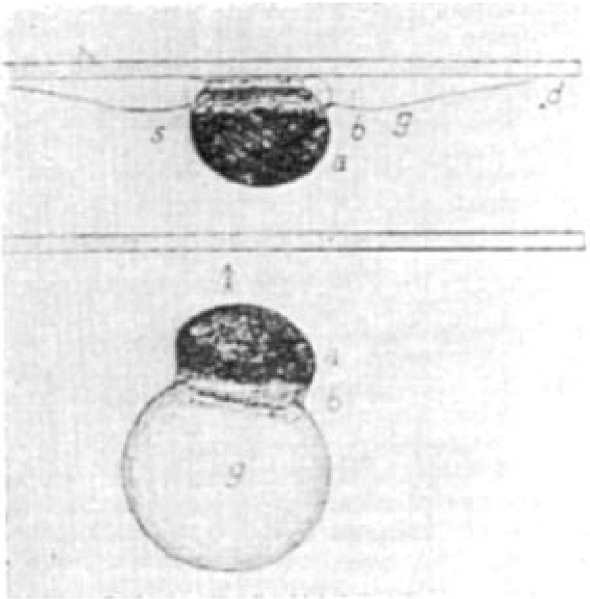

Figure 5. Impact and adhesion of *Pilobolus*. Buller's lower sketch shows a sporangium projectile with a drop of liquid from the old subsporangial region approaching an object such as a blade of grass (traveling in the direction of the arrow). When the sporangium lands (see upper drawing) the material adhering to the sporangium splatters out, acting as a glue cementing the sporangium to the leaf where it may possibly be eaten by a horse. This line drawing is after A. H. R. Buller, Langeron, M., and R. Vanbreuseghem. 1952. Précis de mycologie. Libraires de L'academie de Medecine, Masson et Cie, Paris. p. 306. Used by permission of the publisher, Masson et Cie.

"scatter pattern" of sporangia found glued close to the region surrounding the pin hole of light will be a testimony to the accuracy of *Pilobolus!*[2]

Here in a "lowly" fungus is a light sensing ballistic system that points the sporangiophores unerringly toward a light source (usually the rising sun). Here too is a biological clock which causes the subsporangial swelling to explode at the time when the angle of trajectory will insure the greatest horizontal distance of travel. Here is a fungus that literally "blows its top" at just the right time and in just the right manner to guarantee its spores a better chance to enter the digestive tract of a horse! Here is a fully planned system which fits well with the design expected in a wise Creator's handiwork. But here too is a significant problem to anyone who holds that life developed by chance.

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[1] Excellent line drawing of this growth process and other steps involved in the development of *Pilobolus* were made by the careful Canadian researcher, A. H. Reginald Buller. Buller produced a series of volumes on fungi. Reference material regarding *Pilobolus* in particular may be found in Part I, chapters 1 and 2 of: Buller, A. H. R. 1934. Researches on fungi. Vol. 6. Longmans Green, London.

[2] The author is indebted to Dr. Ralph Emerson, noted mycologist, for this suggestion regarding classroom use of *Pilobolus*. The author's own introduction to this fascinating fungus came during a lecture by Dr. Emerson at the National Science Foundation Summer Institute of Botany held in conjunction with the Botanical Society of America at Washington State University, Pullman, Washington, 1961.

WHY GENETIC VARIATION BETWEEN NEW GUINEA COMMUNITIES? (MIGRATION-DISPERSION MODEL APPLIED)*

R. DANIEL SHAW**

As members of small populations migrating from a relatively large common source are subjected to premature death through warfare, epidemic disease, and other unusual events, genetic drift is greatly accelerated. Migration coupled with unusual events is offered as the primary mechanism in producing genetic variation between the populations of New Guinea. This theoretical interpretation fits well with the facts, presented in table form, and solves a distribution problem of some complexity.

Introduction

The island of New Guinea offers an excellent opportunity to apply and develop theories and concepts in all areas of anthropology. The diversity in linguistic and genetic make-up displayed by populations on the island is particularly striking. Until very recently, isolation has been a fact of life and is still the key to understanding existing diversity.

From the genetic standpoint, New Guinea provides opportunity to use the Migration-Dispersion theory[1,2] and note its application to living populations. It must be made clear at the outset that this is in no way considered to be a validation of the theory since conclusive evidence necessary for validation is not available. Much of the material is in the form of tribal tradition and folklore which, while apparently supporting the hypothesis, can not be considered conclusive. It is, however, interesting to combine

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this material with genetic data available and note the similarity between an application of the theoretical model and the actual known diversity.

Migration-Dispersion Model

Briefly described, the Migration-Dispersion theory recognizes that as individuals migrate in small numbers from a common gene pool, the new group becomes more variable than the source group. Since migrants have isolated themselves from the parent stock, new generations come only from a limited gene pool, making the migrant group more variable. Selective forces acting on this new group would produce further diversification from the original genetic source.

Previously,[3] I have applied this theory to the distribution of hominid fossils throughout the Old World. That distribution shows that the most "primitive" types appear on the periphery, while the most morphologically "advanced" forms appear closer to the center of the Old World, the Mesopotamian Valley. People migrating from this region, encountering conditions as they existed prior to the Biblical Flood, and finally being subjected to the Flood itself could produce great variation resulting in the hominid fossil record we observe today.

Genetic Diversity Noted

The origin of the New Guinea peoples remains in dispute. Coon[4] sees the people as an outgrowth of the Pithecanthropoid Pleistocene population, while Macintosh[5] feels the "Papua-Melanesians" appear to have developed in Southeast Asia and may have somewhat hybridized there before migrating to Oceania. I would tend to agree with Macintosh on this point, since, as noted previously, any Pleistocene populations that may have existed would have been destroyed by the Biblical Flood.

Regardless of their origin, the New Guineas have in the past tended to isolate themselves into relatively small local groups which have become linguistically[6] and genetically[7, 8] diversified from their neighbors. Reasons for such diversification have been open to question for some time and yet have received relatively little attention in the literature. One possible reason for this is the relative lack of data available.

However, I have compiled genetic data (ABO, MNS and Rh blood groups) for thirty-seven areas spread over the entire island of New Guinea in an attempt to discover any relationships or factors which might correlate with this diversity (See accompanying map and table).

These data present a near random distribution that eludes any attempt to correlate frequencies with linguistic groups, culture areas, disease, or environment. Though each of these factors may have a part in shaping the frequencies in any given group, there are no correlations apparent which can be attributed to any one factor.

Populations of close proximity exhibit quite dissimilar gene frequencies (compare Telefolmin, Kopiago and Oksapmin), while they compare with other groups in dissimilar conditions. Frequencies between highlands and lowlands do not indicate any overall environmental trends of selection, high and low frequencies of any one gene being found in adjacent populations which are presumably subject, at least, to the same environmental pressures. Therefore it is impossible, at least with the present data, to plot any gradients, or clines, due to the apparent sudden shifts in frequencies from one region to the next.

Factors Contributing to Diversity

What factors could contribute to this type of near random distribution? I would like to briefly discuss two interrelated factors, unusual events and migrations, and note how these relate to the theory at hand.

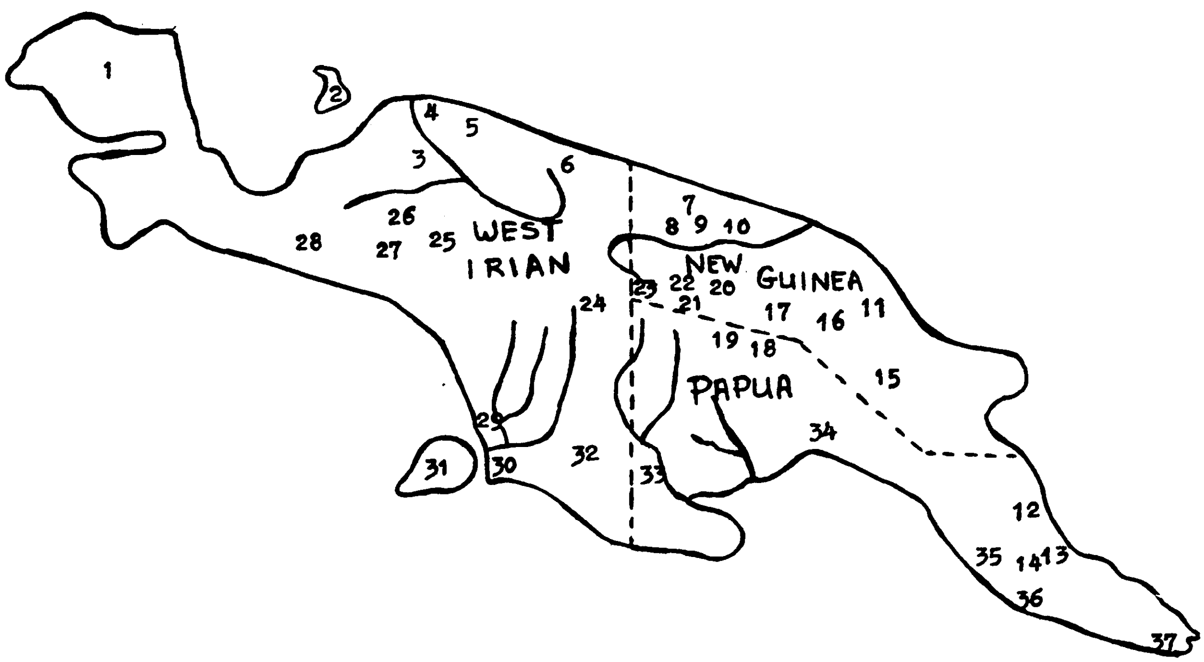
Unusual Events: Physical anthropologists have long agreed that populations are subject to selective forces. Gajdusek[30] has proposed another factor which could also play an important role. "Strange historical accidents," or unusual events, can singly or collectively have a varied effect in changing the gene frequency patterns.

Populations ravaged by disease, natural calamity, or social disruption leave only a relatively few men and women to propagate the next generation. Selective forces, of course, can only act upon the genes present, and if some are dropped, either through genetic drift, migration, or unusual event, they will be lost to future generations which reflect the genetic make up of the "founders."

An example of an unusual event could be the occurrence of disease in a community. Epidemic diseases are known to be prevalent throughout New Guinea. Malaria is endemic up to 5000 feet elevation and filariasis is prevalent as is yaws and, more recently, leprosy, tuberculosis, and influenza. Infant mortality due largely to infections, malaria and malnutrition has been high until very recently.[31]

Warfare, headhunting practices and sorcery disputes could be considered unusual (or not so unusual) events with social overtones. When individuals are thus removed from the gene pool, future generations are deprived of their genetic potential.

Therefore, epidemic disease, near continuous warfare, and headhunting and sorcery practices, continuing to the present in remote areas, undoubtedly have had an effect on the diversity of the New Guinea peoples. Furthermore, all such "removals" reduce the population and create



Northern (lowlands)
1. Sorong
2. Biak
3. Mamberamo
4. Martewar
5. Sarmi
6. Nimboran
7. So. Arapesh
8. Mid-Sepik
9. Maprik
10. Boiken
11. Madang
12. Ewa Ge
13. Orokaiva

Central (highlands)
14. Goilala
15. Kukukuku
16. Chimbu
17. Mt. Hagen
18. Mendi
19. Tari
20. Wabag
21. Kopiago
22. Oksapmin
23. Telefolmin
24. Star Mtns.
25. Pyramid
26. Mulia
27. Uhunduni
28. Wissel Lakes

Southern (lowlands)
29. Asmat
30. Auyu
31. Fredrik Hendrik Is.
32. Mandobo
33. Western Dist.
34. Kikori
35. Motu
36. Koita
37. Milne Bay

a greater chance of inbreeding with the associated likelihood of variability as a consequence.

Migrations: Macintosh[32] maintains that the introduction of new genes through migrations may also help to explain the diversity. He feels that the original population had a common origin and became fairly homogeneous. This stable situation may have been subsequently modified by later intrusions which reached the coasts and followed the rivers altering the existing gene pools as they went. The extent of inter-mixture would, of course, depend upon selective forces acting on the newcomers, including environmental and cultural factors.

The Migration-Dispersion model is almost the antithesis of Macintosh's ideas, viewing the diversity as a result of migration away from a common gene pool rather than movement into a stable pool. Linguistic classifications, especially in the highlands, "indicate the probability of a common source, or related sources."[33]

As people moved out from a common source, probably in relatively small groups, they would become isolated by natural geographic barriers (which abound in New Guinea). This separation would reduce the gene flow, forcing the individuals to inbreed.

Small groups tend toward greater diversity since mutant genes are more frequently brought together in the homozygous condition and are thus expressed phenotypically. A small isolated population gives rise to individuals who represent the limits of potential variability in the original population which may not show up otherwise

TABLE 1

Locality	Number tested		ABO			MNS				Rh	
		A	B	O	mS	ms	nS	ns	R_1	R_2	R_0
Northern (lowlands)											
1. Sorong[9]	25	0.15	0.10	0.75	0.	0.24	0.06	0.70	0.94	0.02	0.04
2. Biak[9]	183	0.10	0.12	0.78	0.	0.26	0.04	0.70	0.93	0.06	0.01
3. Mamberamo[10]	122	0.12	0.20	0.68	0.04	0.22	0.01	0.72	0.99	0.01	0.00
4. Martewar[11]	199	0.15	0.30	0.55	0.12	0.04	0.07	0.77	0.98	0.02	0.00
5. Sarmi[11]	59	0.36	0.09	0.55	0.01	0.24	0.	0.75	0.93	0.05	0.02
6. Nimboran[12]	127	0.24	0.08	0.68	0.	0.03	0.	0.97	0.91	0.09	0.00
7. So. Arapesh[13]	85	0.19	0.15	0.66	0.04	0.08	0.15	0.73	0.87	0.12	0.01
8. Mid-Sepik[13]	47	0.45	0.14	0.41	0.06	0.03	0.17	0.75	0.81	0.15	0.04
9. Maprik[13]	71	0.28	0.21	0.51	0.	0.18	0.12	0.70	0.92	0.07	0.01
10. Boiken[14]	158	0.21	0.18	0.61	0.	0.04	0.22	0.74	0.87	0.08	0.05
11. Madang[15]	26	0.29	0.19	0.52	0.	0.12	0.32	0.56	0.92	0.08	0.
12. Ewa Ge[16]	191	0.34	0.14	0.52	0.00	0.11	0.20	0.69	0.94	0.04	0.02
13. Orokaiva[16]	49	0.26	0.09	0.65	0.08	0.18	0.22	0.52	0.88	0.07	0.05
Central (highlands)											
14. Goilala[17]	433	0.12	0.09	0.79	0.	0.05	0.06	0.89	0.97	0.02	0.01
15. Kukukuku[18]	111	0.34	0.06	0.60	0.	0.10	0.04	0.86	0.83	0.13	0.04
16. Chimbu[19]	864	0.25	0.16	0.59	0.	0.02	0.15	0.83	0.89	0.08	0.03
17. Mt. Hagen[20]	473	0.21	0.20	0.59	0.	0.04	0.15	0.81	0.95	0.04	0.01
18. Mendi[21]	59	0.22	0.11	0.66	0.	0.01	0.14	0.85	0.97	0.03	0.
19. Tari[21]	54	0.20	0.16	0.63	0.	0.01	0.09	0.90	0.91	0.09	0.
20. Wabag[22]	2608	0.24	0.12	0.64	0.00	0.05	0.20	0.75	0.93	0.05	0.02
21. Kopiago[23]	188	0.15	0.21	0.64	0.	0.08	0.02	0.90	0.90	0.05	0.05
22. Oksapmin[24]	147	0.06	0.10	0.84	0.	0.06	0.01	0.93	0.78	0.12	0.10
23. Telefolmin[25]	134	0.22	0.06	0.72	0.	0.06	0.01	0.93	0.85	0.08	0.07
24. Star Mountains[26]	166	0.08	0.18	0.74	0.	0.02	0.	0.98	0.97	0.02	0.01
25. Pyramid[11]	386	0.19	0.25	0.56	0.	0.10	0.01	0.89	0.98	0.02	0.00
26. Mulia[27]	184	0.17	0.39	0.44	0.	0.10	0.	0.90	0.91	0.08	0.01
27. Uhunduni[27]	47	0.11	0.15	0.74	0.	0.12	0.	0.88	0.96	0.04	0.
28. Wissel Lakes[27]	214	0.03	0.12	0.85	0.	0.10	0.02	0.88	0.82	0.15	0.03
Southern (lowlands)											
29. Asmat[27]	338	0.21	0.13	0.66	0.	0.02	0.04	0.94	0.95	0.03	0.01
30. Auyu[27]	71	0.22	0.15	0.63	0.	0.03	0.09	0.88	0.87	0.09	0.04
31. Frederik Hendrik Is.[27]	22	0.07	0.10	0.83	0.	0.09	0.05	0.86	0.91	0.09	0.
32. Mandobo[27]	39	0.12	0.03	0.85	0.	0.17	0.18	0.65	0.83	0.17	0.
33. Western District [15]	52	0.22	0.11	0.67	0.	0.06	0.11	0.83	0.91	0.04	0.05
34. Kikori[28]	339	0.21	0.12	0.67	0.	0.04	0.10	0.86	0.95	0.04	0.01
35. Motu[29]	459	0.13	0.18	0.69	0.	0.24	0.06	0.70	0.94	0.06	0.00
36. Koita[29]	294	0.12	0.16	0.72	0.	0.18	0.09	0.73	0.86	0.14	0.
37. Milne Bay[15]	74	0.20	0.10	0.70	0.	0.28	0.15	0.57	0.91	0.04	0.05

(Note that frequencies represented by 0.00 indicate a frequency of less than 0.005 before rounding to two significant figures.)

since a large population reduces the likelihood of closely related individuals mating.

Related individuals are more certain to have mutant genes at the same loci and in isolated communities these are brought together more frequently resulting in offspring which show greater variability. Therefore, variability in small populations is also directly related to the corresponding increase in inbreeding, accelerating the genetic change affected by natural forces of selection. These natural forces are, in turn, affected by disease, social disruption and other calamities which further change the genetic inheritance of succeeding generations.

Such subdivision of populations was noted by Wright[34] and is considered to be very conducive to rapid change. Neel[35] feels that the type of dispersion noted here is "the single most important step" in the formation of a genetically distinct population. He goes on to say:

> These villages . . . tended to consist of related individuals, thus providing unusual scope in man for what we have termed the 'lineal effect' in establishing subpopulations

whose gene frequencies are quite different from those of the parent population.[36]

Such genetic and cultural isolation could thus be vital forces in creating the variations observed today. In nearly every tribe there are traditional origin stories which mention prehistoric migration of all or part of the tribe. In many instances there are accounts of migrations during the past century, indicating that migration is a continuing process affecting the present genetic distribution. As new waves of migration occur, the earlier migrants appear to be pushed further in the same direction. Observe the present spreading of large languages in the highlands at the expense of smaller, more closely related languages which have in some cases been surrounded, assimilated, or pushed to peripheral lands.[37]

Model Applied

Remembering the theoretical nature of the Migration-Dispersion model, and that this is an application not a validation, I would like to briefly hypothesize a series of events using the model and note the results.

Beginning with the assumptions made by Macintosh,[38] the "Papua-Melanesians" possibly migrated to New Guinea, in relatively large numbers, from somewhere in Southeast Asia. Arriving on the coasts of what was probably a largely uninhabited island, they settled down to living off the land and establishing their position on it.

As the population began to grow, it is natural to expect that it would expand geographically, eventually moving up the river valleys and into the highlands. Pushed by new waves of migrants, these small, relatively mobile groups were affected by unusual events as well as other selective forces which resulted in varying degrees of genetic drift, and produced after several generations a population which was not only distinct from other isolated groups but quite different from the source group as well.

Continuous change that brought about such conditions would result, in fact, in considerable variation within a relatively short time as noted by Cavalli-Sforza.[39] In the highlands, lexical material indicates a continuous development of linguistic diversity of about 6000 years,[40] a time span which agrees well with the archaeologists.[41]

Conclusion

Diversity, then, is a fact of life in New Guinea. I have attempted here to apply a theoretical model to a problem and note the results. The Migration-Dispersion model appears to answer some of the questions in a relatively plausible manner. This is not to say that other explanations are not valid, it simply presents one possibility. It could well be that when further data are available the apparent genetic diversity will not appear as great. Only thirty-seven areas are included here, thus the sampling is very small considering there are probably nearly 1000 tribal (language) areas on the whole of New Guinea. Clearly more data are necessary.

Another factor contributing to the variability is that published figures are only *estimates* of gene frequency, being based on a sample taken from the population. The smaller the sample the larger the standard error, and sample size varies considerably. For this reason all figures noted have been reduced to two significant figures.

Natural forces of selection have without doubt had an affect on New Guinea populations. Premature death through epidemic disease, warfare, and other unusual events acts upon small migrating groups to accelerate genetic drift, thus increasing variability. Migration, then, coupled with unusual events and natural forces could well have produced the genetic diversity noted in data available among populations on the island of New Guinea. While evolutionists posit gradual processes to produce such change, it is here suggested that the change was rapid as a result of small populations living in isolated circumstances and being subjected to unusual events. Thus long periods of time would not be necessary to produce the differences seen.

The type of data presented here could be offered as evidence of what might have occurred on a much larger scale to produce the "living races of man" since the Biblical Flood. Since that Flood, man has proliferated at a much slower rate than other creatures, producing only distinct *races,* the cross breeding of which all produce viable offspring.

The races do, of course, display a high degree of adaptability to the environmental conditions in which they find themselves *e.g.* the Australian Aboriginies and natives of the Magellan Straights are highly adapted to extreme cold while natives in the high Andes are adapted to living in high altitudes. Others entering these areas of environmental stress can, however, cope by using cultural items (clothing, housing, heating devices and oxygen). It probably is man's ability to use culture to his advantage thereby manipulating the environment that has enabled him to exploit new situations and reduce genetic variation.

The very action of God at the Tower of Babel may have had a direct bearing on the mechanism discussed here. As a result of this incident the tongues and languages were suddenly and rapidly developed and man was dispersed throughout the Earth. As he went, man carried his genetic heritage with him and as he moved from the large common gene pool at Babel and dispersed, the result was small migratory populations scattered about the Earth.

The populations within New Guinea though by no means approaching racial distinctions do provide for observation and recording of the mechanisms at force to produce genetic variation. As indicated earlier, the Migration-Dispersion model fits with the data presented. Though more data are needed and perhaps other creationist models are valid at this point, the Migration-Dispersion model provides a description which fits with the Biblical account and solves a population distribution problem of some complexity.

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