SOUTH PACIFIC COMMISSION

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PROGRESS REVIEW OF GENETIC ANALYSIS OF SKIPJACK BLOOD SAMPLES
BY THE SKIPJACK SURVEY AND ASSESSMENT PROGRAMME

(Paper Prepared by the Skipjack Programme)

1.0 INTRODUCTION

The Skipjack Survey and Assessment Programme has collected a sizeable data base from which to assess skipjack population structuring, and the impact of population structuring on fisheries for skipjack in the region. These data, collected between October 1977 and August 1980, include electrophoretic analyses of 58 skipjack blood samples and releases of some 140,000 tagged skipjack.

The analysis and interpretation of tuna blood genetics data is a complex technical subject. For this reason the Skipjack Programme hosted two workshops during which invited experts in the fields of fishery genetics, population genetics, and fishery population biology, met with the Programme´s scientists to jointly consider the data, statistical analyses and resulting preliminary interpretations. This allowed the Skipjack Programme to proceed with a line of analyses, utilising blood genetics, tagging and ancillary data that was most efficient in terms of the Programme´s overall objectives and time deadlines.

This working paper for the Twelfth South Pacific Commission Regional Technical Meeting on Fisheries summarizes deliberations from the two workshops.

2.0 WORKSHOP ONE

In July 1979, scientists from the South Pacific Commission´s Skipjack Programme, the Inter-American Tropical Tuna Commission (IATTC), and the Research School of Biological Sciences, Australian National University (ANU) met to review preliminary results from the Skipjack Programme blood sampling data. ANU scientists, in addition to carrying out the basic biochemical analyses of skipjack blood samples collected by the Skipjack Programme, have independently collected a sizeable set of skipjack electrophoretic data, which they kindly made available to the meeting participants. The workshop suggested a particular line of statistical analyses, based in large measure on a statistical and computer simulation approach developed by the IATTC. The analyses were completed several months after the meeting, and the results were published early in 1980 (Anon, 1980). The salient feature of data in this report was the linear (clinal) relationship between esterase gene frequency and longitude in the South Pacific Commission (SPC) study area.

3.0 WORKSHOP TWO

Field work for the Skipjack Programme ended in August of this year. In September, once the last blood samples had been analysed at ANU, the Skipjack Programme hosted a second and final workshop. The goal of this workshop was to establish to what extent interpretation of the available blood genetic data could be used in formulating fisheries policy for skipjack resources in the SPC area. The workshop addressed the general question of whether there was genetic evidence of population structuring in the resource that could affect fishery exploitation of the resource, either overall or in smaller areas, now or in the future. In particular, the workshop considered how far the blood genetics data could be used in determining degree, timing and geographical extent of skipjack intermingling. All participants from the first workshop, and two invited experts in population genetics, attended the final workshop.

It was planned that this workshop would review results from as complete a set of Pacific Ocean skipjack blood genetics samples as possible. Participants from IATTC and ANU kindly provided additional unpublished data and analyses for consideration. Unfortunately, some of the data were not in a form amenable to detailed consideration at the meeting, and this included a large set of published Japanese data for the central and western Pacific.

4.0 SUMMARY OF WORKSHOP TWO

Additional data available to the second workshop confirmed the apparent clinal gradient in esterase gene frequency in the SPC area, and endorsed the suggestion that the cline did not continue through the eastern Pacific Ocean (Figure 1), i.e. esterase gene frequencies were relatively constant from French Polynesia to the east. Results for a second polymorphic locus for transferrin did not show a correllation between gene frequency and longitude (Figure 2). The only other locus, of 43 examined, to show a degree of polymorphism useful for genetic analysis of population structuring was the locus for guanine deaminase (GDA). However, the low number of GDA samples (38), and the weak correlation between GDA gene frequency and longitude limited the usefulness of these data. It was agreed that the apparent esterase cline constitutes evidence that Pacific Ocean skipjack do not comprise a panmictic population, in which complete mixing would occur across the extremes of the population range, within a single generation. Thus there is some resistance to complete mixing of skipjack across the Pacific, but the nature and magnitude of that resistance was not ascertainable from the genetics data. Several skipjack population structure models were advanced by the meeting, all consistent with the genetics data and based on varying assumptions about dispersal, homing, recruitment, school integrity, breeding areas, and degree of genetic selection. The meeting considered additional non-genetic data on skipjack, including preliminary results from analysis of Skipjack Programme tag returns; and general skipjack ecological data, such as distribution of skipjack juveniles and larvae. Yet, even with this ancillary information, the underlying assumptions of the various models were still not resolvable.

One feature of all but one of the models is the isolation-by-distance concept. This states that fish in any one region mingle with fish in neighbouring regions, and that the degree of mingling between any two regions decreases with an increase in distance between these regions. While we could not rule out the possibility of genetically isolated skipjack subpopulations, we would not, on the basis of available data, anticipate stable geographical boundaries between genetically isolated subpopulations, as has been advanced by Fujino (1970, 1976). And, it follows that we would not at this stage propose any barriers to the interaction of fisheries between neighbouring regions.

It was noted that blood samples from skipjack which are caught by pole-and-line gear, when considered alone, will only provide a very general view of skipjack intermingling, and little insight into the details of population structuring.

The meeting suggested some further analyses of the genetic data in combination with the tagging data, which may shed light on some of the assumptions mentioned previously and may give more insight into timing and geographical extent of skipjack intermingling. Nevertheless, it must be recognized that there will continue to be serious gaps in our knowledge of skipjack population structure and ecology. These gaps must be filled after careful, comprehensive analysis of all blood genetics, tagging and ancillary data from well-designed field experiments, in order to provide the best possible advice to those formulating fisheries policy for skipjack resources in the South Pacific Commission area.

A summary report of the second workshop will be released early in 1981.

5.0 REFERENCES

ANON (1980). Review of preliminary results from genetic analysis of skipjack blood samples collected by the Skipjack Survey and Assessment Programme. South Pacific Commission, Noumea. Skipjack Survey and Assessment Programme, Technical Report No.1, 22 pp.

FUJINO, K. (1970). Range of skipjack tuna subpopulations in the western Pacific Ocean. In Proc. Second CSK Symp., Tokyo, 1970. p 373-384.

FUJINO, K. (1976). Subpopulation identification of skipjack tuna specimens from the south-western Pacific Ocean. Jap. Soc. Sci. Fish., Bull. (11): 1229-1235.

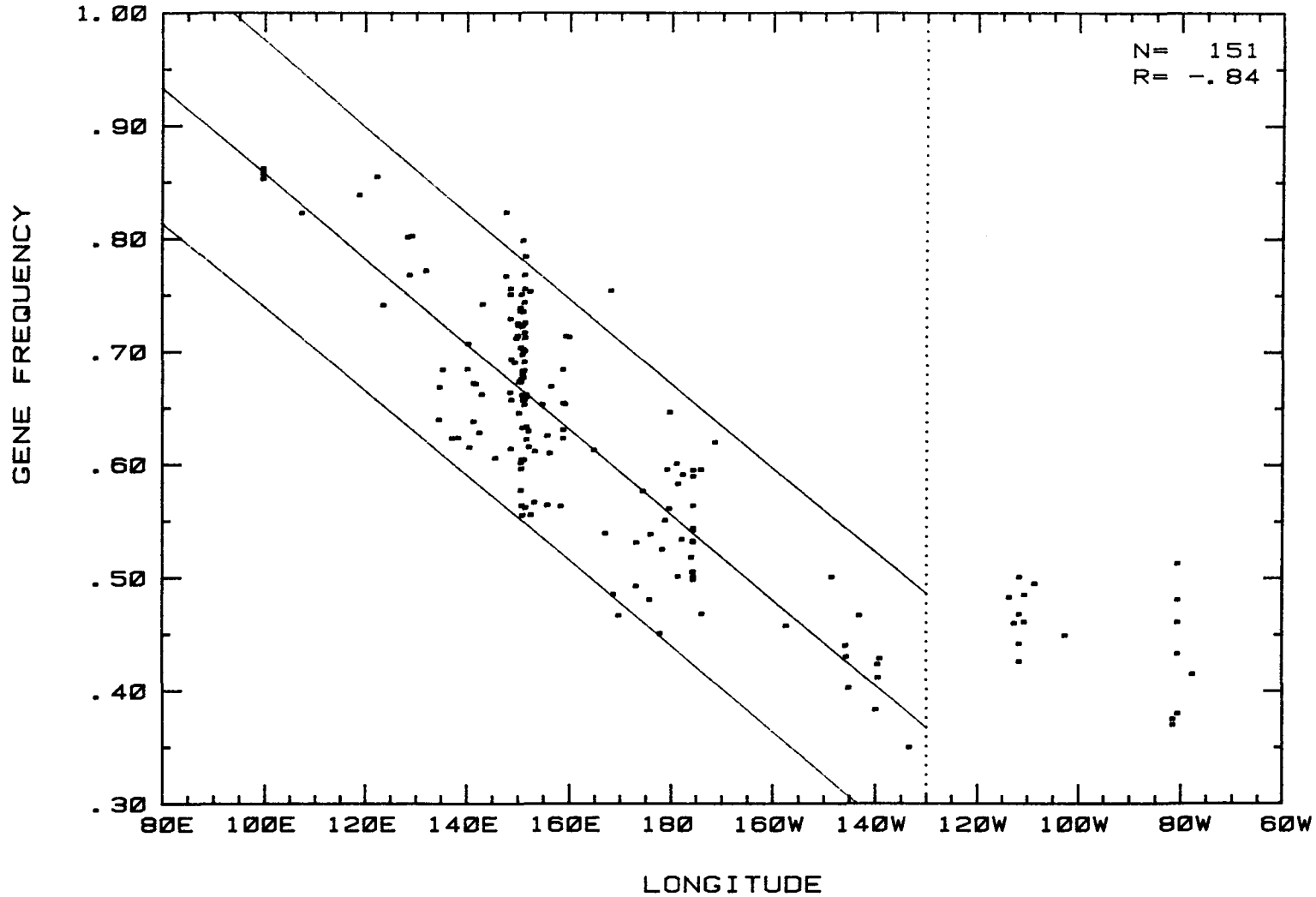# ESTERASE GENE FREQUENCY VERSUS LONGITUDE

Figure 1 - Graph of esterase sample gene frequency plotted against longitude where
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
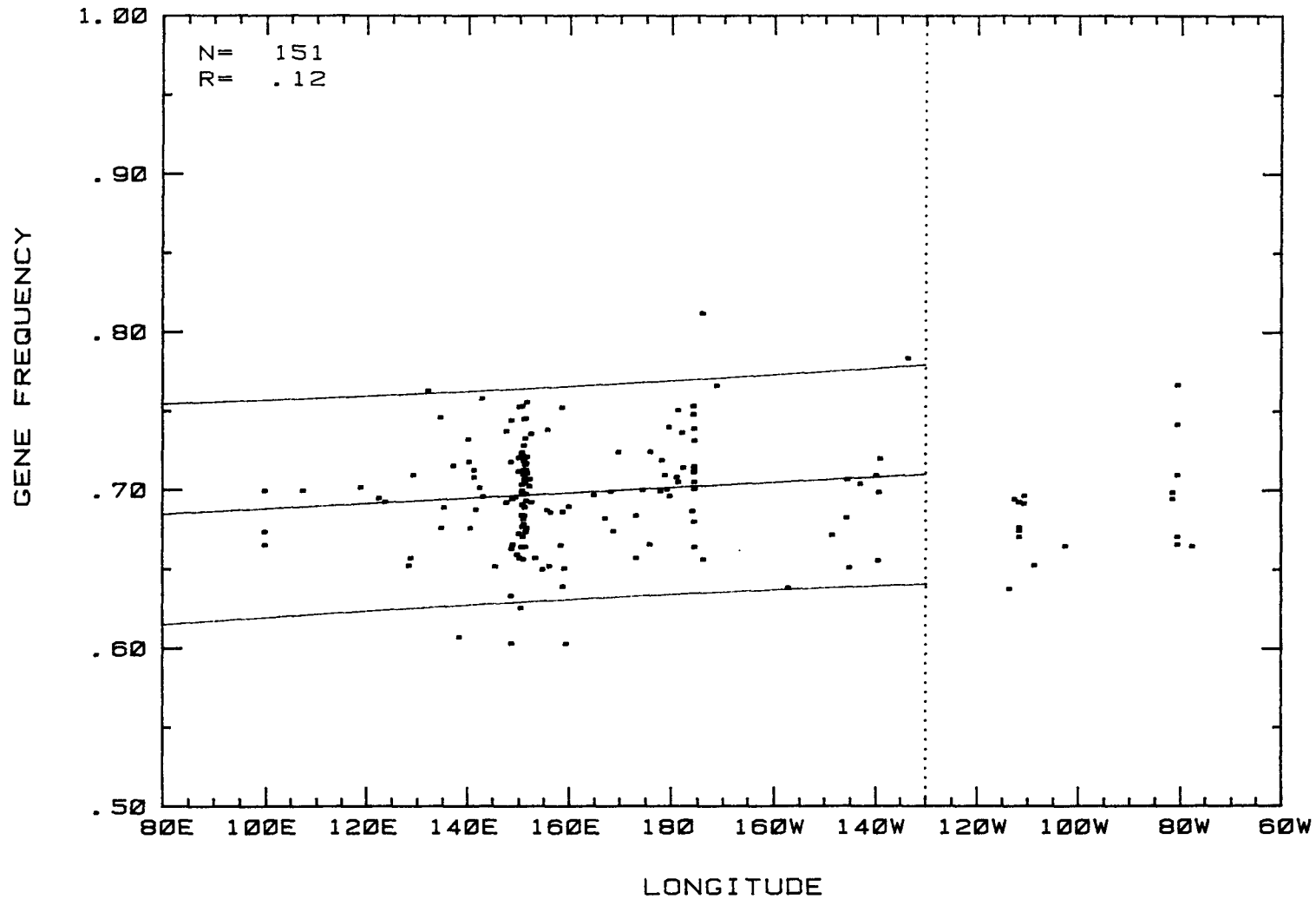from a total of 169 samples are plotted.

Figure 2 – Graph of transferrin sample gene frequency plotted against longitude where
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 169 samples are plotted.