Linear Polymer Solutions Viscosity Effect on Bacterial Swimming Speed: A Mathematical Analysis

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Description

It is known that viscosity sometimes increases the speed at which bacteria swim. Bacterial motion is the only instance of this phenomenon. Turner and Berg (Nature.278:349–351, 1979) suggested that a loose, quasi-rigid network of polymer molecules added to increase viscosity was the cause of the phenomenon. By introducing two apparent viscosities, we mathematically developed their concept and obtained results that are comparable to the previously reported experimental data. The swimming speed increased with viscosity, and the addition of polymer led to an improvement in propulsion efficiency that was greater than the decrease in the flagellar rotation rate. Numerous bacteria swim by rotating their helical cell bodies and/or flagellar filaments. The swimming speed of Leptospira interrogans (helical cell body without any external flagella) monotonically increases with viscosity in medium supplemented with methylcellulose until the viscosity exceeds 300 Numerous researchers have relied on this idea to guide their experimental investigation of bacterial motion [1].

However, they did not mathematically express it, and there has been no quantitative analysis based on the suggestion. With regard to the motion of single-polar-flagellated bacterium like aeruginosa and Vibrio alginolyticus, we interpreted and mathematically developed the suggestion made by Berg and Turner in this study. In addition, we demonstrated that the peculiar phenomenon of bacterial motion in polymer solutions could be quantitatively explained by the equations we obtained. Long linear polymer solutions are highly structured. The solute forms a loose, quasi-rigid network that is simple for microscopic particles to penetrate. The network is able to exert forces that are normal to a portion of a slim body as a result, the motion of microorganisms, as well as cilia and flagella, in solutions containing viscous agents defies conventional hydrodynamic treatments. It is presumed that the motion of a slender body, such as a bacterial flagellar filament, is faster than that of a polymer network because its length is significantly greater than the mesh size. As a result, the network mostly pulls in the normal direction on a part of the slim body. To put it another way, the slim body is surrounded by a virtual tube created by the network; the body moves easily inside the tube but with difficulty outside of it [2,3].

The hydrodynamic force and torque acting on the entire helix can be obtained by integrating the force acting on a small element of the helix; this concept is almost identical to the "reptation model" in polymer physics. The following straightforward idea has frequently been adopted to obtain hydrodynamic force acting on a moving helix: A combination of forces in parallel and perpendicular to the element constitute the force exerted on the element. We assumed that the polymer network does not affect the tangential

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motion of a microscopic slender body but does affect the normal motion in the same way that the motion of a macroscopic body does in order to calculate the bacterial swimming speed in polymer solutions. T equals the viscosity of the solution without the polymer in this extreme approximation, regardless of the concentration of the polymer. Additionally, is the same as the polymer solution's macroscopic viscosity and increases with polymer concentration. The values of the other parameters that were used in the calculation the ratio of swimming speed to flagellar rotation rate (-f ratio) is a measure of how efficiently the bacterial flagellar system propels itself by measuring the distance traveled per flagellar revolution. Despite the fact that the traditional RFT's -f ratio increased with viscosity. This indicates that the addition of polymers increased swimming speed with viscosity and compensated for a decrease in flagellar rotation rate [4,5].

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Conflict of Interest

None.

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