

Primary structure of a soluble matrix protein of scallop shell: Implications for calcium carbonate biomineralization

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ABSTRACT

Soluble proteins in the scallop (*Patinopecten yessoensis*) foliated calcite shell layer were characterized using biochemical and molecular biological techniques. SDS PAGE of these molecules revealed three major protein bands, 97 kD, 72 kD, and 49 kD in molecular weight, when stained with Coomassie Brilliant Blue. Periodic Acid Schiff staining and Stains-All staining indicated that these proteins are slightly glycosylated and may have cation-binding potential. N-terminal sequencing of the three proteins revealed that all three share the same amino acid sequence at least for the first 20 residues. A partial amino acid sequence of 436 amino acids of one of these proteins (MSP-1) was deduced by characterization of the complementary DNA encoding the protein. The deduced sequence is composed of a high proportion of Ser (31%), Gly (25%), and Asp (20%), typifying an acidic glycoprotein of mineralized tissues. The protein has a basic domain near the N-terminus and two highly conserved Asp-rich domains interspersed in three Ser and Gly-rich regions. In contrast with prevalent expectations, (Asp-Gly)_n-, (Asp-Ser)_n-, and (Asp-Gly-X-Gly-X-Gly)_n-type sequence motifs do not exist in the Asp-rich domains, demanding revision of previous theories of protein-mineral interactions.