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CHAPTER 21 : *VIBRIO SPLENDIDUS*

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Abstract:

Bacterial pathogenicity is known to be associated with structural components of the cells or active secretions of substances that either damage host tissues or protect the bacteria against host defenses. Recently, pathologists have begun to describe genes in order to

understand the regulation of virulence factors. Nevertheless, little is known about marine bacterial pathogens, and until now there has not been any information concerning the *Vibrio splendidus* group. *V. splendidus* was defined initially as a luminous marine species with two biotypes distinguishable by phenotypic features. Genotyping by ribotyping, amplified fragment length polymorphism (AFLP), or PCR-restriction fragment length polymorphism has revealed a remarkably high genetic diversity within this group and suggested its polyphyletic nature. A new concept, the ecotype, has been proposed. This theory is based on the principle of multilocus sequence typing (MLST)-based population genetics. Most *V. splendidus*-related strains isolated from diseased marine animals and suspected to be the etiological agent of disease have been identified by means of classical phenotypic schemes. The antigenic characteristics of *V. splendidus*-related strains isolated from diseased turbot or cod have been reported, with authors observing that lipopolysaccharide (LPS) and outer membrane protein profiles were correlated with the origin of strain and the virulence in experimental challenge. Bacterial pathogenicity is associated with structural components of the cells or active secretions of substances that either damage host tissues or protect the bacteria against host defenses.

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KEY CONCEPT RANKING

Outer Membrane Proteins



Multilocus Sequence Typing

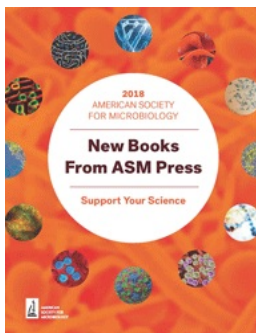


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Type II Topoisomerase






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