

PHOSPHOGLUCOMUTASE POLYMORPHISM IN WHITE SHRIMP, *PENAEUS SETIFERUS**

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Abstract—1. Ten phenotypes of phosphoglucumutase (PGM), were detected in abdominal muscle extracts from white shrimp (*Penaeus setiferus*) by starch-gel electrophoresis.

2. The assumption that these phenotypes were under the control of five allelic genes was supported by the observed distribution of the phenotypes.

3. There were no significant differences in PGM phenotype distribution between sexes or among samples of shrimp collected from Matagorda and Galveston Bays, Texas; Rockefeller Refuge and Barataria Bay, Louisiana; and the north Edisto River, South Carolina.

4. The five PGM alleles observed in white and brown shrimp appear to be the same in the two species.

5. Comparisons of PGM phenotype distributions and allele frequencies of white and brown shrimp suggest that the two species are closely related.

INTRODUCTION

THE ENZYME phosphoglucumutase (PGM), which plays an important role in carbohydrate metabolism, exhibits genetic polymorphism in many animals. PGM was first reported to be polymorphic in a penaeid, the brown shrimp (*Penaeus aztecus*) by Proctor *et al.* (1974). Their work and ours represent part of a search for subpopulations within commercially important species of penaeid shrimp in the Gulf of Mexico (Caillouet & Baxter, 1973).

This paper describes PGM polymorphism in white shrimp, and presents data on distribution of PGM phenotypes and frequency of PGM alleles in white shrimp from four locations in the northern Gulf of Mexico and one location on the Atlantic coast of the

United States. Similarities of alleles and phenotypes between white and brown shrimp are also noted.

METHODS

White shrimp were collected from Matagorda and Galveston Bays, Texas; Joseph Harbor Bayou and Royalite Canal in Rockefeller Refuge and Barataria Bay, Louisiana; and the North Edisto River, South Carolina (Fig. 1). One hundred or more specimens of each sex from each location were frozen immediately on "dry ice" after capture. Upon arrival at the laboratory, all samples were stored at -20°C or lower until analyzed.

Extracts were prepared following Proctor *et al.* (1974). Frozen abdominal muscle samples ground in cold phosphate-buffered physiological saline were centrifuged 31,000 *g* for 10 min at 5°C . Each supernatant was drawn into a 4 × 6 mm piece of Whatman No. 3 (or equivalent) filter paper which was blotted slightly and inserted in starch gel prepared according to Kristjansson (1963). Horizontal electrophoresis was conducted with a buffer system

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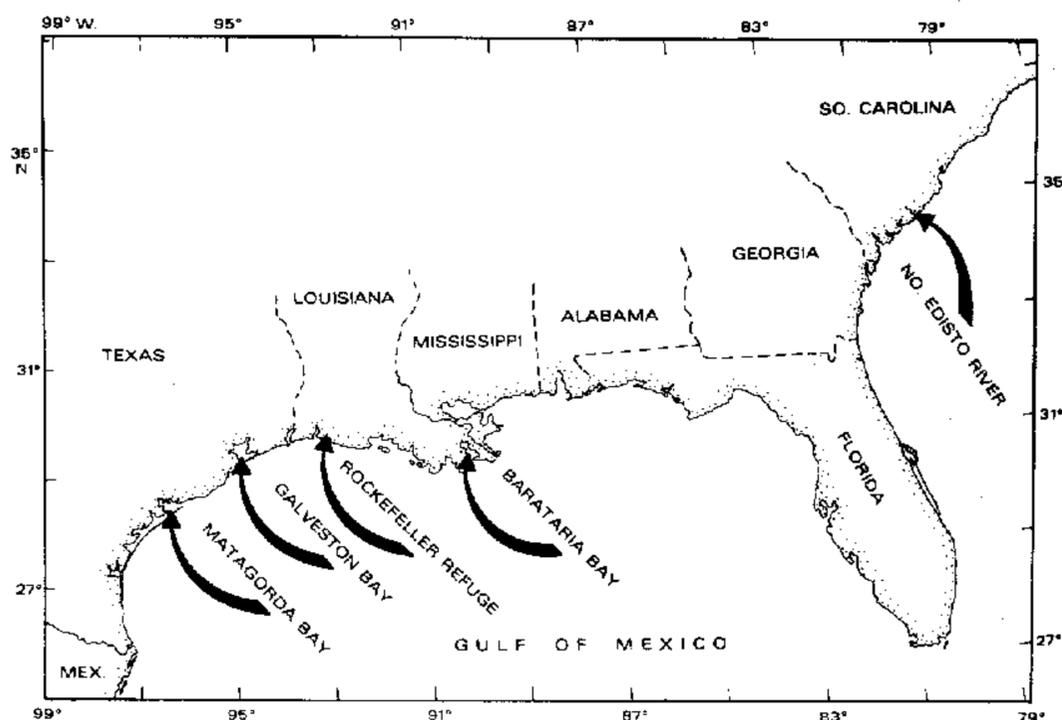


Fig. 1. Locations from which white shrimp were collected.

Table 1. Distribution of PGM phenotypes and frequency of PGM alleles in samples of white shrimp from Matagorda and Galveston Bays, Texas; Joseph Harbor Bayou and Royalite Canal in Rockefeller Refuge and Barataria Bay, Louisiana; and the North Edisto River, South Carolina

Location	Total length* ranges, mm	Phenotypes										Number of specimens	Alleles				
		ab	ac	bb	bc	bd	be	cc	cd	ce	dd		a	b	c	d	e
Matagorda Bay	66-137	0	5	3	50	2	0	135	16	0	0	211	0.0118	0.1374	0.8081	0.0427	0.0000
Galveston Bay	59-96	1	3	6	55	4	0	118	20	4	0	211	0.0095	0.1706	0.7536	0.0569	0.0094
Rockefeller Refuge	63-98	0	5	8	48	3	1	129	11	1	1	207	0.0121	0.1643	0.7802	0.0386	0.0048
Barataria Bay	72-147	0	2	4	52	2	0	128	12	1	2	203	0.0049	0.1527	0.7956	0.0443	0.0025
N. Edisto River	79-137	0	3	7	55	7	0	125	17	2	0	216	0.0069	0.1759	0.7569	0.0556	0.0046

Comparison of phenotype frequencies†	d.f.	Chi square†
Males vs Females (Matagorda Bay)	2	0.809
Males vs Females (Galveston Bay)	2	0.140
Males vs Females (Rockefeller Refuge)	2	3.605
Males vs Females (Barataria Bay)	2	0.558
Males vs Females (North Edisto River)	2	0.253
Comparison among the five locations (sexes combined)	8	8.859

* Tip of rostrum to tip of telson.

† Frequencies for phenotypes containing a, b, d, and e alleles were pooled under one category for the Chi square calculations.

described by Ridgeway *et al.* (1970), and staining of PGM followed the method described by Johnson *et al.* (1972). A horizontal section of each gel also was treated with a non-specific protein stain (Coomassie Blue) to confirm species identification (Fig. 2).

RESULTS AND DISCUSSION

Zymograms of white shrimp abdominal muscle extracts exhibited one region of PGM activity represented by five anodal bands labeled a, b, c, d, and e (Fig. 3). These bands were assumed to be under the control of five codominant allelic genes, because observed distributions of one- and two-banded phenotypes did not differ significantly* from expected distributions based upon Hardy-Weinberg equilibrium (Stern, 1943). Ten of 15 possible phenotypes were detected, and nine of the ten are shown in Fig. 3. The ab phenotype was detected in only one specimen which was not saved, and we were unable to find another to portray this phenotype. The remaining five phenotypes were not observed, but this might be expected since alleles a, d, and e are rare.

There were no significant differences in phenotype distribution among the five locations (Table 1); the distribution of observed phenotypes was not significantly dependent on sex, so data for males and females were combined for the comparison among locations. The sample from South Carolina was included because the white shrimp of this area are assumed to be reproductively isolated from those of the Gulf. According to Farfante (1969), the population of white shrimp probably extended from the Carolina coast southward across the Suwannee straits into the Gulf of Mexico prior to

when it became discontinuous, probably toward the close of the Pleistocene, with the consolidation of the Florida Peninsula. Although recent genetic interchange between the Atlantic population and the Gulf population seems unlikely, extensive biometric studies have failed to show any significant morphological differences between these two populations of white shrimp (Farfante, 1969).

Lack of significant differences in the distribution of PGM phenotypes in white shrimp among the five locations is not necessarily indicative of strong gene flow throughout these locations (F. M. Utter, personal communication). Even a small amount of gene flow with large populations and an absence of strong selection could maintain these frequencies at the same levels.

Conversely, selective forces could be acting to maintain PGM phenotypes at similar levels in the absence of interchange among the locations. The PGM alleles of white shrimp appear to be the same as those of brown shrimp (Fig. 4) and occur at similar frequencies (Table 2). These similarities indicate that the two species are closely related and suggest that selective forces may be maintaining the alleles at these frequencies in the absence of gene flow between species (see Koehn & Mitton, 1972). The same also may apply to different

Table 2. Frequency of PGM alleles in white shrimp (1048 specimens) and brown shrimp (600 specimens)*

Species	Alleles				
	a	b	c	d	e
White shrimp	0.0091	0.1603	0.7786	0.0477	0.0043
Brown shrimp	0.0025	0.2175	0.7642	0.0142	0.0017

* Refers throughout this paper to the 95% level of confidence.

* Adapted from Proctor *et al.* (1974).

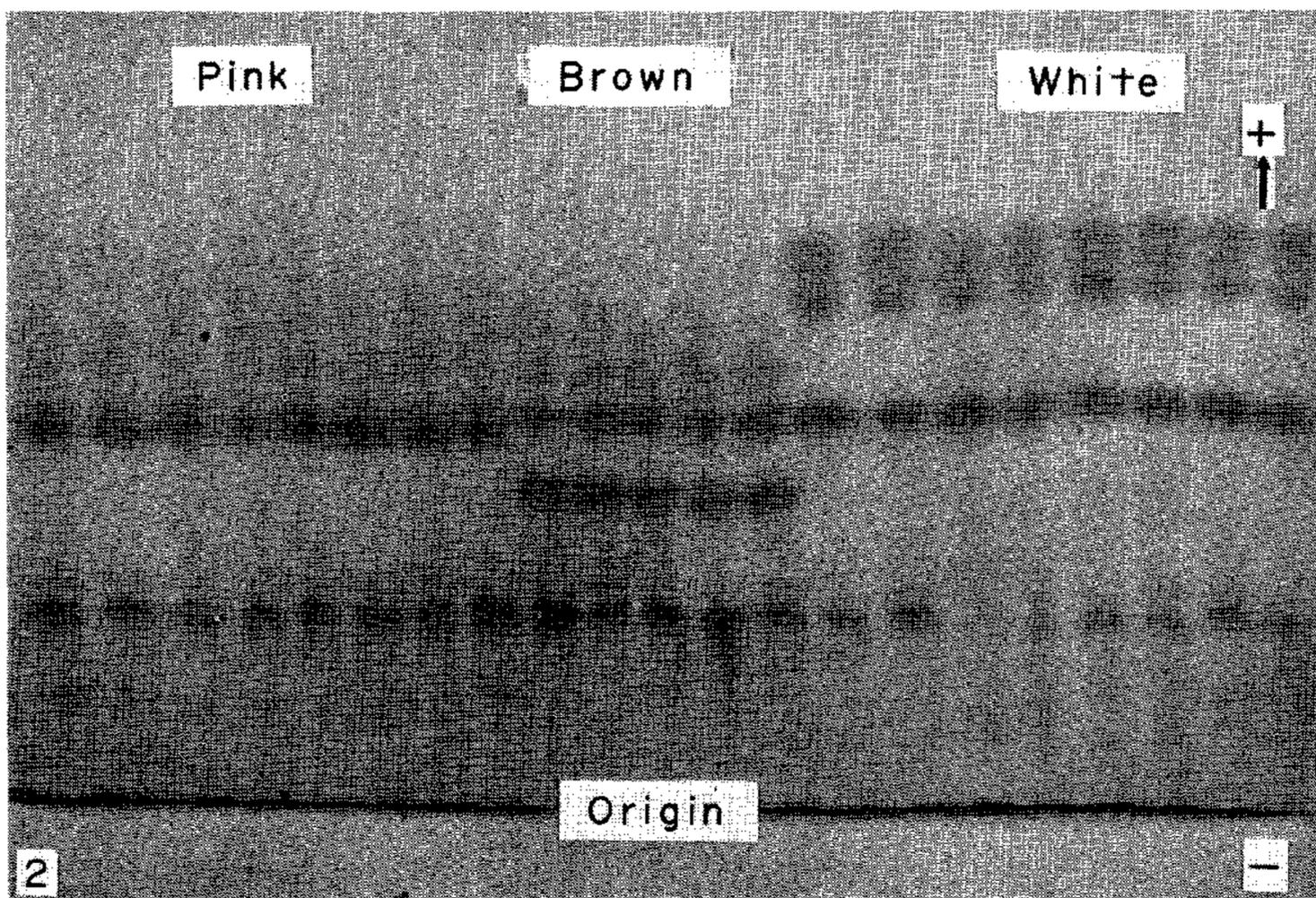


Fig. 2. Starch-gel electropherograms of pink (*Penaeus duorarum*), brown, and white shrimp abdominal muscle proteins stained with the nonspecific stain, Coomassie Blue. Direction (↑) of protein migration toward the anode (+) is shown.

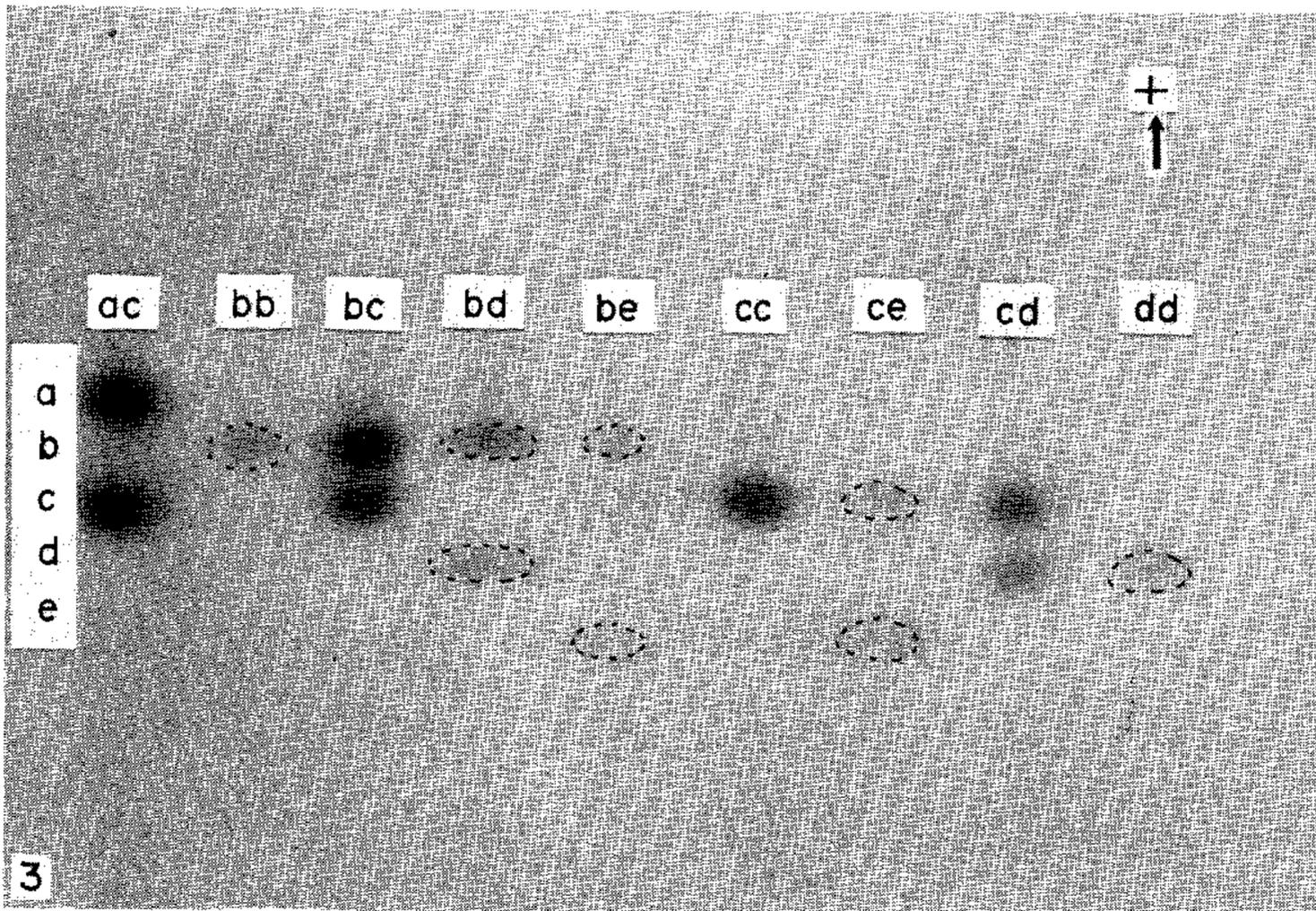


Fig. 3. Zymogram showing nine of the ten PGM phenotypes observed in white shrimp. Alleles a-c are also labeled. Direction (\uparrow) of protein migration toward the anode (+) is shown. Alleles that were too faint to be photographically reproduced are encircled (---).

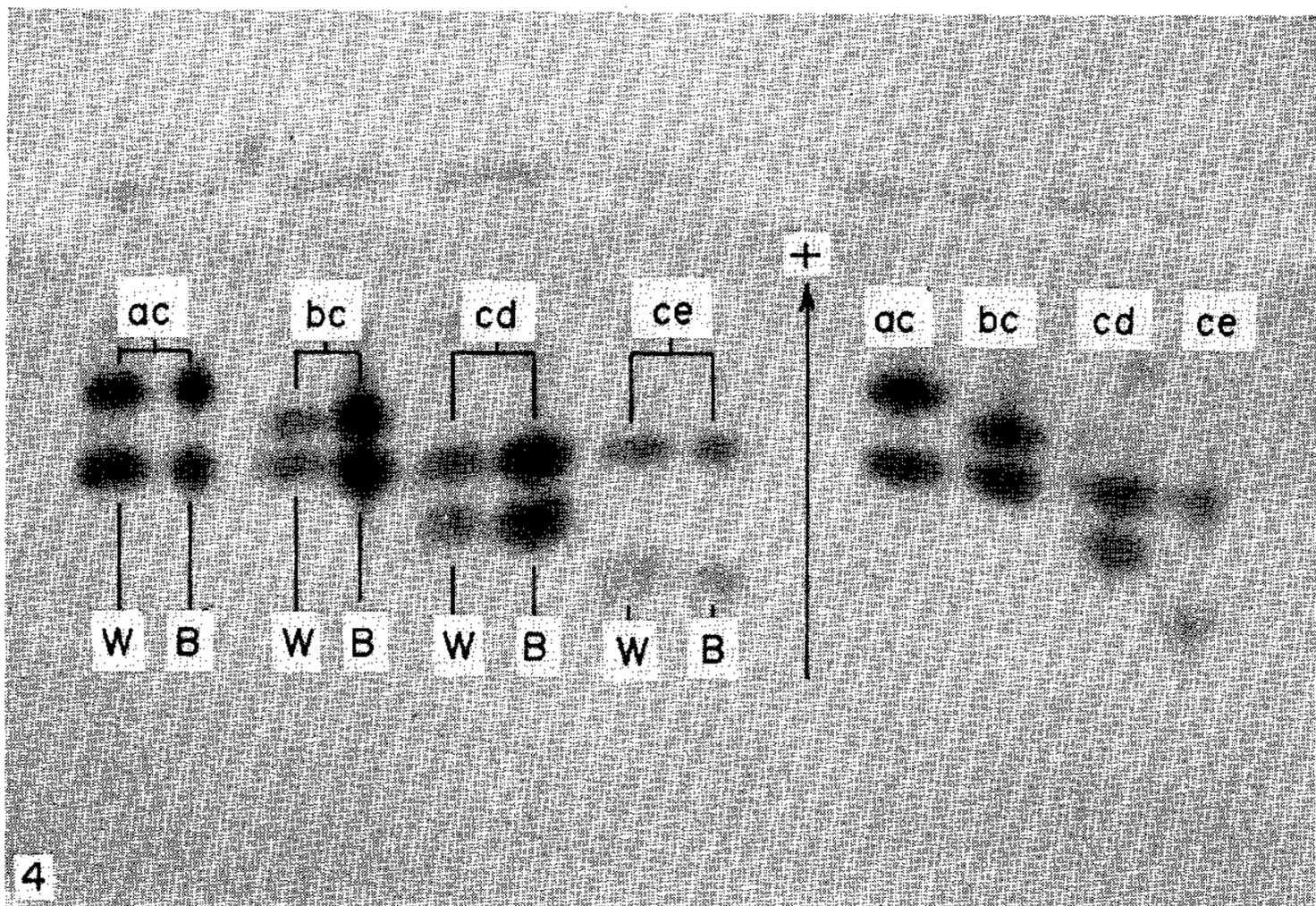


Fig. 4. Zymogram showing similarity of alleles in white (W) and brown (B) shrimp. Comparisons between species are to the left of the arrow. Extracts from both species were mixed together to obtain the patterns to the right of the arrow. Direction (\uparrow) of protein migration toward the anode (+) is shown.

subpopulations of the same species if selective forces are similar in the different locations in which they occur.

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