volume 1 had five issues) had a photograph of a waterfall on the cover (I do not know the location of the waterfall). Since then, the traditional cover with the line drawing of a trout (presumably a rainbow), deer, and quail depicting three of the wildlife species of interest in 1914 (original artist unknown). The cover drawing remained unchanged until volume 61(2) when it was cleaned-up and modified, presumably to improve legibility. However, the deer looked like a white-tail with an unlikely antler configuration, and the quail appeared to be a Mearn's with a California quail top-knot.

The phrase "Conservation of wild life through education" is the theme of the journal, and has remained on the cover since the beginning. Issue 38(2) however,

changed the phrase slightly by converting it from drawn text to typestyle and joined the words "wild" and "life" into "wildlife." I recently changed the phrase back to its original two word configuration, but not without comment in the office that I had made a mistake! At its inception, this theme was spawned by controversial issues such as the selling of waterfowl in the markets of California and the closing of Catalina Island waters to net fishing. The first issues of California Fish and Game dealt heavily with the growing concern about utilization and conservation of wildlife (see Volume 25(3):206). The focus was to get the message out to the public about the importance of fish and wildlife conservation. Initially then, the primary target audience was not the scientific or professional reader as it is today.

The cover stock was gray from volume 1(2) to 17(2) and since then has been a variation of green depending on stock available at the printing plant (cover stock is purchased by the plant in bulk orders for a variety of jobs). For its' 75th year in 1989, the journal was printed using a gold cover.

Previous editor Dr. Robert Lea changed the journal from a January-April-July-October format to Winter-Spring-Summer-Fall because he could not guarantee when the issue would come out (it is largely up to the vagaries and priorities of the State Printing Plant). I've recently found that lack of a state budget can also affect publication schedules, I can't guarantee which season an issue will come out!

In the fall of 1990 we implemented some major overhauls related to producing and distributing the journal by converting production to a desktop publishing format on a PC and easily justified from a cost-benefit perspective, the purchase of a computer, printer, and software. Using a scanner, I scanned a recent version of the cover into a graphics "paint" program and modified it to improve the clarity of the line drawings, and most importantly as a California deer ecologist, changed the apparent white-tailed deer with the unlikely antler configuration into a mule deer with more likely antlers. We also modified the quail into a more reasonable (albeit robust) facsimile of the California quail!

The other major change is that the mailing list has been completely re-entered into a PC-based software package (DBASE) to cut costs and hopefully improve efficiency in updating the list. Previously, the mailing list was maintained on a VAX-main frame machine that we could access remotely, was overly cumbersome, and was dependent upon others. These changes have cost little except time. The journal is still considerably off schedule in production and delivery because of the time required to implement these changes, but it is slowly creeping back. The benefit to the subscriber is that the journal is produced more economically and we are able to keep the subscription cost at the same level it has been for several years, which is fantastic given the budgetary problems that have faced the Department of Fish and Game and the state of California.

The Department of Fish and Game regards this publication as an information tool designed primarily to provide its professional biological staff and cooperating scientists with information of specific interest and application to California flora and fauna. Any employee of the Department of Fish and Game may receive the journal free of charge. Additionally, we have a large exchange subscription base with domestic and foreign subscribers and receive many comparable publications for our reference

libraries. Paid subscriptions round out the distribution list. At last look, the journal went to 47 states and 45 countries, as well as most major libraries in California and many other state and federal agencies.

A few articles have been published twice or more. For example, *Bird Life as a Community Asset* by Joseph Grinnell was originally published in 1914. I read it recently and thought it so pertinent to current ecology that I re-ran the article in volume 77(1). Shortly thereafter, I found that editor Richard Croker had also thought it a worthy article when he re-ran it in volume 25(3)! Among the most impressive issues have been the trout, salmon, hawk, and warm-water fish issues which had beautifully done color plates in every copy [e.g., Volumes 3(1), 5(3), 7(3), and 35(4)]. A trout issue was done again in volume 19(2).

During the 1930s, the non-technical aspects of the journal such as editorials, news items, photographs, and observational reports gradually declined. Part of this was due to the establishment of the "*California Conservationist*" in 1936, the official publication of the Department of Natural Resources. This information-packed monthly publication appears to have lasted only until 1941? *Outdoor California*, which apparently was a weekly newsletter beginning in the 1930s, became a monthly publication in 1953. It too, contained similar news items and reports. By the 1940s, all the editorial, news-style information, photographs, and similar information was eliminated from the journal and it became more technical, primarily publishing peer-reviewed articles and notes, with occasional items of interest.

The journal flourished with technical and informative articles from many Department personnel on fish and wildlife during the 1950s-60s. I consider articles published on wildlife during that time to be the most informative, data-rich articles on terrestrial wildlife that the journal has ever published. For example, there were numerous individuals contributing to research efforts on deer and upland game from the late 1940s until the 1960s which spawned many publications in the journal. Efforts from the marine resources and inland fisheries programs however, have likely been the most steady and productive units in the journal's history.

However, an unfortunate trend I have seen in the journal has been a decline in articles published by Department of Fish and Game employees. I think this is symptomatic of a long-term decline in research effort by the Department, increasing responsibilities on the environmental protection front, and the passing of research projects to outside contractors such as the University of California and private contractors. Our current director, Boyd Gibbons, recently expressed his desire to see the Department become more highly respected in the scientific community. Hopefully, this will ultimately translate into a renewed commitment by the Department to strengthen investigation about how California's fish, wildlife, and native plants interact with each other, with their habitats, and with human-induced impacts.

This Department has established quite a prestigious vehicle to carry the message of "Conservation of Wild Life Through Education" for almost 80 years. Take a look back to the past and you'll see that many conservation concerns haven't changed much, we've just made them more complicated.

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