

Phosphoglucumutase Polymorphism in Brown Shrimp, *Penaeus aztecus*¹

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Eight phenotypes of phosphoglucumutase (PGM) were detected in abdominal muscle extracts from brown shrimp (*Penaeus aztecus*) by starch-gel electrophoresis. The observed phenotypes were assumed to be under the control of five allelic genes. This assumption was supported by the observed distribution of phenotypes.

There were no significant differences in PGM phenotype distribution between sexes or among samples of shrimp taken from Galveston Bay, Texas, and Vermilion and Barataria bays, Louisiana.

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Nous avons décelé, par électrophorèse de gel amidon, huit phénotypes de phosphoglucumutase (PGM) dans des extraits du muscle abdominal de la crevette grise (*Penaeus aztecus*). Nous supposons que les phénotypes observés sont sous le contrôle de cinq gènes allèles. La répartition des phénotypes, telle qu'observée, confirme cette hypothèse.

Il n'y a pas de différences significatives dans la répartition des phénotypes de PGM entre les sexes ou entre les échantillons provenant de la baie Galveston, Texas, et ceux des baies Vermilion et Barataria, Louisiane.

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PHOSPHOGLUCOMUTASE (PGM) is a phosphotransferase that catalyses a reaction converting glucose-1-phosphate to glucose-6-phosphate. Genetic variation of PGM was first reported in man by Spencer et al. (1964). Hopkinson and Harris (1965, 1968) reported

three independent loci in man, each locus having two or more allelic forms.

Genetic variants of PGM also have been described in several teleosts. A two-allele system was reported in rainbow trout (*Salmo gairdneri*) by Roberts et al. (1969). Lush (1969) presented evidence for two PGM loci (one was polymorphic) in Atlantic herring (*Clupea harengus*). A two-allele PGM system was also reported in sockeye salmon (*Oncorhynchus nerka*) by Utter and Hodgins (1970).

The objective of our research was to find genetically controlled biochemical variants that can be

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used to determine whether or not different stocks exist within each of the three most important commercial shrimp species (*Penaeus aztecus*, *P. setiferus*, and *P. duorarum*) in the Gulf of Mexico. This paper describes PGM polymorphism in brown shrimp (*P. aztecus*) and presents data on distribution of phenotypes and frequency of alleles for brown shrimp taken from three locations in the northwestern Gulf of Mexico.

Methods — Juvenile brown shrimp between 60 and 100 mm in total length (tip of rostrum to tip of telson) were collected from three locations: Galveston Bay, Texas; Vermilion Bay, Louisiana; and Barataria Bay, Louisiana (Fig. 1). Two hundred specimens (100 of each sex) from each location were frozen immediately with dry ice for transportation to the laboratory where they were stored at -80°C until analyzed.

Equal parts (about 0.5 cm^3 each) of partially thawed abdominal muscle and phosphate buffered physiological saline (Johnson et al. 1972) were blended to extract PGM from each specimen. A glass rod was used to grind and mix the muscle and saline in a 10- by 75-mm culture tube, and the mixture was centrifuged at $31,000 \times g$ for 10 min at 5°C . Without further treatment, the cleared extract was drawn into a 4- by 6-mm Whatman No. 1 filter paper insert. The insert was blotted lightly, then placed with inserts representing other specimens in starch-gel prepared according to Kristjansson (1963). A buffer system by Ridgway et al. (1970) was used, and horizontal starch-gel electrophoresis and subsequent staining of PGM followed the method described by Johnson et al. (1972).

Results — Zymograms of abdominal muscle extracts exhibited a single region of PGM activity

occupied by five anodal bands labelled a, b, c, d, and e (Fig. 2). These bands are assumed to be under the control of five codominant allelic genes, designated herein as PGM^a through PGM^e . This assumption was supported by observed distributions of one- and two-banded phenotypes (Table 1) which did not differ significantly from expected distributions based upon Hardy-Weinberg equilibrium (Stern 1943). Eight of the 15 possible phenotypes were detected, and their observed distribution in samples from the three bays is shown in Table 1. Our failure to detect the seven remaining phenotypes was not surprising, because PGM alleles a, d, and e were rare (Table 1).

A three-banded pattern (Fig. 2) observed in one female shrimp from Galveston Bay was counted as a bd phenotype. The extra band may have resulted from a nongenetic modification of one of the bands. Such conformational isozymes are common for PGM in vertebrates (Brewer 1970). An alternate explanation for the extra band would be that this particular individual was trisomic for the chromosomes carrying the PGM locus, with each chromosome carrying a different allele. A similar situation for LDH in brook trout (*Salvelinus fontinalis*) was discussed by Davisson et al. (1972).

The distribution of observed phenotypes was not significantly dependent on sex (Table 1); therefore, the samples of males and females from each bay were combined for the comparison among the three bays (Table 1). There was no significant difference in phenotype distribution among the three bays (Table 1). This means that separate stocks of brown shrimp were not detected in these

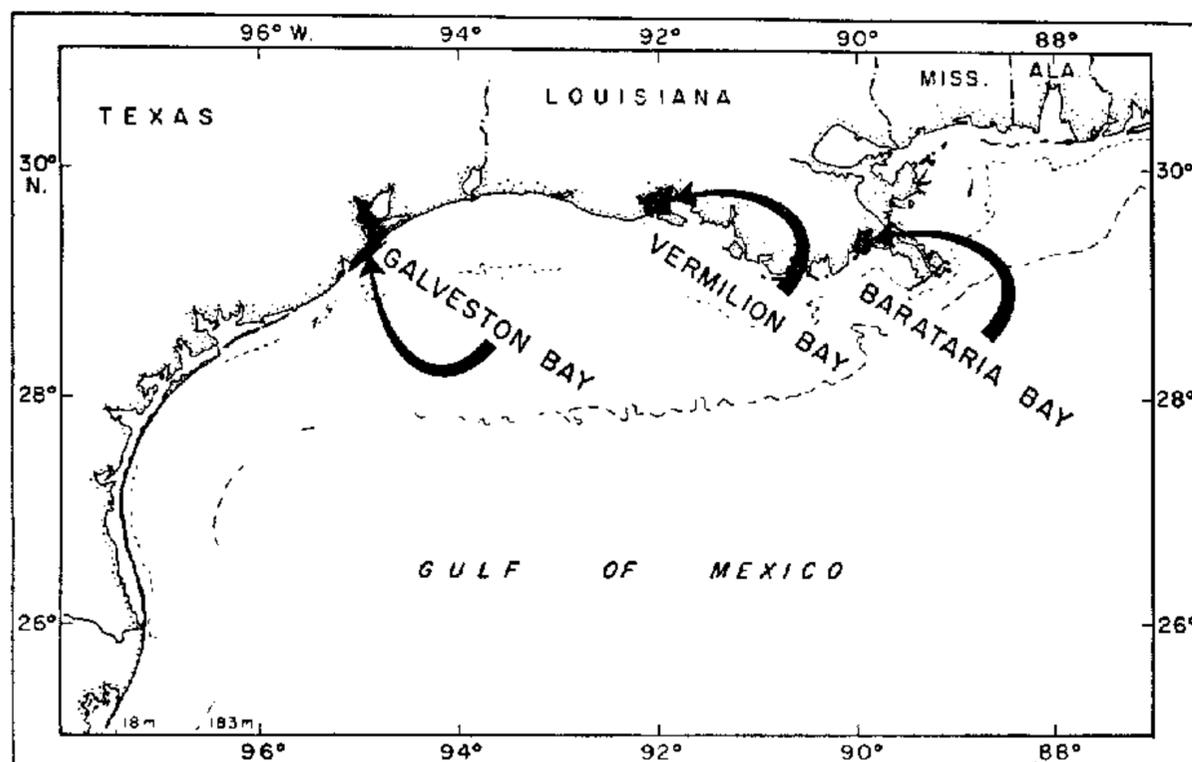


FIG. 1. Bays from which brown shrimp (*Penaeus aztecus*) samples were collected.

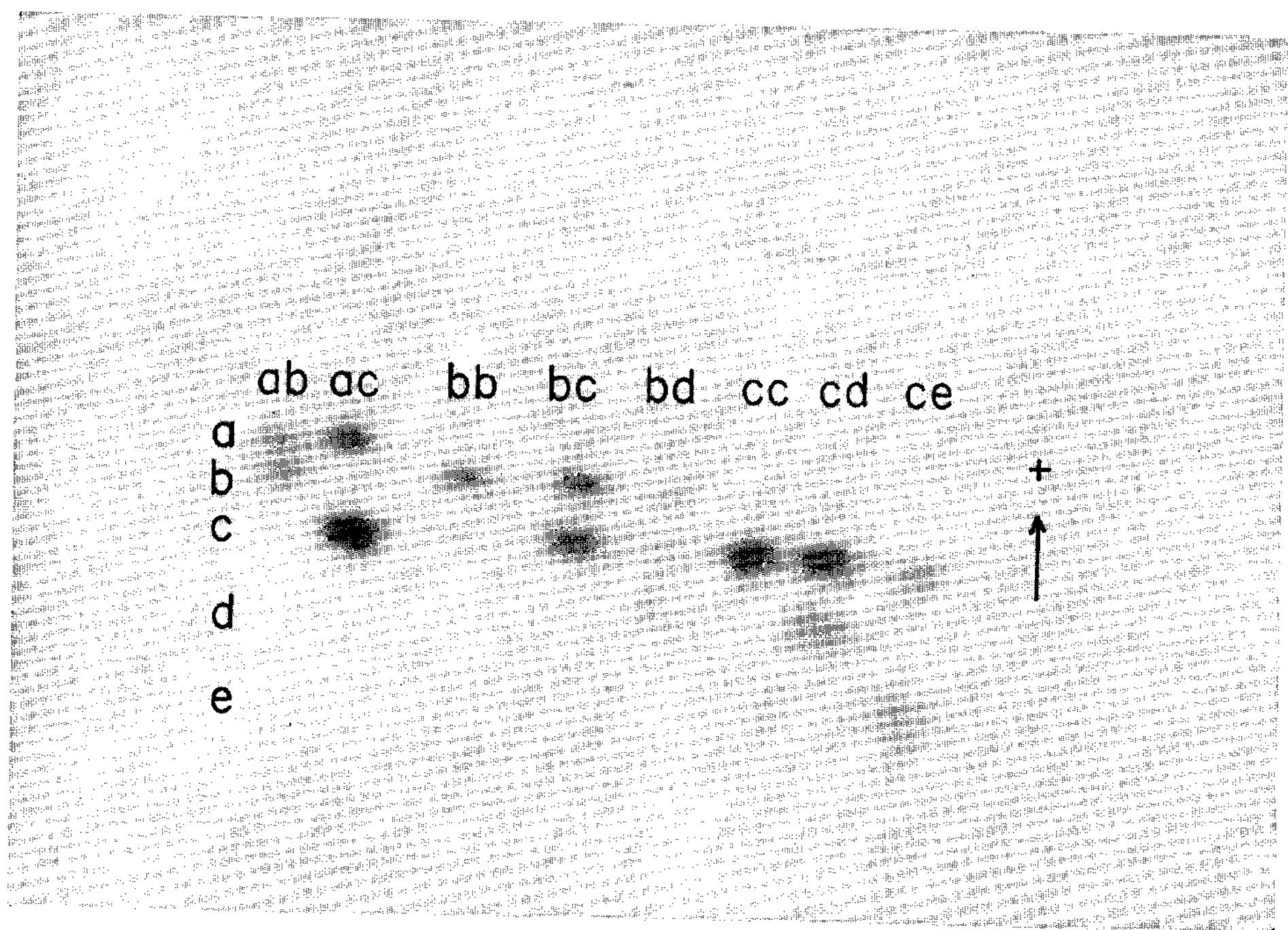


FIG. 2. Bands in starch-gel illustrating five PGM alleles and eight PGM phenotypes detected in brown shrimp. Direction (↑) of protein migration toward the anode (+) is shown.

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TABLE 1. Distribution (number of specimens) of eight PGM phenotypes and frequency of PGM alleles in samples of brown shrimp (*Penaeus aztecus*) from Galveston Bay, Texas, and Vermilion and Barataria bays, Louisiana.

Location	Phenotypes								Alleles				
	ab	ac	bb	bc	bd	cc	cd	ce	a	b	c	d	e
Galveston Bay	1	1	9	74	3	110	2	0	0.0050	0.2400	0.7425	0.0125	0.0000
Barataria Bay	0	1	5	68	2	119	4	1	0.0025	0.2000	0.7800	0.0150	0.0025
Vermilion Bay	0	0	8	69	0	116	6	1	0.0000	0.2125	0.7700	0.0150	0.0025
Comparison of phenotype distributions										df	Chi* square		
Males vs. females (Galveston Bay)										2	4.109		
Males vs. females (Vermilion Bay)										2	0.745		
Males vs. females (Barataria Bay)										2	0.151		
Comparison among the three bays (sexes combined)										4	2.642		

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

three bays. It is possible, however, that sample size was too small to detect a significant difference in phenotype distribution among the three bays, under the assumption that such slight differences were real.

To our knowledge this is the first report of PGM polymorphism in a penaeid shrimp. We believe that the PGM genetic system described herein has considerable potential as a tool in population studies of brown shrimp and other *Penaeus* spp. in the Gulf of Mexico. As no differences in PGM phenotype distribution were detected among samples from Galveston Bay, Vermilion Bay, and Barataria Bay, future comparisons will include samples from areas separated by greater distances and by presumed barriers to shrimp migration (e.g. discharge from the mouth of the Mississippi River).

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