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The Use of Parasites in Discriminating Stocks of Pacific Halibut (Hippoglossus stenolepis) in the Northeast Pacific

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Abstract—The use of parasites as indicators of the stock structure of Pacific halibut (*Hippoglossus stenolepis*) in the northeast Pacific was investigated by using 328 adult (>55 cm fork length) halibut from 15 composite localities ranging from northern California to the northern Bering Sea and 96 juvenile (10–55 cm) halibut from five localities ranging from the northern Queen Charlotte Islands to the Bering Sea. Counts of eight selected parasite species (the juvenile acanthocephalans *Corynosoma strumosum* and *C. villosum*, the metacestode *Nybelinia surmenicola*, the digenean metacercaria *Otodistomum* sp., and the larval nematodes *Anisakis simplex*, *Pseudoterranova decipiens*, *Contracaecum* sp., and Spirurid gen. sp.) that produce infections of long duration, do not multiply in the host, and that have a relatively high abundance in at least one geographic locality were subjected to discriminant function analysis. Juvenile Pacific halibut showed no separation and, even though they were not heavily infected with parasites, the analysis suggested that juveniles could be a mixed stock. Three groups of adults were identified: fish from California to the southern Queen Charlotte Islands, those from the northern Queen Charlotte Islands to the central Bering Sea, and those from the central and northern Bering Sea. These groups suggest that the single stock concept be more thoroughly evaluated.

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The Pacific halibut (*Hippoglossus stenolepis*) is an Arctic–Boreal Pacific pleuronectid flatfish ranging throughout the North Pacific from southern California to northern Japan, but is most abundant in the Gulf of Alaska. The halibut supports one of the top five commercial fisheries in North America, with average annual landings of approximately 25,000 metric tons from 1991 to 1995 (IPHC, 1996), and is also widely sought in the sport fishery, thus contributing significantly to west coast economies. The International Pacific Halibut Commission (IPHC) is responsible for management of the resource. From the 1930s through the 1950s the IPHC recognized at least three stocks of halibut from tagging experiments, egg and larval drift, anatomical differences, and differences in growth rate: 1) those in the Bering Sea; 2) those from the Gulf of Alaska south to Cape Spencer, Alaska; and 3) those south of Cape Spencer (Skud, 1977). These boundaries roughly followed the zoogeographic zonation in the North Pacific. Skud (1977) re-analyzed the data and concluded that there was extensive intermingling of fish among areas and that there was no evidence to indicate that fish north and south of Cape Spencer, Alaska, constituted different stocks. Available biochemical evidence (Tsuyuki et al., 1969; Grant et al., 1984), although limited in scope and by sampling effort, suggests little genetic variation throughout the northeast Pacific. As a result, the IPHC manages halibut as a single population, but with statistical divisions for management of data.

Parasites have been used successfully to distinguish populations or stocks of fishes and, as a result, provide information useful in fisheries management (see

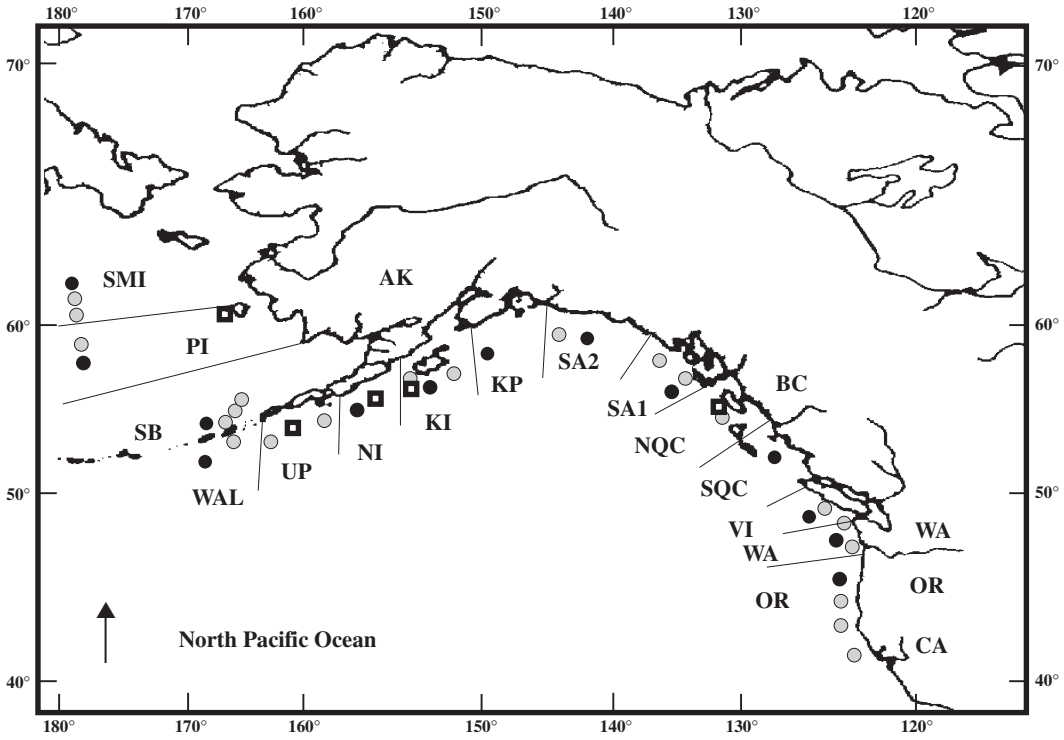

Figure 1

Sampling localities for 328 adult (circles) and 96 juvenile (squares) Pacific halibut, *Hippoglossus stenolepis*, in the northeast Pacific. OR = Oregon–northern California, WA = Washington, VI = Vancouver Island, SQC = southern Queen Charlotte Islands, NQC = northern Queen Charlotte Islands, SA1 = southeast Alaska site 1, SA2 = southeast Alaska site 2, KP = Kenai Peninsula, KI = Kodiak Island, NI = Nagai Island, UP = Unimak Pass, WAL = western Aleutian Islands, SB = southern Bering Sea, PI = Pribilof Island, SMI = St. Matthew Island. Individual hauls with at least 10 fish (for a total of 202 fish) are shown as solid circles. Other collection sites are shown as stippled circles. See Table 1 for sample sizes.

reviews by Lester, 1990; Moser, 1991; Williams et al., 1992). With respect to flatfish, Gibson (1972) used parasitological data to distinguish three groups of *Platichthys flesus* and Krzykawski and Wierzbicka (1982) used parasitological data and other information to distinguish between Barents Sea and Labrador stocks of Greenland halibut, *Reinhardtius hippoglossoides*. Khan et al. (1982) and Arthur and Albert (1993) used parasites to distinguish between Atlantic and Gulf of St. Lawrence stocks of *R. hippoglossoides*, and Boje et al. (1997) used parasites to indicate differences among Greenland stocks of Greenland halibut and stocks from the western Atlantic. No similar work on flatfishes has been done in the Pacific and, with the exception of Krzykawski and Wierzbicka (1982) and Boje et al. (1997), there has been no attempt to distinguish between stocks of a species across a significant portion of the species' range.

In this article, we use discriminant analysis on counts of some of the parasites from adult Pacific halibut to determine if they form discrete groups or stocks in the northeast Pacific. We do a similar analysis on the juvenile fish and compare the results to the adult analysis to determine when separation is likely to occur.

Materials and methods

A total of 328 adults (>55 cm fork length) from 15 composite localities, ranging from northern California to the vicinity of St. Matthew's Island in the Bering Sea and 96 juveniles (10–55 cm) from five localities ranging from the northern Queen Charlotte Islands to the Bering Sea (Fig. 1), were caught by staffs of the IPHC and the U.S. National Marine Fisheries Service during the summers of 1990–92 (using longlines and trawls). Most localities (for the adult samples) included fish taken from several hauls; however, 202 fish came from 13 individual hauls, each of which contained at least 10 fish. Fish were bagged individually and immediately frozen at sea for later examination.

Fish and parasites were processed by using standard parasitological techniques (see Blaylock et al., 1998a). We followed Bush et al.'s (1997) definitions for prevalence, abundance, and intensity. Parasites used in the analyses were chosen according to the guidelines of Arthur and Albert (1993). Only those species with infections of long duration, that do not multiply in the host, and that have a relatively high abundance in at least one geographic locality were used. Of the 59 parasite taxa identified from

Pacific halibut (Blaylock et al., 1998a), eight taxa met these criteria: the juvenile acanthocephalans *Corynosoma strumosum* (body cavity) and *C. villosum* (body cavity), the metacestode *Nybelinia surmenicola* (stomach wall), the digenean metacercaria *Otodistomum* sp. (stomach wall), and the larval nematodes *Anisakis simplex* (body cavity, organs, musculature), *Pseudoterranova decipiens* (body cavity, organs, musculature), *Contracaecum* sp.(body cavity), and Spirurid gen. sp. (stomach wall). A ninth taxon, the larval nematode *Hysterothylacium aduncum* (body cavity and organs) was included for the analysis of juveniles.

Because individual fish varied extensively in size (fork length), and the number of a parasite individuals was strongly correlated with fish size (Blaylock et al., 1998a), parasite numbers were corrected for differences in host size. Counts of individual parasites were first log-transformed ($\ln(x+1)$). To adjust for the effect of fish length, a regression of the transformed parasite numbers on fish length for each species in each locality (and haul) was calculated. This relationship was then used to adjust the number of parasite individuals within each fish in each locality (and haul) to that expected for the average-size fish in the overall sample (80.9 cm for adults, 39.2 cm for juveniles). These data were then used in discriminant function analyses. We applied the most widely used (and available) method of discriminant function analysis, in which the data were divided into training and test sets, and a discriminant function calculated on the training set was used to classify the test set. Interpretations were based on patterns in the test sets. To insure that any identified patterns were due to differences among localities rather than simply differences among individual hauls, we performed the same analysis on both the locality and the individual haul data.

Our training set consisted of six fish randomly selected from each haul ("haul" training set) or these fish plus four from the northern Queen Charlotte Islands and six from Unimak Pass ("locality" training set). Discriminant functions calculated from data on these "training" fish were used to classify each of the remaining fish from each haul ("haul" test set) or those fish plus all remaining fish ("locality" test set). The test set fish were first classified into one of the 13 hauls or 15 localities. Classification matrices were examined for the degree of misclassification. Hauls or localities were then grouped and regrouped into four and three groups based on patterns in the 13 or 15 category analyses and the zoogeographic zones from Blaylock et al. (1998b). Analyses were then repeated. Classifications were examined for misclassification, and boundaries adjusted for retesting. Results presented are those from the best fit "test" classifications. Statistical analyses were performed in SYSTAT for Windows version 5.05 (Wilkinson et al., 1992). The entire data set from which the data for this analysis came is available for purchase from the Depository of Unpublished Data, Document Delivery, CISTI, National Research Council of Canada, Ottawa, ON K1A 0S2, Canada.

Results

Of the taxa that met the Arthur and Albert (1993) criteria, *N. surmenicola* was most common and abundant in northern localities and fairly common and abundant in central localities. *Corynosoma strumosum*, although variable in prevalence and abundance, was much more common in the northernmost localities. *Corynosoma villosum*, although prevalent everywhere, was more abundant in northern fish. *Otodistomum* sp. and Spirurid gen. sp. were more common and abundant in southern localities. *Anisakis simplex*, although present in virtually every fish from every locality, was more abundant in southern fish. *Pseudoterranova decipiens* and *Contracaecum* sp. appeared to be more common in central areas (Table 1). In the juveniles, *A. simplex* and *P. decipiens* were more common in central localities, whereas *C. villosum*, *C. strumosum*, and *Hysterothylacium aduncum* were more common in northern localities (Table 2).

The haul analyses indicated that the majority of fish from some hauls (12/14 Vancouver Island [VI] fish, 3/4 Southeast Alaska 1 [SA1] fish, 3/5 from the Pribilof Islands [PI], and all 4 from St. Matthew's Island [SMI]) could be correctly classified but that fish from surrounding areas also were incorrectly classified to these hauls. Moreover, the percentage of fish correctly classified by the haul functions was, in all cases, within only a few percentage points of that correctly classified by the equivalent locality function. Thus, patterns do not appear to be associated with independent hauls. Therefore, we present only the results of the locality analyses.

Fifteen category discriminant analyses revealed severe misclassification in most areas. Only 39% were correctly classified to locality (Table 3). The functions did assign correctly the majority of test fish from two localities (19/26 from Vancouver Island [VI] and 14/22 from the southern Bering Sea [SB]). However, misclassification of fish from surrounding areas to these localities indicated less than accurate discrimination. The clearest indications from these analyses were that localities from the vicinity of the Queen Charlotte Islands south should be grouped together and that there is a suggestion that the two northern Bering Sea locations (PI and SMI) should be grouped.

Regrouping the localities into four categories by using boundaries from zoogeographic analyses (Blaylock et al., 1998b) plus the apparent northern Bering Sea grouping (PI–SMI), considerably improved the predictive ability of the functions. The "best fit" four-category grouping gave approximately 62% correct classification at the locality level (Table 4). The four-category functions were good predictors for the California–Oregon (OR) to southern Queen Charlotte Islands (SQC) fish; over 80% of these southern fish were correctly classified, and only about 6% of the other fish were misclassified to this group. Over 70% of the Pribilof–St. Matthew Island (PI–SMI) fish were correctly classified, and only 7% of the other fish were incorrectly classified to this group. There was much misclassification in the two central groups, and adjustment of the boundary between these two groups did not produce marked improvement (not shown).

Grouping into three categories by combining the two central groups resulted in substantial improvement in discrimination (83% correct) (Table 5). Shifting of the boundary between the northern and central group revealed that discrimination broke down when the southern

Table 1

Summary of parasites used for discrimination of stocks of adult Pacific halibut by locality. OR = Oregon–northern California, WA = SA1= southeast Alaska 1, SA2 = southeast Alaska 2, KP = Kenai Peninsula, KI = Kodiak Island, NI = Nagai Island, WAI = western bc = body cavity, o = organs, m = musculature, sw = stomach wall. Intensity = mean number of parasites per infected host.

			OR (n=23)		WA (n=14)	
Parasite	Site	Stage	%	Intensity	%	Intensity
Anisakis simplex	bc, o, m	larva	100	258.2 ±520.2	100	122.2 ±101.0
Corynosoma villosum	bc	juvenile	74	7.9 ±5.4	71	6.3 ±7.3
Corynosoma strumosum	bc	juvenile	52	5.6 ±6.4	50	6.3 ±5.2
Nybelinia surmenicola	sw	metacestode	17	2.8 ±2.9	14	4.0 ±4.2
Otodistomum sp.	sw	metacercaria	44	14.3 ±13.8	36	32 ±55.7
Pseudoterranova decipiens	bc, o, m	larva	44	2.5 ±2.1	21	2.3 ±1.5
Contracaecum sp.	bc	larva	0	0	0	0
Spirurid gen. sp.	sw	larva	22	1.4 ±0.5	50	11 ±24.7

	KP (n=21)		KI (n=26)		NI (n=13)	
Parasite	%	Intensity	%	Intensity	%	Intensity
Anisakis simplex	100	33.6 ±22.1	100	29.5 ±27.3	100	80.3 ±62.0
Corynosoma villosum	95	11.1 ±12.4	100	11.2 ±18.4	85	12.6 ±15.0
Corynosoma strumosum	19	1 ±0.0	27	1.3 ±0.5	8	2.0 ±0.0
Nybelinia surmenicola	43	4.2 ±3.9	65	29.5 ±106.6	39	42.2 ±89.0
Otodistomum sp.	14	2.0 ±1.7	4	1 ±0	8	1 ±0.0
Pseudoterranova decipiens	29	1.5 ±1.2	50	1.9 ±1.4	61	2.5 ±2.0
Contracaecum sp.	62	3.0 ±3.08	50	3.2 ±3.2	0	0
Spirurid gen. sp.	9	1.0 ±0	4	1 ±0.0	0	0

Table 2

Summary of parasites used for discrimination of stocks of juvenile Pacific halibut. NQC = northern Queen Charlotte Islands, NI = Nagai Island, UP = Unimak Pass, PI = Nunivak Island (central Bering Sea). bc = body cavity, o = organs, m = musculature, sw = stomach wall. Intensity = mean number of parasites per infected host.

			NQC (n=20)		KI (n=13)		NI (n=20)		UP (n=20)		PI (n=23)	
Parasite	Site	Stage	%	Intensity	%	Intensity	%	Intensity	%	Intensity	%	Intensity
Anisakis simplex	bc, o, m	larva	25	1.2	8	1.0 ±0	65	3.1 ±1.9	70	3.6 ±3.1	30	1.7 ±0.8
Corynosoma villosum	bc	juvenile	5	1 ±0.0	46	1.3 ±2.4	75	3.4 ±2.6	80	5.8 ±7.4	9	1.5 ±0.7
Corynosoma strumosum	bc	juvenile	0	0	8	1.0 ±0	0	0	5	1 ±0.0	48	1.2 ±0.4
Hysterothylacium aduncum	bc, o	juvenile	15	1 ±0.0	92	4.4 ±3.2	95	8.7 ±10.7	85	5.4 ±8.8	74	2.8 ±1.5
Nybelinia surmenicola	sw	metacestode	0	0	0	0	0	0	5	1 ±0.0	26	1.3 ±0.8
Pseudoterranova decipiens	bc, o, m	larva	0	0	8	1.0 ±0	25	1.4 ±0.9	15	1 ±0.0	4	6 ±0.0
Contracaecum sp.	bc	larva	0	0	15	1.0 ±0	10	5 ±5.7	0	0	0	0
Spirurid gen. sp.	sw	larva	0	0	0	0	5	2.0 ±0.0	0	0	0	0

Table 1

Washington, VI = southern Vancouver Island, SQC = southern Queen Charlotte Islands, NQC = northern Queen Charlotte Islands, Aleutian Islands, SB = southern Bering Sea, PI, Pribilof Island (central Bering Sea), SMI = St. Matthew Island (northern Bering Sea).

VI (*n*=32)		SQC (*n*=31)		NQC (*n*=8)		SA1 (*n*=20)		SA2 (*n*=29)	
%	Intensity	%	Intensity	%	Intensity	%	Intensity	%	Intensity
100	381.4 ±357.1	100	167.8 ±101.4	100	76.1 ±47.6	100	81.8 ±141.1	100	44.0 ±57.0
94	8.8 ±7.4	94	13.7 ±24.3	100	5.9 ±7.4	90	10.9 ±16.6	93	16.1 ±32.0
44	3.6 ±5.2	39	1.8 ±1.5	25	2.0 ±0.9	15	1.7 ±0.6	52	1.9 ±1.0
19	16.0 ±31.9	3	1.0 ±0.0	50	13.3 ±23.8	30	11.8 ±25.1	52	4.1 ±2.0
9.4	18.3 ±30.0	39	8.3 ±13.9	38	4.7 ±2.3	35	13.0 ±11.0	21	8.3 ±11.0
16	1.2 ±0.4	13	1.5 ±0.6	25	2.0 ±0.0	25	3.2 ±4.4	69	3.1 ±3.0
3	1.0 ±0	0	0	50	3.8 ±4.9	40	3.5 ±2.2	45	2.0 ±2.0
3	1.0 ±0	0	0	0	0	15	2.3 ±1.2	10	2.8 ±2.0
UP (*n*=20)		WAI (*n*=20)		SB (*n*=29)		PI (*n*=14)		SMI (*n*=28)	
%	Intensity	%	Intensity	%	Intensity	%	Intensity	%	Intensity
100	53.3 ±43.8	100	41.5 ±55.0	100	40.6 ±33.6	100	21.5 ±22.3	84	10.9 ±10.0
85	29.6 ±57.4	95	13.8 ±14.0	97	16.8 ±18.3	86	34.4 ±37.0	90	34.4 ±55.9
30	2.0 ±1.5	40	2.1 ±2.0	38	8.5 ±20.2	79	9.0 ±9.3	77	23.2 ±25.4
55	2.7 ±2.1	35	16.1 ±33.8	52	6.7 ±13.1	57	34.6 ±69.2	58	25.0 ±69.8
0	0	5	1 ±0	0	0	0	0	0	0
45	1.4 ±0.7	45	2.3 ±2.0	38	2.3 ±1.5	29	2.3 ±1.3	23	2.4 ±1.8
15	2.0 ±1.0	30	1.3 ±1.0	38	3.0 ±4.5	14	1.0 ±0	7	4.0 ±3.5
5	1.0 ±0.0	0	0	4	1 ±0.0	0	0	0	0

Bering Sea (SB) was included in the northern group (not shown). Inclusion of the northern Queen Charlotte Islands (NQC) in the southern group had little effect (81% correct classification) (not shown). These analyses indicated a southern (OR–SQC) group, a central (NQC–SB) group, and a northern (PI–SMI) group.

Classification into two categories (with SQC as the dividing line) provided no substantial improvement (87% correct) (not shown). Inclusion of NQC in the southern group had little effect (88% correct classification).

Discrimination of juveniles was poor with any organization of localities. The "best fit" classification correctly classified only 66% of the fish and there was substantial misclassification among the localities (Tables 6 and 7). Fish from the northern Queen Charlotte Islands (NQC) through Nagai Island (NI) separated reasonably well, but the majority of fish from the northernmost locality were also misclassified to this group. Note that parasite numbers and prevalences were low in the juveniles (Table 2).

Discussion

Our results show four things: 1) parasites clearly differentiate a group of southern adults; 2) parasites provide some evidence for a separation of the northernmost adults; 3) the differentiation is not always unequivocal; and 4) parasites do not differentiate groups of juvenile fish.

Skud (1977) concluded that southern and northern groups mixed extensively at all ages of their life history and that, although populations of adults may be largely discrete in the summer, any such discreteness was temporary because tagging evidence suggested more extensive winter migrations associated with spawning. Our data, on the other hand, suggest that there is some merit to the IPHC's early recognition of three stocks of adult halibut. Parasite data support the existence of two major groups of halibut and suggest the possibility of a third group in the central and northern Bering Sea. The high proportion of correct classifications based on parasites suggest that these differences are well established.

Recognition of three such groups is also supported by several of Skud's (1977) observations. He presented data suggesting that after fish home to spawning areas, southern and northern fish maintain reasonably separate migration circuits between feeding and spawning grounds. Data from Skud (1977) and more recent tagging data (Geernaert, 1996) also suggest that southern fish move less than their northern counterparts. Skud also recognized a resident population in the Bering Sea. These con-

Table 3

Cross validation results of a 15-category discriminant function classification of adult Pacific halibut in the northeast Pacific based on parasite data. Numbers of fish assigned to each locality and the corresponding percentage of the sample assigned to that category are shown. See Table 1 legend for key to abbreviations. Correct classifications are shown in bold (28% of 240).

True category	Assigned category														
	OR	WA	VI	SQC	NQC	SA1	SA2	KP	KI	NI	UP	WAL	SB	PI	SMI
OR	**4** **17%**	2 9%		1 4%	2 9%						2 9%		3 13%		
WA	2 25%	**2** **3%**			1 13%									1 13%	2 25%
VI		1 4%	**19** **73%**	2 8%	3 12%							1 4%			
SQC	1 4%	1 4%	10 40%	**11** **44%**							2 8%				
NQC					**2** **50%**	2 50%									
SA1		1 7%			1 7%	**4** **29%**		1 7%	1 7%	1 7%				3 21%	
SA2	1 4%				1 4%	2 9%	**1** **4%**	3 13%	3 13%	1 4%	1 4%		8 35%	1 4%	1 4%
KP						7 50%	1 7%	**1** **7%**	1 7%	1 7%	2 14%		1 7%		
KI						7 35%	2 10%	1 5%	**2** **10%**	1 5%	2 10%		3 15%	2 10%	
NI			1 14%		1 14%				2 29%	**1** **14%**	1 14%				
UP			2 14%			1 7%			2 14%	2 14%	**1** **7%**	2 14%	3 21%		1 7%
WAI						3 21%	1 7%	1 7%		2 14%	2 14%	**0**	5 36%		
SB		1 7%			1 7%	4 29%	3 21%	1 7%	2 14%	1 7%	2 14%	5 36%	**1** **7%**		2 14%
PI													1 13%	**3** **38%**	4 50%
SMI						1 5%			3 14%			3 14%		1 5%	**14** **64%**

clusions pose two questions. First, do fish from different groups mix extensively? Second, do such groups represent reproductive units or stocks?

Our analysis was based on a small set of larval parasites, all of which are known to be long-lived and do not multiply in the host. Other long-lived parasites such as the myxosporeans have been used in stock discrimination but were not included here because of a lack of abundance data. However, the decreased ability to detect differences because of the small data set was offset by an increased ability to detect the host's past activities. Most of these parasites live for at least several years; therefore, the presence and abundance of these parasites may indicate where the host has been over that time period. At least some of the individuals of each of the parasite species, however, were probably short-term acquisitions (lasting a few years); thus, there may be some bias in the data of the recent past.

Our data suggest less extensive movement of Pacific halibut in southern areas. Because parasites are generally more abundant in the south, southern fish may be more easily classified. Nevertheless, if the southern fish mingle extensively with more northern fish, there should be more similarity in the parasite faunas. In particular, central area fish should develop characteristics of southern fish. This did not happen, as is shown by the very low proportion of central fish misclassified as southern fish (Table 5). Our information cannot completely rule out the movement of southern fish to central areas during the spawning season, and then back to southern areas for the feeding season. Their long-lived parasite fauna, having been established in the distinct southern areas, would probably

Table 4

Cross validation results of a four-category discriminant function classification of adult Pacific halibut in the northeast Pacific based on parasite data. Numbers of fish assigned to a category and the corresponding percentage of the sample in that category are shown. Correct classifications are shown in bold (63% of 240). OR–SQC = Oregon–northern California to southern Queen Charlotte Islands, NQC–KP = northern Queen Charlotte Islands to Kenai Peninsula, KI–SB = Kodiak Island to southern Bering Sea, PI–SMI = Pribilof Islands to St. Matthew Island.

True category	Assigned category			
	OR–SQC	NQC–KP	KI–SB	PI–SMI
OR–SQC	**60**	3	7	6
	79%	4%	9%	8%
NQC–KP	3	**28**	21	4
	5%	**50%**	42%	7%
KI–SB	7	23	**41**	7
	9%	30%	**53%**	9%
PI–SMI		1	6	**23**
		3%	20%	**77%**

Table 5

Cross validation results of a three-category discriminant function classification for adult Pacific halibut in the northeast Pacific based on parasite data. Numbers of fish assigned to a category and the corresponding percentage of the sample in that category are shown. Correct classifications are shown in bold (83% of 240). OR–SQC = Oregon–northern California to southern Queen Charlotte Islands, NQC–SB = southeast Alaska to southern Bering Sea, PI–SMI = Pribilof Islands to St. Matthew Island.

True category	Assigned category		
	OR–SQC	NQC–SB	PI–SMI
OR–SQC	**63**	7	6
	83%	9%	8%
NQC–SB	10	**112**	12
	7%	**84%**	9%
PI–SMI		5	**25**
		17%	**83%**

Table 6

Cross validation results of five-category discriminant function classification for juvenile Pacific halibut in the northeast Pacific based on parasite data. Numbers of fish assigned to a category and the corresponding percentage of the sample in that category are shown. Correct classifications are shown in bold (44% of 62). NQC = northern Queen Charlotte Islands, NI = Nagai Island, UP = Unimak Pass, and PI = Nunivak Island (central Bering Sea).

True category	Assigned category				
	NQC	KI	NI	UP	PI
NQC	**9**	4			
	69%	31%			
KI	1	**5**	1		
	14%	**71%**	14%		
NGI	5	3	**3**	2	
	39%	23%	**23%**	15%	
UP	5		2	**5**	1
	39%		15%	**39%**	8%
PI	6	4		1	**5**
	38%	25%		6%	**31%**

Table 7

Cross validation results of a three-category discriminant function classification for juvenile Pacific halibut in the northeast Pacific based on parasite data. Numbers of fish assigned to a category and the corresponding percentage of the sample in that category are shown. Correct classifications are shown in bold (66% of 62). NQC = northern Queen Charlotte Islands, NI = Nagai Island, UP = Unimak Pass, PI = Nunivak Island (central Bering Sea).

True category	Assigned category		
	NQC–NI	UP	PI
NQC–NI	**30**	3	
	91%	9%	
UP	6	**6**	1
	46%	**46%**	8%
PI	10	1	**5**
	63%	6%	**31%**

not lose their southern character. Winter sampling could potentially determine if this is the case.

With respect to the Bering Sea, we suggest that the majority of the mixing occurs in the southern Bering Sea because classification breaks down when the southern Bering Sea is included in the northern region. This mixing is consistent with larval studies that show that larvae enter the Bering Sea through the Aleutian chain. Those fish may not disperse far into the Bering Sea. Rather, they either remain in the southern Bering Sea or migrate back to the Gulf of Alaska area (Skud [1977] believed that both occurred). A migration may explain why fish tagged in the Bering Sea tend to be recovered at greater distances from the tagging site than those tagged elsewhere (Geernaert, 1996). Migrations of the central and northern Bering Sea group appear to be in a more northerly direction (Skud,

1977), which would preclude mixing in the Aleutians and the Gulf of Alaska. Zoogeographic analysis with patterns of prevalence showed that Bering Sea parasites are rarely found outside the Bering Sea (Blaylock et al., 1998b).

The patterns identified in our analysis agree only in part with zoogeographic analyses (Blaylock et al., 1998b). The southern boundaries in both studies are in the vicinity of the Queen Charlotte Islands, providing additional support for the existence of a southern group of halibut. However, this analysis, unlike the zoogeographic analyses, indicated no sign of a division in the vicinity of Kodiak Island, suggesting that the division near Kodiak Island depends on short-lived species not included in this analysis. The evidence for the existence of a northern Bering Sea group is equivocal; it was supported by the clustering of localities by using prevalences and, to some degree, the clustering of individuals, but was not supported by any other analyses (Blaylock et al., 1998b).

With respect to juveniles, Skud's (1977) analysis clearly indicates compensatory movement from the Gulf of Alaska and southern Bering Sea to southern areas, and, as such, predicts that juveniles should have more similar parasite faunas among areas. Our data show this similarity, but there are significant caveats. First, our samples of juveniles came from areas that form a single group in the classification of adults. The sample from the northern Queen Charlottes is near the southern boundary of that group, and the sample from Nunivak Island is near the northern boundary. Samples of juveniles from other areas, particularly the southern area, should be examined to help clarify this issue. Second, and maybe more important, in these smaller fish, prevalences and intensities are low and perhaps hinder separation. However, because halibut at this stage are susceptible to bycatch in other fisheries (IPHC, 1996), management should probably consider juveniles a mixed stock to prevent impacts on future halibut populations in distant localities.

Overall, our analysis provides a less clear picture than that of Arthur and Albert (1993) for Greenland halibut in the northwest Atlantic. Part of the lack of clarity may be due to our use of the training and test set method rather than the bootstrapping method used by Arthur and Albert, which would increase the likelihood of correctly classifying similar fish. Also, Arthur and Albert were dealing with a very different system. Geological and oceanographic conditions around the Gulf of St. Lawrence are quite complex and create great potential for the isolation of stocks. The northeast Pacific is more open and has fewer isolating mechanisms than the northwest Atlantic. Further, the system is clinal (Blaylock et al., 1998b) and Pacific halibut are quite capable of migrating along the entire Pacific coast; therefore, less clear cut divisions are expected. Nevertheless, we successfully identified groups of fish, some with a high degree of accuracy.

Skud (1977) suggested that juveniles will, as adults, home to the areas in which they were spawned, making the existence of reproductive stocks at least possible. Modern molecular methods could address the issue. For example, molecular methods could potentially address the existence of separate stocks in the south and in the northern Bering Sea. The limited molecular studies done to date, however, have not elucidated any indentifiable stock structure because of limited sampling localities, the limited number of loci examined, and the use of juveniles only. Tsuyuki et al. (1969) examined a single serum hemoglobin transferrin locus in halibut from ten sites from Vancouver Island to the Bering Sea and found that only one southeast Alaska locality was different. Grant et al. (1984) found no differences between Gulf of Alaska and Bering Sea halibut at five loci but were able to distinguish northeast Pacific halibut from Japanese halibut. However, it is important to note that biochemical and genetic information measures differentiation at a different time scale than that reflected in parasite data (Lester et al., 1988). According to Grant (1984), movement of only a few Atlantic herring (*Clupea harengus*) may be sufficient to obscure true differences between different breeding stocks. Thus, even limited gene flow could obscure any differences in the loci examined.

Parasite or tagging information alone, however, can not determine whether or not the groups we identified are reproductive stocks. Therefore, all potential factors that might refine the halibut stock concept should be considered. The parasite data suggest a conservative approach to management that recognizes a mixed stock of juveniles and three potential stocks of adults—one in the south, another in the northern Bering Sea, and a third and largest centered in the Gulf of Alaska.

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