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- Polyadenylated [poly(A)⁺] RNA was purified from the kidney of the VDR^{-/-} mice at 7 weeks (26). The total cDNA was prepared with poly(A)+ RNA (27). The cDNA fragments were subsequently inserted into the Hind III site of the mammalian expression vector pcDNA3 (Invitrogen). The reporter plasmid 17M2-G-lacZ was constructed by inserting yeast GAL4 upstream activating sequence x2 and β-globin promoter into a multicloning site of the Basic expression vector (Clontech). The ligand-binding domain of VDR [VDR(DEF)] fused to the GAL4 DNA-binding domain [GAL4-VDR(DEF)] (11) was used to detect ligand-induced AF-2 function. COS-1 cells cultured with Dulbecco's modified Eagle's medium containing 10% fetal bovine serum were transiently transfected with 0.5 µg of GAL4-VDR(DEF) expression vector, 1 µg of 17M2-GlacZ, 0.2 µg each of the ADX and ADR expression vectors (12), and 0.1 µg of expression cDNA library in OPTI-MEM using lipofection agent (GIBCO BRL).
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Extensible Collagen in Mussel Byssus: A Natural Block Copolymer

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To adhere to solid surfaces, marine mussels produce byssal threads, each of which is a stiff tether at one end and a shock absorber with 160 percent extensibility at the other end. The elastic extensibility of proximal byssus is extraordinary given its construction of collagen and the limited extension (less than 10 percent) of most collagenous materials. From the complementary DNA, we deduced that the primary structure of a collagenous protein (preCol-P) predominating in the extensible proximal portion of the threads encodes an unprecedented natural block copolymer with three major domain types: a central collagen domain, flanking elastic domains, and histidine-rich terminal domains. The elastic domains have sequence motifs that strongly resemble those of elastin and the amorphous glycine-rich regions of spider silk fibroins. Byssal thread extensibility may be imparted by the elastic domains of preCol-P.

Mussel byssal threads are undoubtedly among nature's most peculiar tendons. One end of each thread inserts into the byssal retractor muscles at the base of the foot; the other end is disposed outside the animal and attached to a hard surface by an adhesive plaque. In a process that resembles injection molding, the foot of the mussel is able to make a new thread in 5 min or less (1). Despite their rapid production and vulnerable location, byssal threads are durable and exquisitely engineered fibers (Fig. 1A). They contain a graded distribution of tensile molecular elements that result in a material that is strong and stiff at one end and pliably elastic at the other (2, 3). Overall, byssal threads are five times tougher than Achilles tendon (4).

The collagen content of mussel byssal threads has been well established by wideangle fiber x-ray diffraction, the presence of trans-4-hydroxyproline, and byssus-derived pepsin-resistant peptides with Gly-X-Y repeats (5, 6). Unlike tendon, however, byssus has a nonperiodic microstructure and shrinkage and melting temperatures in excess of 90°C (5). Any attempt to reconcile these unusual biochemical and mechanical features with what is known about collagen provokes the following molecular questions: How is byssal collagen different from tendon collagen, and what role does this difference play in the material performance of byssus?

Because of its highly cross-linked structure, there has been only one recourse for recovering collagen from byssus: acid extraction coupled with extensive treatment with pepsin. We (6) used this approach to characterize two collagen fragments, Col-P and Col-D (both apparently homotrimers), with apparent α -chain masses of 50 and 60 kD, respectively (7). These fragments coexist in complementary gradients along the length of each byssal thread with Col-D predominating at the distal end and Col-P predominating at the proximal end. Similar gradients were found to exist in the mussel foot, which fabricates the byssus one thread at a time. Precursors to Col-P and Col-D (preCol-P and -D) were identified in foot extracts with specific polyclonal antibodies. Apparent masses of 95 and 97 kD were determined for α -chain preCol-P and preCol-D (a-preCol-P and α -preCol-D), respectively. The amino acid compositions for the NH2- and COOH-terminal extensions consist of Gly plus Ala concentrations of 50 (preCol-P) and 60 (preCol-D) mole percent (mol%) (6). Although it was inferred that the extensions or flanking domains might resemble structural proteins such as silk fibroin or elastin or resilin, confirmation of such homology has awaited determination of the complete primary structure. Here we report the primary structure of α -pre-Col-P, a natural block copolymer with putative cross-linking, elastic, and collagen domains (8).

 α -PreCol-P may be divided into seven domains based on its amino acid sequence (Fig. 2). The most prominent feature is a central region consisting of a 435-residue collagenous sequence identified by alignment with amino acid sequences reported previously for peptides derived from the pepsin-resistant fragment Col-P (6). The collagen domain consists of 146 Gly-X-Y repeats in which X and Y are frequently Pro. Only the Pro residues at position Y appear to be converted to *trans*-4-hydroxyproline (6). Gly also occurs in the X (10 times) and Y (once) positions. The continuity of Gly-X-Y repeats is interrupt-

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byssus subdivided into four morphologically distinct regions: adhesive plague, stiff distal thread, elastic proximal thread, and stem. For clarity, all but one thread were cut from the stem. Insertion denotes point of attachment to mussel. Typically, threads are 2 to 4 cm long with diameters of 0.10 to 0.15 mm. (B) Model of the block-like structure of domains in a homotrimer of α -preCol-P from the proximal portion of a byssal thread. Mass estimates of domains are based on the molecular sequence indicated in Fig. 2 and analyses of pre-Col-P by matrix-assisted laser desorption-ionization mass spectrometry (17).

ed after the eleventh repeat (Gly-Ser-Thr) by a single missing Gly. The effect of this on the triple-helical structure of collagen is unclear at this time; however, it is noteworthy that this region is not susceptible to cleavage after extensive treatment of the native homotrimer with pepsin (6). It is tempting to suppose that omission of one Gly in each α chain induces a kink or bend in the triple helix. However, the best studied kinked collagen, complement Clq, is a heterotrimer in which one chain has no triplet discontinuity, another has an Ala for Gly substitution, and the third is missing Gly-X of the triplet (9). The collagen domain of α -preCol-P is followed by an acidic patch about 15 residues long that is enriched in Glu and Asp.

The elastic domains flank the collagen domain on both sides (Fig. 2) and exhibit sequence and solubility similarities with elastin (10). Both are dominated by Gly, Pro, and bulky hydrophobic residues and have Pro-containing pentapeptide repeats (that is, $X^1-X^2-X^3-Pro^4-X^5$). The Pro is not hydroxylated (6). In the elastic domains of preCol-P, X is usually Gly but can be Phe (nine cases), Ala (four cases), Ile (two cases), or Val (two cases) (Fig. 3). These resemble the pentapeptide repeats of elastin, the most common of which is Val-Gly-Val-Pro-Gly (11). Gly, Pro, and the hydrophobic residues of elastin are critical to the elastic recoil, which is entropically driven (12). The entropy is derived from dynamic hydrophobic interac-



Reports Fig. 2. Predicted amino acid sequence (34) of α -preCol-P. Full sequence from cDNA is arranged to exhibit the block copolymer structure of preCol-P and to align the characteristic repeat motifs of each domain. Thus, elastin-like pentapeptides (boldface) are aligned at P to distinguish them from intervening GGX clusters and Alarich runs (double underline), and collagen is arrayed as a series of tripeptides. The nucleotide sequence has been deposited in the GenBank database (accession number AF015539). Lowercase, signal peptide; bold italics, histidines in His domain; •, missing G; single underline, acidic patch; and dashed

underline, partial peptide se-

auences from (6).

HAHAFGGLGGGSASAGSHSSSSSHSFGGHVFHSVTHHGPSHVSSGGHGGBGGGPYKPGY 902 His

tions or "librations," which are maximized in unstretched protein and accommodated by the flexible structure imposed by Gly and Pro. Similar librations are predicted for the elastic domains of preCol-P. All in all, there are 6 pentapeptide repeats in the NH₂-terminal side and 12 in the COOHterminal side of the flanking elastic domains. Both elastin and preCol-P also have poly(Gly) clusters peppered with hydrophobic residues (Leu, Ile, Val, and Phe) and Ala-rich regions (Figs. 2 and 3). Many of these features are evident in lamprin (13) and spider silk fibroins (14) as well. The Ala-rich regions of α -preCol-P are more substituted than the poly(Ala) tracts of elastin, in which substitutions are limited to Lys, and spider silk fibroins,

F

F

E

which lack substitutions except for occasional Ser residues (Fig. 3). Curiously, in spider silk fibroins, poly(Ala) runs evidently form nanocrystalline β sheets (15), whereas in elastin they form α helices (16)

His-rich regions are located at the NH₂- and COOH-termini. The only Tyr and noncollagenous Lys residues of pre-Col-P are also found there. The presence of trace 3,4-dihydroxyphenyl-L-alanine (dopa) in hydrolyzed preCol-P suggests that, as in other byssal precursors, Tyr may be posttranslationally hydroxylated to dopa in the mature protein (17). The Hisrich domains comprise about 80 and 50 residues at the NH₂- and COOH-termini, respectively. At both ends, His represents

Fig. 3. Sequence alignment of repeated motifs in the elastic flanking domains of α -preCol-P with consensus repeats of the known extensible proteins bovine elastin (10) and spider dragline protein ADF-3 (12). X denotes hydrophobic residues such as F, V, L, I, and A; Z denotes polar residues such as

Protein	Pro repeat	GGX clusters	Poly(Ala) runs
reCol-P:	GXGPG(6) GGGPG(5) XGGPG(4) GGXPG(2)	GSVGGGIGGIGGIG(2)	ASAZAAAZAN (3)
lastin:	XGXPG(17) GXXPG(8) GGXPG(4) GXGPG(3)	G-VGG-IGGVGGLG(5)	AAAKAAAKAA (10)
ragline silk:	GYGPG(12) QQGPG(26)		ASA-AAA-AA (12)

S, N, and R. Number of repeats in each protein is indicated in parentheses after the sequence. Shaded areas represent conserved sequences.

20 mol% of the composition or one in five residues. Other prominent residues are Gly, Ala, and Ser (Fig. 2). His-rich domains occur in several other proteins including high molecular weight kininogen (18), plasmodial His-rich protein HRP (19), blood Hisrich glycoprotein HRG (20), and trematode eggshell precursors (21). Sequence homology is limited to short repeats-for example, Ala-His compared with Ala-His-His repeats in plasmodial His-rich protein, and His-Gly-Gly or Gly-Gly-His compared with Gly-His repeats in the kininogen and eggshell precursors. The function of the His-rich tracts in almost all known cases is connected with metal binding such as zinc in kininogen and HRG and heme iron in HRP. His-rich nereid jaws are high in complexed copper or zinc (22), and poly(His) tracts are routinely added to recombinant proteins for facile recovery by metalloprecipitation or metalloligand affinity chromatography (23). Of the transition metals detected in Mytilus edulis byssus, zinc levels are consistently the highest at about 1 mg per gram of dry weight (24). Studies are under way to determine whether the recovery of initial stiffness in distal byssal threads after yield to 0.5 extension (25) is related to the breakage and re-formation of protein-zinc complexes.

The results reported here are unusual in several respects. PreCol-P is the first known protein to contain both collagenous and elastin-like domains. Indeed, elastins were thought to be absent in invertebrates (26). In addition, the tandem array of collagenous and elastic domains is remarkably reminiscent of synthetic block copolymer designs with their hard and soft segments (27) (Fig. 1B). In this case, "blocks" of elastin (breaking strain, ≤ 1.6 ; tensile stress, $\leq 5 \times 10^{6}$ Pa) would improve the extensibility of the collagen (breaking strain, ≤ 0.1 ; tensile stress, $\leq 1 \times 10^8$ Pa) (28). This results in a material with breaking strength lower than that of tendon but with significantly greater toughness (3, 4). Block copolymer design has also been detected in another byssal precursor, preCol-D, which has silk fibroin-like instead of elastic flanking domains in a sequence that is otherwise homologous with that of preCol-P (29). Future studies would profit from a closer scrutiny of the mechanism of preCol fibrillogenesis as well as the interplay of hard

(collagen) and soft (elastin) segments in determining the peculiar mechanical properties of byssal threads.

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- We constructed a cDNA library in a λ ZAP expression vector (Stratagene) from mRNA extracted from foot tissue of Mytilus edulis. We initially screened the library with polyclonal antibodies specific to preCol-P (6, 30). We subcloned positive clones by in vivo excision into pBK-CMV phagemids for sequencing and made nested deletions with the double-stranded nested deletion kit (Pharmacia) of one clone to facilitate sequencing. We sequenced plasmids with the Taq DyeDeoxy terminator cycle sequencing kit (Applied Biosystems) and analyzed sequencing reactions on a model 373A sequencer (Applied Biosystems). Overlapping sequences in both directions were aligned by the computer program CAP (contig assembly program) (31). To obtain the 5' end of the sequence for the largest partial preCol-P cDNA, we prepared a digoxigeninlabeled RNA probe by in vitro translation with a MAXIScript in vitro RNA transcription kit (Ambion). The cDNA library was plated and overlaid with nitrocellulose membranes (Nitropure, Micron Separations). We incubated the membranes overnight at 50°C with a 1:10⁴ dilution of the RNA probe. The location of the probe on the membrane was detected with alkaline phosphatase-conjugated antidigoxigenin (DIG) (Boehringer Mannheim, Indianapolis, IN) and visualized with nitroblue tetrazolium and 5-bromo-4-chloro-3-indolylphosphate toluidinium (NBT/BCIP). The full-length sequence for α-preCol-P is 2800 bases with an open reading frame of 2706 bases and a translated amino acid sequence of 902 residues. We verified the size of the cDNA transcript by Northern blot analysis. The absence of preCol-P mRNA in non-foot tissue confirmed its tissue-specific expression in adult mussels. Double-stranded DNA probes for Northern blots were synthesized by incorporation of DIG-11deoxyuridine triphosphate into products during polymerase chain reaction (PCR) amplification (32). We synthesized a probe specific for preCol-P by PCR amplification of deletion plasmid P14-7aF and with T3 and T7 primers. This deletion plasmid includes the last 900 bases of the sequence for pre-Col-P. We synthesized a second probe for actin in the same manner from a cloned actin cDNA from the sea scallop Placopecten magellanicus (a generous gift from M. Patwary, National Research Council of Canada). Probes constructed from the actin clone of this sea scallop have been shown to

cross-react with actin RNAs from other bivalve species, including *M. edulis* (*33*). We fractionated mRNA from foot and non-foot tissue on a 0.44 M formaldehyde gel in duplicate and transferred them to positively charged nylon membranes (Boehringer Mannheim) by standard techniques. We incubated the blots overnight at 42°C in separate chambers: one with the preCol-P probe and the other with the actin probe. The probe–mRNA hybrid on the membranes was localized by incubation with alkaline phosphatase–conjugated anti-DIG and visualized with NBT/BCIP.

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