

# **Supporting Data: Stiff Coatings on Compliant Biofibers: The Cuticle of *Mytilus californianus* Byssal Threads<sup>†‡</sup>**

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## Four Items

Figure S1. Isolation and purification of mcfp-1.

Figure S2. Chromatography of the pooled fractions (36-41min) from gel filtration chromatography by C8 HPLC.

Figure S3. MALDI TOF mass spectrometry of mgfp-1.

Figure S4. cDNA-deduced protein sequence of *Mytilus californianus* foot protein 1 variant 2

Figure S1. Isolation and purification of mcfp-1. A. Acid-Urea polyacrylamide gel electrophoresis of key steps in purification of mcfp-1. Lanes 1 and 2 were loaded with 20 µl, and 40 µl crude PCA extract of mcfp-1, respectively, and stained with Coomassie Blue R-250. Lanes 3 and 4 were loaded with 20 µl, and 40 µl crude extract of mcfp-1, respectively, and stained for Dopa with NBT in 2 M glycinate. Lane 5 through 10, which correspond to fractions under the bracketed peak (36-41 min), were loaded with 10 ul of mcfp-1 purified by chromatography with Shodex KW-803 column and stained with Coomassie Blue R-250. B. Gel filtration chromatography of mcfp-1 crude extract with Shodex KW-803. Bracketed peak contains pure mcfp-1.

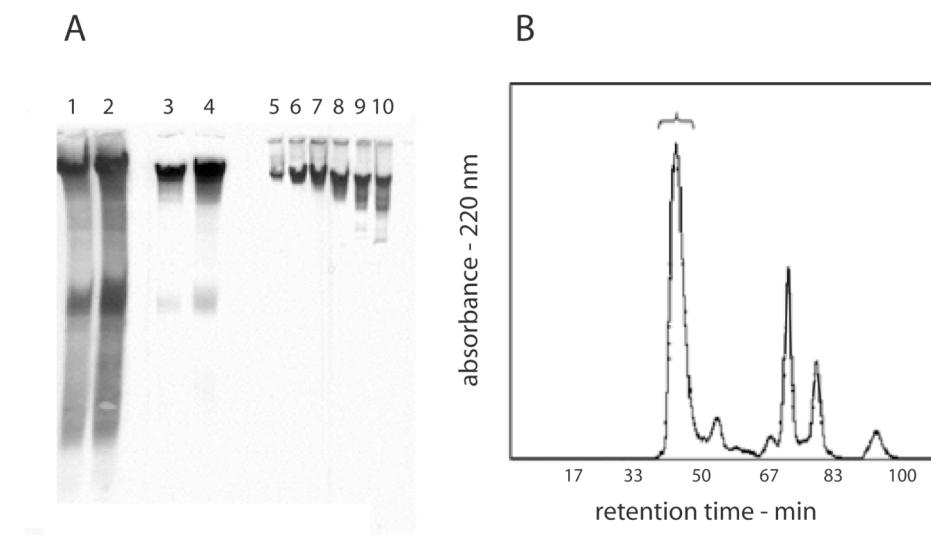


Figure S2. Chromatography of the pooled fractions (36-41min) from gel filtration chromatography by C8 HPLC. Bracketed peak contains more pure mgfp-1 preparations. Inset is fractions under peak subjected to acid-urea gel electrophoresis and stained with Coomasie Blue R-250.

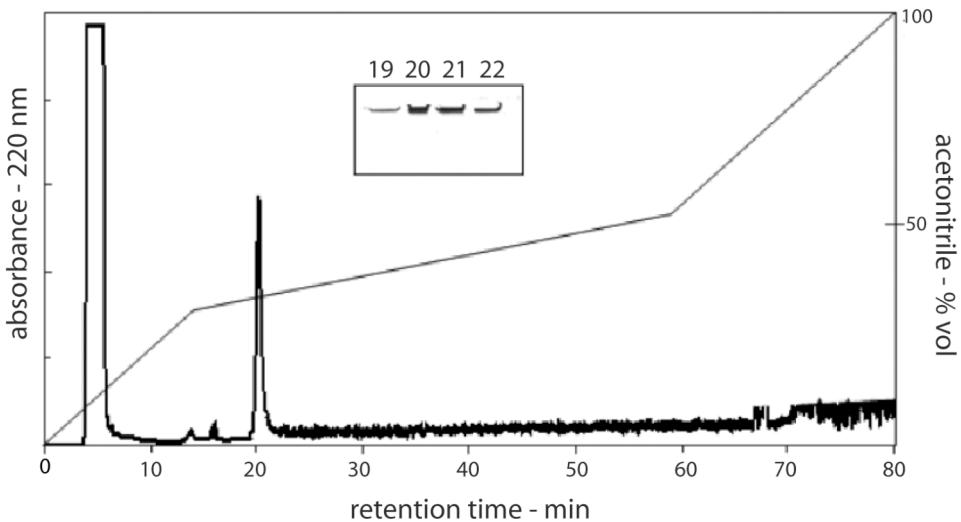


Figure S3. MALDI TOF mass spectrometry of mgfp-1. Protein was purified as described by Sun and Waite (2005). Operating parameters were delayed extraction (200 ns) in positive ion mode with accelerating voltage of 25000V, grid voltage at 93%, and guide wire voltage at 0.1%. Spectrum represents average of 254 scans with laser at 75% full strength.

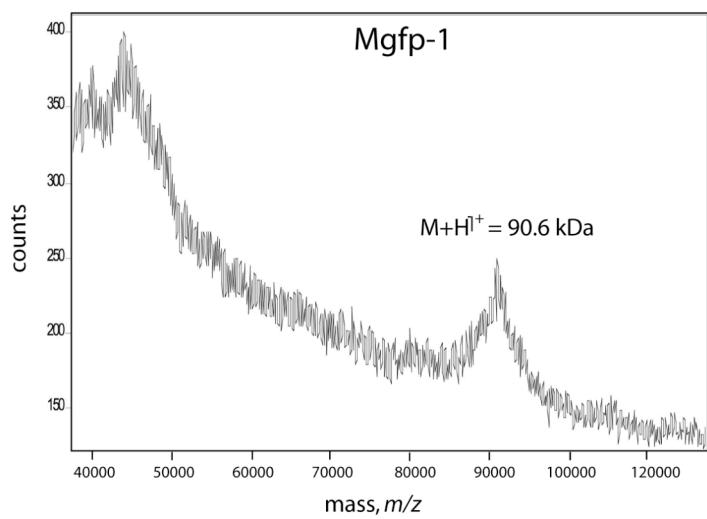


Figure S4. cDNA-deduced protein sequence of *Mytilus californianus* foot protein 1 variant 2 - (mcfp1) (GenBank AY960602 and Swiss Prot Q2TCK9). Variant 2 is 7 decapeptide repeats shorter than variant 1. The location of sequence is between the two residues denoted by a box. Signal peptide is italicized.

*MEGIKLNLCLLCIFSCDVFALSNGFIHNAYGSAYAGASAGAYKPLPGSYGSKHVPVYKPMNKIPT*  
SYISKKSYPAPYKPKGYHPTNSYQPTYG

SKTNYPPIYK PVAKKLSSYK AIKTTYLVYK AKTSYPPVYK HKITNPPTYK PKITYPPTYK  
PKPSYPPTYK PKPSYPPTYK AKKTYPPTYK PKPSYPPTYK PKITYPPTYK PKPSYPPSYK  
AKKSYPSTYK **PKPSYPPTYK** PKITYPPTYK PKPSYPPTYK AKKTYPPTYK PKITYPPTYK  
PKPSYPTSYK SKKTYPPTYK PKITYPPTYK PKPSYPPSYK PKITYPPTYK PKKSYPPAYK  
SKASYPPSYQ PKKTYLPSYK PKKTYPPTYK RKISYPPTYK TKPSYPSSYK RKTSYPPSTYK  
RKTSYPPPTYK PKISYPSTYK TKPSYPPTYK AKKTYPPTYK PKITYPPTYK PKPSYPTSYK  
SKKTYPPTYK PKITYPPTYK PKPSYPPSYK PKITYPPTYK PKKSYPPAYK SKASYPPSYQ  
PKKTYLPSYK PKKTYPPTYK RKISYPPTYK TKPSYPASYK RKTSYPPSTYK RKTSYPPPTYK  
PKISYPSTYK TKPSYPPTYK PKPSYASSYK PKIRYPPTYK PKPSYASSYK PKITYPPTYK  
PKISYPPTYK PKITYPPSYK PKISYLPAYK PKISYPSQY

Sun, C. J., and Waite, J. H. (2005) Mapping chemical gradients within and along a fibrous structural tissue: Mussel byssal threads, *J. Biol. Chem.* 280, 39332-39336.