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Selander R K, Smith M H, Yang S Y, Johnson W E & Gentry J B. Biochemical polymorphism and systematics in the genus *Peromyscus*. I. Variation in the old-field mouse (*Peromyscus polionotus*). *Studies in Genetics*, VI. Univ. Texas Publ. 7103:49-90, 1971.
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An analysis by enzyme electrophoresis of allelic variation in 32 structural genes revealed that populations inhabiting beaches on Santa Rosa Island and several peninsulas on the Florida Gulf coast were only 1/4 to 1/2 as variable as those on the mainland. Both this and the fact that the beach populations were strongly heterogeneous in allele frequencies were attributed to genetic drift. A "cookbook" of laboratory protocols for multilocus enzyme electrophoresis was appended. [The SC1® indicates that this paper has been cited in more than 1,165 publications, making it the most-cited paper published in this journal.]

Genetic Drift in Isolated Populations

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In the late 1960s, S.Y. Yang and I were using the then-new multilocus enzyme electrophoresis (MLEE) to analyze the genetic structure of natural populations of the house mouse and had discovered an unusual degree of microgeographic subdivision. As a result of the founder effect and genetic drift in small demes maintained by the territorial behavior of the polygamous adult males, allele frequencies often vary markedly among barns on the same farm and even within single large barns.¹ Because a comparative analysis of a monogamous rodent was desirable, we arranged a collaboration with M.H. Smith, an authority on mammalian ecology, to study the old-field mouse of the southeastern US.

Our study demonstrated that genic heterozygosity in isolated populations on a barrier island and several peninsulas is greatly reduced compared to that of the mainland populations and revealed a relatively high degree of allele frequency variation among the various beach popu-

lations. Because the beach environment is relatively simple, uniform, and seasonably stable, an adaptive ecological explanation (the "ecological amplitude hypothesis") for the reduced genetic variation might have been invoked. But we rejected selectionist hypotheses and opted instead for genetic drift as the cause. Knowing that the beach populations were relatively small and periodically bottlenecked, we also attributed the interpopulation variation to genetic drift rather than to natural selection. This interpretation undoubtedly raised the eyebrows of many mammalogists and evolutionists, because, in the dogma of the New Synthesis of evolutionary theory, genetic drift had been effectively dismissed as an evolutionary factor. Drift was, however, soon to return with a vengeance in the form of M. Kimura's neutral theory of molecular evolution.²

Our paper was a model for the population genetic analysis of geographic variation, but the primary reason for its heavy citation record is that it includes an appendix containing detailed descriptions of our methods. A "cookbook" for MLEE was much in demand, for application to such varied organisms as elephant seals and slime molds. In the next decade, research in population genetics and systematics came to be dominated by application of this technique.³

Soon after this paper appeared, my interests turned to mollusks when MLEE revealed that some land snails and many slugs practice self-fertilization,⁴ just like plants. Beginning in 1980, we applied MLEE to the population genetics of bacteria and soon discovered that, for any one pathogenic species, most disease is caused by one or a few globally distributed clones.⁵ Now we are busy playing the newest game in population genetics research—the complete nucleotide sequencing of PCR-amplified genes—in order to determine the role of lateral transfer and recombination in bacterial evolution.⁶ But, MLEE is still widely used, because it is the quickest and least expensive method of assessing levels of genetic variation in populations, estimating genetic distances, and determining population structure.

- Selander R K. Behavior and genetic variation in natural populations. *Amer. Zool.* 10:53-66, 1970. (Cited 205 times.)
- Kimura M. *The neutral theory of molecular evolution*. Cambridge, England: Cambridge University Press, 1983. (Cited 525 times.)
- Lewontin R C. Electrophoresis in the development of evolutionary genetics: milestone or millstone? *Genetics* 128:657-62, 1991.
- Selander R K & Kaufman D W. Self-fertilization and genetic population structure in a colonizing land snail. *Proc. Nat. Acad. Sci. USA* 70:1186-90, 1973.
- Selander R K, Caugant D A & Whittam T S. Genetic structure and variation in natural populations of *Escherichia coli*. (Neidhardt F C, Ingraham J L, Low K B, Magasanik B, Schaechter M & Umberger H E, eds.) *Escherichia coli and Salmonella typhimurium: cellular and molecular biology*. Washington, DC: American Society for Microbiology, 1987. Vol. 2, p. 1625-48.
- Nelson K, Whittam T S & Selander R K. Nucleotide polymorphism and evolution in the glyceraldehyde-3-phosphate dehydrogenase gene (gapA) in natural populations of *Salmonella* and *Escherichia coli*. *Proc. Nat. Acad. Sci. USA* 88:6667-71, 1991.

Received January 27, 1992