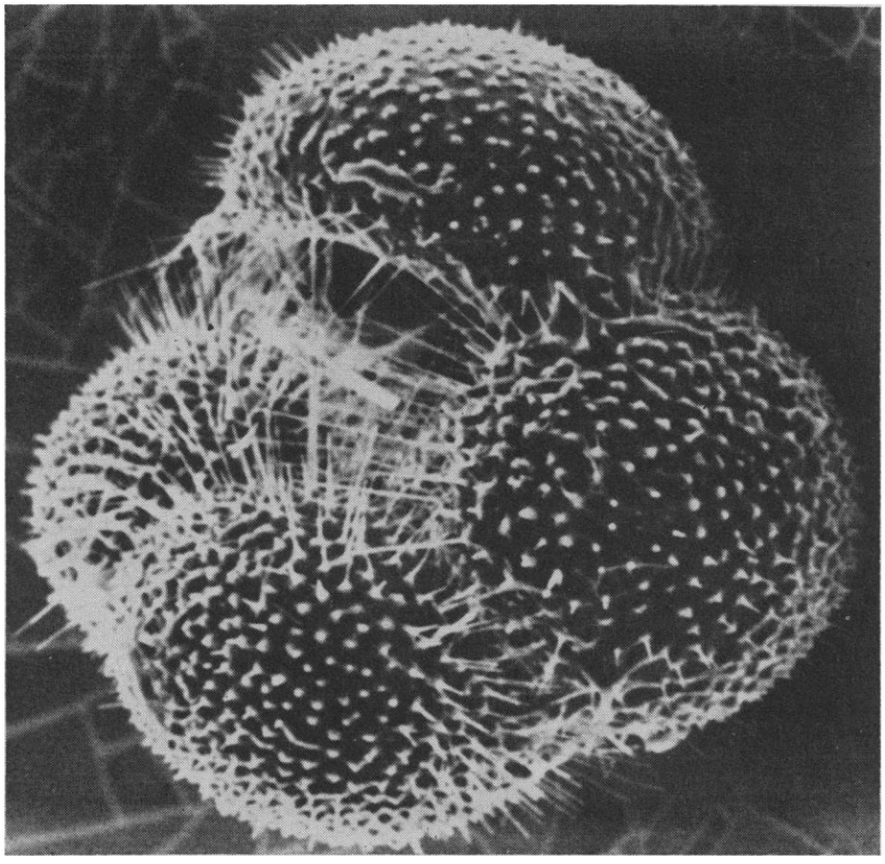

Fig. 2. *Globigerina bulloides* (d'Orbigny); Recent, Scotian Shelf at 50 m. Note narrow elongate spines over entire surface, concentration of spines in apertural region, and absence of any form of bilamellar or secondary thickening (× 400).

The secondary layers can be counted by focusing on individual pores. Both bilamellar and secondary thickening support the hypothesis (*3*) that shell thickening occurs at depth in adult stages of planktonic Foraminifera. Spinal development in *G. bulloides* at depth is contrary to findings of Bé and Hamlin (*4*), who found spines only in juveniles living at or near the surface of the ocean.

I have also investigated differences in microstructure of other foraminiferal species (*5*). *Globoquadrina dehiscens dehiscens* (Chapman, Parr, and Collins) differs radically from *Globigerina* in wall structure as well as in having prominent apertural flaps covering each aperture. *Globigerinoides trilobus trilobus* (Ruess) displays a heavy cancellate pore pattern, characteristic of the *Globigerinoides* group. However, *Globigerinoides trilobus immaturus* LeRoy, considered by many to be a member within the *G. trilobus* (s.l.) evolutionary sequence, has a surface covered with irregularly spaced knobs and small circular pores; this wall structure resembles that of *Globigerina*.

I have mentioned only a few morphologic characteristics. Many detailed features of various microorganisms, hitherto unavailable, are being investigated and will now add greatly to the determination of evolutionary sequences and specific, generic, and familial relations; they will enable more natural classification of these microorganisms. This new insight can be attributed to the scanning electron microscope.

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6. I thank Charles Godden, Marine Geology Division, Bedford Institute of Oceanography, for his active interest and the photographs [taken with the aid of the Jeolco scanning electron microscope; Jeolco (U.S.A.) Inc., 477 Riverside Drive, Medford, Mass.].

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Electrophoretic Variants of α-Glycerophosphate Dehydrogenase in Drosophila melanogaster

Abstract. *Two alleles of* Gdh, *the locus specifying the electrophoretic mobility of α-glycerophosphate dehydrogenase, are found in* Drosophila melanogaster. *The gene is located on the second chromosome at a map position of 17.8. Hybrid enzyme molecules are found in heterozygotes.*

The enzyme α-glycerophosphate dehydrogenase (GDH) catalyzes the oxidation of α-glycerophosphate to dihydroxyacetone phosphate and the reverse reaction. Extraordinarily high activity of this enzyme is found in thoracic muscle of insects (*1*, *2*), where it plays an important role in the rapid production of energy from carbohydrate [see reviews by Sacktor (*3*) and Chefurka (*4*)].

Electrophoretic variants of at least 12 enzymes are known in *Drosophila melanogaster* [see review by Shaw (*5*)]. More than one electrophoretic type of an enzyme is more the rule than the exception in this species. The genetic loci responsible for the variations have in most cases been located on the linkage map of *Drosophila*.

A method for acrylamide gel electrophoresis of α-glycerophosphate dehydrogenase of *Drosophila* has been described by Sims (*6*). Hubby and Throckmorton (*7*) examined GDH electrophoretic patterns of several species of the virilis group of *Drosophila* and found differences between but not

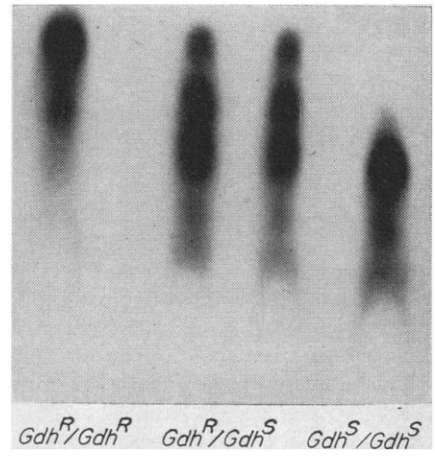

Fig. 1. Acrylamide-gel electrophoresis of α-glycerophosphate dehydrogenases of *Drosophila melanogaster*. On the left is the homozygote of the rapid type of GDH. On the right is the homozygote of the slow type of GDH. In the center are two heterozygotes of the two alleles.

within species. Hubby and Lewontin (*8*) surveyed many strains of *D. pseudoobscura* and found no electrophoretic variants of GDH, although variants of some other enzymes were common.

For this investigation, Sim's (*6*) technique was used with modifications to accommodate flat-bed electrophoresis equipment (EC Apparatus Corp.). Strips of polyacrylamide gel (5 percent acrylamide) were cast according to the method of Raymond and Wang (*9*). Before use, the gels were equilibrated with buffer of 0.025*M* tris brought down to *p*H 6.0 with H_3PO_4. Buffer in electrode vessels was 0.05*M* trisphosphate, *p*H 6.0. Flies were squashed on small squares of filter paper and inserted between cut ends of the gel. The top and bottom of the apparatus were cooled with running tap water. A potential of 24 volt/cm and a current of about 45 ma was applied across the gel for 2 to 4 hours.

The mixture to give color to regions of GDH activity contained 90 ml of tris buffer (0.05*M*, *p*H 8.5), 0.18 g of disodium dihydrogen ethylenediaminetetraacetate, 0.8 g of disodium glycerophosphate pentahydrate (α and β mixture; Calbiochem), 4 ml of nicotinamide-adenine dinucleotide solution (10 mg/ml), 4 ml of phenazine methosulfate solution (0.2 mg/ml), and 20 mg of nitro blue tetrazolium. Gels incubated in this mixture for about 1 hour at 20°C begin to show purple formazan in areas of GDH activity. One fly has sufficient enzyme activity to give dark areas. To insure that minor components were detected, the gels were incubated overnight in this mixture.

It was found that inbred strains of *D. melanogaster* may be divided into two types according to the electrophoretic mobility of their GDH. When the procedures described above are used, it is found that one type contains GDH that migrates more rapidly to the anode than the other. Canton-S, Samarkand, and Oregon-RC are examples of common wild-type strains that contain the more rapidly migrating enzyme. Swedish-c and Oregon-R have the slower migrating enzyme (see Fig. 1). There appears to be a family of enzymes in each inbred. There is a major component and two slower-moving minor components. The whole pattern is displaced when the slower and faster types are compared. Larvae, pupae, and adults have the same patterns. Whether these multiple forms are present in the living animal or are artifacts cannot be determined at this time. Sims (*6*) did not observe this heterogeneity in her experiment; however, Hubby and Lewontin (*8*) observed two areas of GDH activity in all strains of *D. pseudoobscura*.

Crosses between the two different types yield hybrids which have five visible components with GDH activity. There are three major components: the two parental ones and a hybrid with intermediate mobility (Fig. 1). The only minor components that are detectable are those of the slow-type parent. Other minor components in the hybrid are obscured by the three major components. The presence of a hybrid major component indicates that the GDH molecule contains at least two protein subunits. The parental major components contain two subunits that are alike; the hybrid contains two unlike subunits (*10*). Flies trapped from a wild population in Oak Ridge, Tennessee, are polytypic. The rapid, slow, and hybrid patterns of GDH are all found in this one population.

Genetic analysis shows that the differences in electrophoretic mobility of GDH are based on there being two alleles of a genetic locus. This locus (called Glycerophosphate dehydrogenase, symbol *Gdh*) is located on the second chromosome. On the standard linkage map of *D. melanogaster* (*11*) it has a genetic map position of about 17.8. It is between the loci of clot eye color (map position 16.5) and Sternopleural bristles (map position 22.0). Homozygotes of the allele Gdh^R have the rapid pattern. Homozygotes of the allele Gdh^S have the slow pattern of GDH. The hybrid pattern is produced by Gdh^R/Gdh^S heterozygotes.

The approximate cytological position of the *Gdh* locus is known from analysis of *Df(2L)GdhA*. This second chromosome deficiency was selected from x-irradiated chromosomes which lacked the wild-type allele of *cl* (clot eye color). In one case the irradiation induced a deficiency which included both cl^+ and *Gdh*. The electrophoretic pattern of $Df(2L)GdhA/Gdh^S$ is like that of Gdh^S homozygotes, and $Df(2L)GdhA/Gdh^R$ is like Gdh^R homozygotes. In salivary gland chromosomes there are a few bands missing. On Bridges' (*11*) salivary chromosome map the left break of *Df(2L)GdhA* is between 25E1 and 25F1. The right break is between 26B1 and 26C1. The locus of *Gdh* must therefore be between 25E1 and 26C1.

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Detergent-Solubilized RNA Polymerase from Cells Infected with Foot-and-Mouth Disease Virus

Abstract. *The foot-and-mouth disease virus RNA polymerase complex was dissociated from cellular membranes with deoxycholate in the presence of dextran sulfate. The soluble polymerase complex was active in the cell-free synthesis of virus-specific RNA; solubilization of the complex permitted direct analysis of the cell-free reaction mixtures without recourse to RNA extraction. A major RNA-containing component found early during cell-free incubation ranged from approximately 140 to 300*S. *The final major products of the cell-free system were 37*S *virus RNA, 20*S *ribonuclease-resistant RNA, and a 50*S *component containing RNA.*

Detailed studies of replication of animal virus RNA in cell-free systems have been hindered by high levels of nuclease or membrane-bound polymerase complexes, or of both (*1*, *2*). The RNA polymerase induced by the foot-and-mouth disease virus (FMDV) is reportedly bound to cellular mem-