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AN APPRAISAL OF THE GENETIC ANALYSIS OF SKIPJACK BLOOD SAMPLES

(Paper Prepared by the Skipjack Programme)

1.0 INTRODUCTION

Population structure of skipjack is important for a full understanding of fishery interactions. In the past, several population structures for Pacific Ocean skipjack have been inferred from electrophoretic analysis of blood samples. Fujino (1970 and 1976) hypothesized two genetically isolated subpopulations, one in the western Pacific and one in the central/eastern Pacific; Sharp (1978) hypothesized five Pacific Ocean subpopulations. Estimates of the degree to which fisheries in different locations exploit skipjack of the same genetic origin would obviously depend on what the population structure actually is; hence it is important to determine which, if either, of the above hypotheses is correct.

The Skipjack Survey and Assessment Programme sought to clarify the issue of skipjack population structuring by simultaneously collecting blood samples and tagging skipjack from selected skipjack schools. During 30 months of field work the Programme obtained blood samples from approximately 100 individuals in each of 58 schools; a total of 32,000 skipjack were tagged and released in these schools. An additional 108,000 skipjack were tagged in other schools. Many of the blood samples and tag releases occurred in little studied parts of the central and western Pacific. This working paper briefly reviews results and interpretations from our analysis of blood genetics data. The limitations of these data when inferring skipjack population structure and fishery interactions are discussed.

2.0 WORKSHOPS

The Skipjack Programme hosted two workshops at which specialists in the fields of population genetics and fishery population biology met with the Programme's scientists to jointly consider the statistical analysis and resulting interpretations of the blood genetics data. Both workshops dealt with additional unpublished blood genetics data for the eastern, central and

western Pacific Ocean that were provided by participants from the Australian National University and the Inter-American Tropical Tuna Commission. Skipjack Survey and Assessment Programme Technical Report No.1, published after the first workshop, summarized preliminary results from statistical analysis of blood genetics data (Anon, 1980). The second workshop focused on interpretation of this data, in concert with preliminary information from tag returns and limited biological data on distribution of larvae, juveniles and spawners. A report of the second workshop (Anon, 1981) is presented as a background document to this meeting.

3.0 WORKSHOP INTERPRETATIONS

Scientists at the Australian National University surveyed 42 loci from SPC and other skipjack blood samples for electrophoretically detectable polymorphisms. Three showed polymorphisms that were suitable for traditional population analysis; of these, only serum naphthyl esterase was considered suitable for detailed consideration at the workshops.

Esterase gene frequencies in skipjack showed a pronounced longitudinal gradient across the SPC area, with flattening of this gradient occurring to the east of 130°W longitude (Figure 1). This gradient is consistent with the concept of a cline. Underlying the acceptance of a clinal hypothesis is the idea that reproducing fish in neighbouring areas mingle, and the degree of mingling between any two areas decreases with increasing distance between them. In other words there is a dominant isolation-by-distance component to the population structure.

Alternatively, one could view the gradient as simply the zone of contact between two (or more) relatively homogeneous breeding units near the longitudinal extremes. Under this genetic model the zone of mixing, i.e. the gradient, could represent the mingling of primarily migrants from breeding units, or a zone of weak hybridization where there may be lowered breeding success. For example, skipjack in the eastern Pacific, where successful reproduction is thought to be less, could be considered to be migrants that return to spawn in the central Pacific.

Existence of the esterase gradient was considered to be strong evidence that Pacific skipjack do not comprise a single panmictic population, in which all adults of one generation have an equal chance of mating.

For skipjack of the size captured by pole-and-line gear, the tagging data demonstrated that within a generation there was movement to varying degrees between adjacent and distant fisheries in the central and western Pacific. This implied that there is some genetic mixing over a wide area, and that mixing would have to be offset by some degree of selection in order to maintain a cline.

No relationship was evident between esterase gene frequency for particular skipjack schools and subsequent movement of tagged skipjack from these schools. Thus gene frequency was not a predictor of skipjack movement. These results also implied that adults undergo a degree of genetic mixing within the study area.

GENE FREQUENCY

ESTERASE GENE FREQUENCY VERSUS LONGITUDE

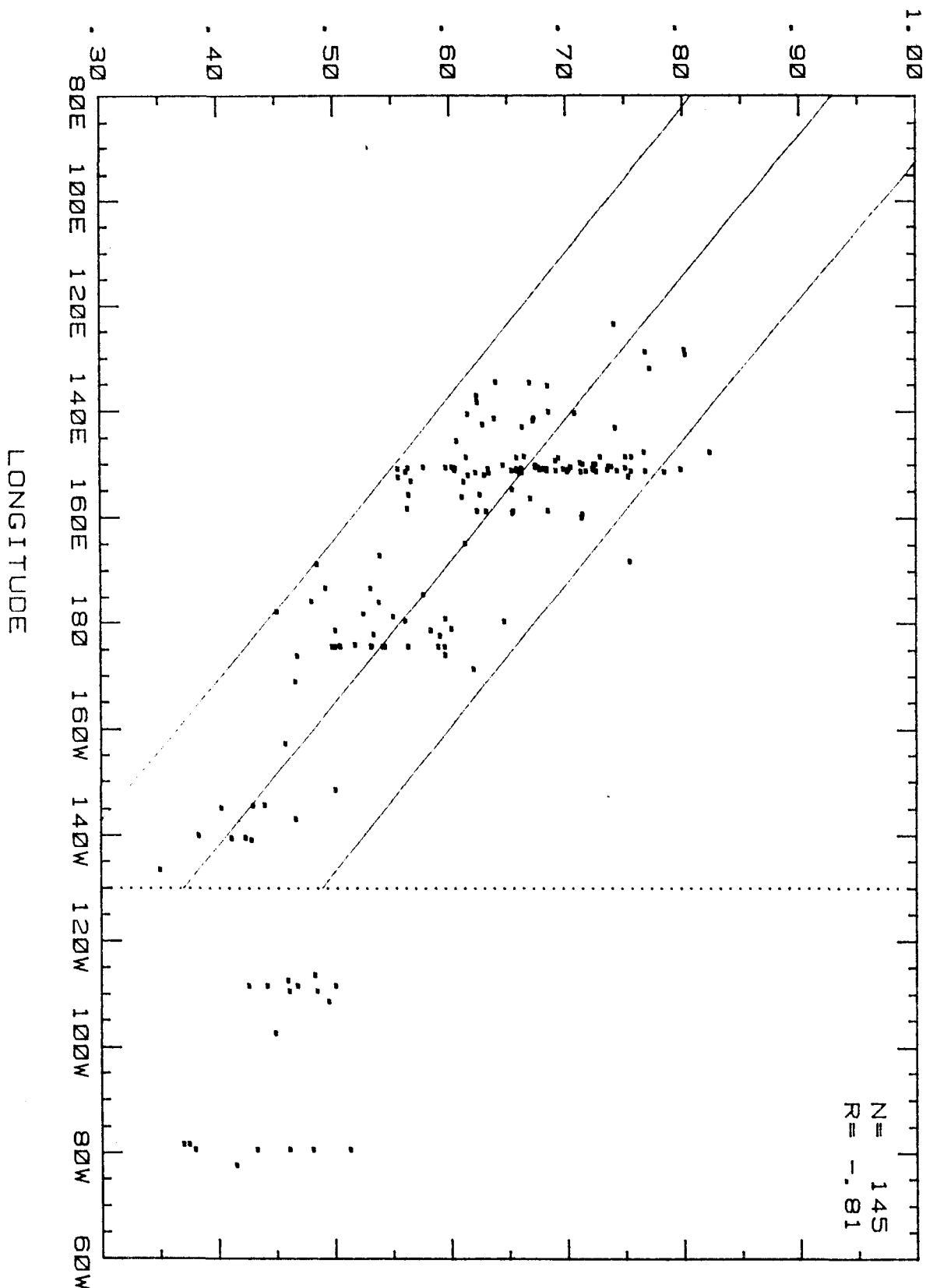


Figure 1 - Graph of esterase sample gene frequency plotted against longitude where the sample was taken. Regression line and 95 percent prediction limits indicated on the graph. The regression excludes samples from east of the SPC area (east of dotted line). N is the number of samples used for the regression and R is the correlation coefficient. Gene frequencies from a total of 163 samples are plotted.

Available biological data were insufficient to determine whether skipjack concentrate spawning activity in particular areas; however, spawning is obviously limited in higher latitudes.

In brief, the workshop participants concluded that a clinal population structure was a reasonable alternate hypothesis to the isolated subpopulation hypotheses advanced by Sharp and Fujino. Thus unconditional support for either one or other of the hypotheses, such as recently proposed by Fujino, Sasaki and Okumura (1981), is questionable and firm predictions of fishery interactions based on either hypothesis are at best premature, and at worst misleading.

4.0 ADDITIONAL QUALIFICATIONS

Further to the above, there are other serious reservations concerning the application of skipjack blood genetics data to questions of skipjack population structure and fishery interactions. Some of these reservations apply to the same use of tagging data.

What Life History Stage Was Sampled?

To infer population structure from blood genetics data, it is important to know the reproductive stage of the sampled fish. Unfortunately, this was usually not the case. For example, it is unclear whether blood samples were from mature pre-spawning skipjack, from post-spawning skipjack, or from immature skipjack. As well, these samples could have been from relatively non-migrant skipjack, from skipjack that had concentrated in spawning areas, or from fish travelling along dispersal or migration pathways.

There are similar problems with interpretation of skipjack movements based on tag returns. Do they represent adults homing to spawning areas, or simply the movement of dispersing fish to any number of spawning or feeding areas? Recent research has demonstrated that skipjack have a highly developed capability to sense the earth's electromagnetic field (Andrew Dizon, personal communication), thus giving them the potential capability to "navigate".

There is also the difficulty of ageing the sampled fish (there are no reliable methods for direct ageing). Since skipjack growth varies widely between neighbouring countries in the SPC area (Working Paper 11), it is questionable to assign even relative ages based on size.

Not knowing with reasonable certainty which life history stage was sampled limits the inferences one can make regarding genetic exchange between areas. Inability to estimate genetic exchange confuses the choice of an appropriate population model. This, in turn, reduces the management value of the data.

Dispersal, Selection, Migration/Homing

The esterase gradient (cline) could be maintained by various degrees of dispersal, selection and migration/homing.¹ If the esterase cline was maintained by high selection coefficients on young skipjack, then dispersal of older fish could be extensive and the cline would still be maintained. To maintain the cline when selection is negligible requires that adults disperse little or else migrate and then home to relatively narrowly defined spawning areas. Simply stated, various reasonable combinations of these variables imply significantly different potentials for fishery interactions. Table 1 presents some examples of these combinations and their potential for fishery interactions. At this time, neither the electrophoretic data nor the analysis of tagging data allow one to choose with confidence from the different alternatives.

Integrity of Skipjack Aggregations (Schools)

The degree to which skipjack stay together in schools or aggregations, over all or part of their lifetimes, is important for some interpretations of the electrophoretic data. As part of our examination of this question we estimated tag dispersal coefficients for individual schools, and tested whether blood schools containing individuals with rare alleles were a random or contagious occurrence. From these analyses there was little evidence that skipjack remained in cohesive groups over long periods of time.

Pre-recruits

Perhaps the major shortcoming of blood genetics sampling and tagging programmes to date is that they have focussed entirely on older post-recruitment skipjack. Larval and very small skipjack (less than 15cm) could undergo extensive movement simply by passive association with ocean currents. Young skipjack of up to 45cm may undergo feeding migrations of great distance from areas in which they were spawned. Kearney (1978) hypothesized that young skipjack followed the 20°C isotherm in a poleward direction until reaching areas where surface waters approached 20°C. If fisheries develop or intensify on skipjack of these sizes then there would appear to be potential for long and short term fishery interactions over large distances.

¹ As used in this paper, dispersal refers to "permanent" movement of some portion of maturing skipjack in an area, to different breeding locations at varying distances from where they were spawned; and migration/homing refers to movement (perhaps for feeding) by some portion of immature skipjack, to areas at varying distances from where they were spawned, followed by some degree of homing to the area where they were spawned.

TABLE 1. SOME EXAMPLES OF SELECTION, DISPERSAL AND MIGRATION/HOMING EFFECTS ON POTENTIAL FOR FISHERY IMPACTS

Case	Selection	Dispersal	Migration/Homing	Potential for Fishery Interactions
<u>Clinal Hypothesis</u>				
A	High	Wide	Negligible	High
B	High	Negligible	Negligible	Low
C	Negligible	Negligible	Extensive	High
D	Negligible	Negligible	Negligible	Low
<u>Two or More Breeding Unit Hypotheses</u>				
E	High	Wide (but little between units)	Negligible	High in mixing zone Low between breeding areas
F	Negligible	Negligible	Extensive	High in both zones

Mortality, Movement, Recruitment

Interactions between fisheries within a single skipjack generation largely depend on rates of fishing and natural mortality, and exchange (movement) of fish between the fisheries. The results from tagging have significantly improved our knowledge of these variables in a little studied portion of the Pacific (Working Paper 9). Blood genetics data, on the other hand, sheds little light on the first two variables; and only by making often unjustified assumptions about selection, dispersal, school integrity, homing, etc., could blood genetics data be used to infer movement patterns between fisheries.

Inferences regarding fisheries interactions over a longer term, that is between generations, could be made from genetics and tagging data. However, in the case of blood genetics data, the existence of reasonable but divergent population hypotheses severely limits the usefulness of genetics data for this purpose.

5.0 RESUME

It is as important to understand the limitations of data collected by following a particular line of research, as it is to recognize alternate hypotheses arising from the data. To this extent we feel that our analysis of skipjack blood genetics data has been most fruitful. For now we conclude that interactions between neighbouring fisheries are possible on both a long and short term basis, and that quantification of these interactions is most appropriate through analysis of tagging data. A more complete understanding of fishery interactions and population structure will depend on future results from well designed field experiments. We would not recommend further blood sampling until knowledge of basic ecology and biology of skipjack, particularly young skipjack, is greatly improved.

6.0 REFERENCES

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