INTRAPOPULATION GENETIC SIMILARITY IN
POGONOMYRMEX CALIFORNICUS (BUCKLEY)
(HYMENOPTERA: Formicidae)

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ABSTRACT
Two color morphs of Pogonomyrmex californicus (Buckley) were studied at twelve enzyme loci by means of starch gel electrophoresis. Neither of the dark phase morph was genetically distinguishable from the typical morph. The results strongly suggest that, at the loci and in the populations studied, the two morphs are members of the same species. These findings provide additional evidence in support of the synonymy of P. c. erichsonii with P. californicus. The suggestion is made that the dark phase morph may have evolved slightly different isoforms to cope with thermal stress.

INTRODUCTION
Pogonomyrmex californicus (Buckley) is a species of harvester ant common throughout most of the southwestern desert states, especially California and Arizona. Identification of the "typical" P. californicus worker presents few problems. It is of comparatively small stature (5.5-6.0 mm in head across eyes), bears coarse cephalic and thoracic rugae, and has a concolorous, ferruginous red body color. With an excel lent electrophoretic in range, however, there is an infatuation of the gaster in one or all of a series, ranging from lateral spotting to concordial black or brown. This is the typical polymorphism in respect to color, with one extreme being repre sented by totally red individuals (typical) and the other by individuals containing substantial postepisteme, and leg red and the gaster entirely black or brown (dark phase). Wheeler (1914) and Cole (1968) noted site differences between the two forms, with typical being somewhat smaller than dark phase. Creighton (1950), however, was unable to detect any size differences that could reliably separate the two forms and concluded that "the two forms are most readily separable on the basis of color."... Color of colonies of typical and dark phase occur throughout California, Arizona, New Mexico, and northern Mexico (Cole, 1968). In some nests, both types are found in admixture with a full range of intergradation. Typical colonies are found mainly in the coastal areas of California and Baja California. In the central Mojave Desert, colonies of dark phase ants are found extending to lower elevations (below 1500 m) than typical colonies, while in southern Arizona, typical and dark colonies are sympatrically distributed (Cole, 1968).

Initially, workers of the dark phase variant were assigned subspecific state (P. c. erichsonii), principally on the basis of their bicolored appearance (Wheeler, 1914). This convention was maintained in a number of subsequent studies of the species (Omen, 1934; Creighton, 1950; Cook, 1953). Creighton (1950) noted, however, that substantial genetic differences between the two forms were not of significant aspects—and stated that "it would be much more in keeping with the concept of erichsonii as a geographical race if it were more clearly a distinctive race of its own." He be lieved that the distinctive race might lie in northwestern Mexico. Cole (1968) has synonymized P. c. erichsonii with P. californicus on the premise that the color difference separates the two is within the "established limits of intraspecific variation." He sup ports this classification with the following facts: 1) no distinct range for erichsonii has been found; 2) the two types have been shown to exist within the same nest; and 3) no characters have been found which could provide erichsonii with the status of a species. With these unresolved conflicts in the existing data, it was felt that new biochemical genetic data could provide further clarification of the taxonomy of this species. We therefore sought to determine those levels of genetic variability between the two morphs that were not an expression of environmental heterogeneity (Johnson et al., 1969). Such findings would provide us with a further test of Cole's statement that erichsonii lacks the characteristics of a species distinct from californicus. Electrophoretic analysis methods were employed to assess questions with the level of genetic variability between the two forms.

MATERIALS AND METHODS
Typical and dark phase workers of Pogonomyrmex californicus were collected from nests in the central Mojave Desert near Pearlbeom, Los Angeles County, California. The collections were restricted to a 45 m area around square kilo meters to the possibility of clinal geographics being factors in the observed variation (Johnson et al., 1969). Approximately 250 individuals were taken from fifteen nests in the area in April.

Colonies of Pogonomyrmex californicus have twelve structural genes coding for enzymes stained. The enzymes: Esterase (Esp), four loci each; phosphoglucose isomerase (PGI); one locus; malate dehydrogenase (MDH); one locus; phosphoglucokinase (PGK); one loci. Whole line ants were homogenized in 50 μl of distilled water by means of a small mortar and pestle. Pooled samples for homogenization were obtained from a single individual from each of two populations. The resulting homogenates were adsorbed onto 4x4 cm gel slices of Whatman No. 1 filter paper and subjected to horizontal starch gel electrophoresis in 12.5% gel for 3.5 hours at a maximum current of 50 μA. A discontinuous buffer system was employed (Parker, 1957). Standard protocols were used. An assay was pri sed (Johnson et al., 1969; Shaw and Proctor, 1970; Kuhn, 1973).

RESULTS
The observed genotypes and allelic frequencies were determined by direct counts of the various bands developed in the gels. A conservative scoring procedure was used by which only unquestionably distinct bands were counted. Alleles at each locus were identified with a relative electrophoretic mobility relative to the most common, lowest allele at each locus was designated 1.00. Alleles slower than this were designated 0.95; faster alleles were designated 1.05. The allele frequencies in Table 1 were calculated from the raw data using the method of Huffy and Lewontin (1966).

Two significant results emerge from the data pre sented in Table 1. First, there are low levels of enzyme polymorphism in all sample studied, with a maximum of three out of twelve loci clearly polymorphic using the 1% criterion of Ayala et al. (1970). Second, each locus examined had an allele in common between samples. P. c. erichsonii is particularly evident at the MDH and PGI loci, which were also consistently monomorphic. The esterase loci, despite the presence of a few rare alleles, each demonstrated an allele in common between samples. The common alleles were revealed by homology tests. The PGM-2 locus is unique in that the 1.00 allele is not represented in any of the dark phase samples.

Estimates of the genetic similarity of the two populations were calculated using Rogers' formula (1972) for similarity and Hedrick's formula (1971) for probability of genotype identity. Rogers' coefficient assumes values from zero for similar populations to one for populations that are completely differentiated genetically. Hedrick's formula compares genotype, rather than gene, frequencies. The probability value ranges from one for identical genotypes to zero for highly dissimilar genotypes. The results of the tests are as follows: Rogers' coefficient: 0.04; Hedrick's probability: 0.98.

Discussion
The principal object of this investigation was to ascertain the level of genetic variability between the two morphs. From the results resulting from environmental heterogeneity. The electrophoretic data and the results of this analysis strongly suggest that the two forms are not genetically distinct and differ considerably from the value expected for members of the same species. While speculation does not seem to require a change of sample size from the one detected here does not indicate any divergence between the two morphs. The slight variations noted at loci other than PGM-2 were of recent origin and are undetectable with the method used.

Polyorphism at the esterase loci is to be expected. Such enzymes, which utilize substrates originating in the environment, are more variable than those utilizing specific substrates which are supplied in a fixed amount (e.g., Lewontin, 1973). The total lack of polymorphism in the dark phase samples could be the result of the conservative scoring procedure and the deliberate attempt to reduce clinal variation. The average of observed levels of polymorphism in all samples, 12.5%, suggests that outbreeding and gene flow are quite restricted in these populations and that selection for certain specialized genotypes may have taken place. We are interested in determining whether the two forms differ most at the PGM-2 locus. Such a difference does not represent potential speciation; however, it could indicate that the two forms are more significantly related by physiological mechanisms to cope with environmental heterogeneity. However, the limited data does not, as yet, enable us to predict whether this particular polymorphism is a common enough occurrence to be significant in the ecology of P. californicus. Further work will be required to determine, for example, if there is a correlation between this variation and the "thermo phobic" character of the dark phase morph (Cowgrien, 1950). While electrophoresis currently represents the best approach to the study of genetic variation, the method is not without its sources of error. One of these is that some amino acid substitutions may occur that do not have any detectable effect on a protein's net charge, thus leading to an underestimation of genetic variability by a factor of three (Lewontin, 1973). Another source of error that cannot be corrected for easily is that not all available genetic variation may not be assayed; assay techniques are available for only a limited number of enzymes. This problem is compounded by the fact that color polymorphism in insects is frequently controlled by a single gene and a single selection gradient, whereas the effects of these and other problems, cannot be ignored the possibility that there is a genetic difference between the two forms. Significant variation may have been obscured or not detected. It may be that for reasons which the result of the present study may be considered highly suggestive rather than conclusive.
On the basis of the biochemical genetic evidence alone, we could not preclude considering estebanius as a subspecies of *P. californicus* since the two are almost certainly conspecific. However, these results do support Cole's statement that estebanius does not display any characters which distinguish it as a species distinct from *P. californicus*. Thus these findings, in combination with those of Creighton (1950) and Cole (1968), provide additional justification for the synonymy of *P. c. estebanius* with *P. californicus*.

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**LITERATURE CITED**


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