Title
Broadly conserved roles of TMEM131 family proteins in intracellular collagen assembly and secretory cargo trafficking.

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Collagen is the most abundant protein in animals. Its dysregulation contributes to aging and many human disorders, including pathological tissue fibrosis in major organs. How premature collagen proteins in the endoplasmic reticulum (ER) assemble and route for secretion remains molecularly undefined. From an RNA interference screen, we identified an uncharacterized *Caenorhabditis elegans* gene *tmem-131*, deficiency of which impairs collagen production and activates ER stress response. We find that amino termini of human TMEM131 contain bacterial PapD chaperone–like domains, which recruit premature collagen monomers for proper assembly and secretion. Carboxy terminal of TMEM131 interact with TRAPPC8, a component of the TRAPP tethering complex, to drive collagen cargo trafficking from ER to the Golgi. We provide evidence that previously undescribed roles of TMEM131 in collagen recruitment and secretion are evolutionarily conserved in *C. elegans*, *Drosophila*, and humans.

INTRODUCTION

Collagen is the major extracellular component of connective tissues and is the most abundant protein in animals (1–3). The production of mature collagen is a multistep process, involving collagen gene regulation, protein biosynthesis, posttranslational modifications in the endoplasmic reticulum (ER), formation of secretion-competent trimers, extracellular C-propeptide cleavage, and cross-linking among trimers (1–3). Dysregulation of collagen production or deposition contributes to a wide variety of human disorders, including diabetes, aging, and pathological tissue fibrosis in major organs such as kidneys, liver, lungs, and heart (4–9). The type I collagen is the most abundant fibril-type collagen; its trimer comprises two α1 (I) procollagen chains and one α2 (I) procollagen chain, encoded by the genes COL1A1 and COL1A2, respectively. Both COL1A1 and COL1A2 contain C-terminal domains (C-propeptide) responsible for initial chain trimerization in the ER. The trimerization occurs via a zipper-like mechanism, initiating from the C-propeptide domain of α1/2 (I) in close proximity to ER membranes (10–13). Although the enzymes responsible for type I collagen modification, extracellular cleavage, and cross-linking have been well described (1, 14), how procollagen monomers are recruited to assemble into secretion-competent multimers in the ER remains poorly understood.

COPII-coated vesicles mediate ER-to-Golgi anterograde transport of secretion-competent cargos, including those containing collagens (15, 16). Tethering COPII vesicles from ER to Golgi membranes requires TRAPP (transport protein particle), a multisubunit protein complex highly conserved in eukaryotes (17–19). TRAPPC8 (trafficking protein particle complex 8) is a key component of TRAPP III, a subtype of TRAPP that acts as a guanine nucleotide exchange factor (GEF) to activate Rab GTPase (guanosine triphosphatase) to promote ER-to-Golgi cargo trafficking. Most COPIII vesicles are approximately 60 to 80 nm in diameter, insufficient to accommodate 300- to 400-nm procollagen fibers (15). Collagen maturation and secretion in large-cargo COPII require HSP47, a procollagen chaperone in the ER, and TANGO1, an ER transmembrane protein that facilitates the export of specialized bulky cargo with collagen (20–22). HSP47 and TANGO1 orthologs are not apparently present in collagen-producing *Caenorhabditis elegans* (23–25), raising the question whether more broadly conserved mechanisms exist to facilitate procollagen assembly into export-competent collagen trimers en route for secretion.

In this study, we identify a previously uncharacterized *C. elegans* gene *tmem-131* that defines an evolutionarily conserved protein family important for procollagen recruitment and secretion. The exoskeleton cuticle of *C. elegans* is a complex collagen matrix that contains many distinct mature collagen proteins, including COL-19, an adult-specific, epithelial synthesized collagen (26). From yeast-two-hybrid (Y2H) screens, we identified two human proteins, COL1A2 and TRAPPC8, that bind to the N- and C-terminal domains of human TMEM131, respectively, and show that COL-19 secretion requires TMEM131 and TRPP-8, the *C. elegans* ortholog of TRAPPC8. We show that TMEM131 proteins are also essential for collagen secretion in *Drosophila* and human cells, supporting the evolutionarily conserved role of TMEM131 protein family in collagen production.

RESULTS

**Genome-wide RNAi screen identifies tmem-131 regulating ER stress response and collagen production in C. elegans**

We performed a genome-wide RNA interference (RNAi) screen for genes that affect levels of the *C. elegans* transgenic reporter *asp-17p::GFP* (Fig. 1A). *asp-17* is a gene encoding an aspartyl protease–like protein that is up-regulated by temperature stress and down-regulated by ER stress (Fig. 1, A to C) (27). From a screen of over 19,100 genes, we identified 574 RNAi clones that either up- or down-regulated the abundance of *asp-17p::GFP* (table S1). In this work, we...
focus on the gene \textit{tmem-131}, as it is uncharacterized but otherwise highly evolutionarily conserved in all animals (see below). \textit{RNAi} against \textit{tmem-131} caused a fully penetrant and strong suppression of \textit{asp-17p::GFP} reporter expression (Fig. 1B). By contrast, \textit{RNAi} against \textit{tmem-131} caused marked up-regulation of \textit{hsp-4p::GFP} (Fig. 1C), an established transcriptional reporter for ER stress and unfolded protein response (UPR) in \textit{C. elegans} (28–30). The screen also identified many other genes, including \textit{ostb-1} and \textit{dlst-1}, that are involved in protein modification and homeostasis in the ER (Fig. 1C). \textit{RNAi} against \textit{ostb-1} or \textit{dlst-1}, as \textit{tmem-131}, also caused marked up-regulation of \textit{hsp-4p::GFP} and down-regulation of \textit{asp-17p::GFP} (Fig. 1C).

To verify the \textit{RNAi} phenotype, we examined \textit{C. elegans} mutants carrying a 323–base pair (bp) genetic deletion allele \textit{tm6119}, which caused a protein-coding frameshift and severe reduction of \textit{hsp-4p::GFP} that can be rescued by transgenic expression of green fluorescent protein (GFP)–tagged wild-type \textit{tmem-131} (Fig. 1F). In addition, high \textit{hsp-4p::GFP} levels in \textit{tm6119} mutants or \textit{tmem-131} \textit{RNAi}–treated animals were completely suppressed by loss of function (LOF) of \textit{xbp-1} (Fig. 1, G to I), a transcription factor that drives a major branch of UPR in \textit{C. elegans} (29–32). Loss of IRE-1, an ER transmembrane protein that senses ER stress, also prevented \textit{hsp-4p::GFP} up-regulation in \textit{tm6119} mutants (Fig. 1I). Besides constitutively activated \textit{hsp-4p::GFP} expression, we found that \textit{TMEM131}–deficient animals by \textit{RNAi} or \textit{tm6119} were smaller in size at higher temperature, more sensitive to the ER stressor tunicamycin as well as cuticle-disrupting osmotic stresses, and developed more slowly compared with wild type (Fig. S1). Nonetheless, unlike \textit{hsp-4p::GFP}, these additional phenotypes were not suppressed by loss of \textit{xbp-1} or \textit{ire-1} (Fig. S1G). Together, these results indicate that loss of \textit{tmem-131} causes various organismic phenotypes and defective ER homeostasis, leading to IRE-1– and XBP-1–dependent activation of \textit{hsp-4p::GFP} and UPR.

To investigate the mechanism by which \textit{TMEM-131} may regulate ER function and proteostasis, we first examined its expression pattern and subcellular localization. The promoter of \textit{tmem-131} drives expression of GFP in a variety of \textit{C. elegans} tissues, most prominently the intestine and hypoderm (Fig. 2A). A translational reporter with GFP fused to the \textit{C}terminus of \textit{TMEM-131} driven by the endogenous \textit{tmem-131} promoter reveals an intracellular perinuclear reticulum pattern (Fig. 2B). The translational reporter rescued the \textit{tm6119} mutant phenotype, indicating that the reticulum-localizing \textit{TMEM-131} is functional (Fig. 1F). In addition, SignalP-4.1 predicts an ER signal
peptide sequence (amino acids 1 to 30) of TMEM-131, supporting its ER endosomal localization (33). To confirm the prediction, we generated an mCherry-tagged ER reporter driven by the tmem-131 promoter, with ER signal peptide at the N terminus and KDEL ER retention sequence at the C terminus. We found that TMEM131::GFP colocalized to the ER sig::mCherry::KDEL signal (Fig. 2B). Its cellular loci and regulation of hsp-4::GFP led us to hypothesize that TMEM-131 normally acts to regulate processing, trafficking, and/or homeostasis of ER-resident proteins. To identify potential client proteins of TMEM-131, we screened a panel of translational fluorescent reporters for ER-resident transmembrane and secreted proteins, seeking any phenotypic defects caused by RNAi against tmem-131 (table S2 and fig. S2). Among 34 various reporters we comprehensively examined, the COL-19::GFP reporter displayed the most notable defect in GFP patterns caused by tmem-131 RNAi.

COL-19 is a C. elegans collagen protein that is secreted by the epithelial system and required for exoskeleton structure of the cuticle (26, 34). COL-19::GFP deposition is enriched in the wild-type adult animal, constituting regular cuticle structures of annular furrows and lateral alae (Fig. 2, C and D). By contrast, cuticle COL-19::GFP is completely absent in the tm6119 mutant, with apparently missing COL-19::GFP–marked annular furrows and weak intracellular

Fig. 2. Ce-TMEM131 is essential for secretion of GFP-labeled collagen COL-19 and COL-101. (A) Exemplar epifluorescence image of tmem-131p::GFP transcriptional reporter. Arrows indicate major tissues of reporter expression. (B) Exemplar confocal images of tmem-131p::tmem-131::GFP and ER transgenic reporter tmem-131p::ERSig::mCherry::KDEL showing colocalization (indicated by arrows) of both reporters with vesicular puncta patterns in the perinuclear areas of epithelial cells. (C) Exemplar epifluorescence image of col-19::GFP (i.e., col-19p::col-19::GFP) and tm6119; col-19::GFP. (D and E) Exemplar confocal fluorescence images with indicated phenotypic penetrance of col-19::GFP in wild-type (D) and tmem-131 mutant (E). (F) Quantification of COL-19::GFP fluorescence intensity (n ≥ 4 for each group) and endogenous col-19 mRNA levels in wild-type and tmem-131(tm6119) mutants. a.u., arbitrary units. (G and H) Exemplar confocal fluorescence images with the indicated phenotypic penetrance of col-19::GFP with xbp-1 RNAi in wild type (G) or tmem-131 mutants (H). ***P < 0.001 (n ≥ 3 biological replicates); n.s., no significant differences. (I) Exemplar SDS-PAGE and Western blot analysis of col-101::GFP and tm6119; col-101::GFP proteins from total animal lysates. IB, immunoblotting. (J and K) Exemplar confocal images with indicated phenotypic penetrance of col-101::GFP in wild-type (J) and tmem-131 mutants (K). Scale bars, 20 μm.

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COL-19::GFP in the hypoderm (Fig. 2E). tm6119 decreased the abundance of COL-19::GFP proteins without affecting the cuticle furrow structure (fig. S2F), the mRNA abundance, or the promoter activity of col-19 (Fig. 2F and fig. S2G). The notable COL-19::GFP phenotype was not caused by UPR via activation of XBP-1, since xbp-1 RNAi restored hsp-4::GFP expression to normal levels (Fig. 1, G and H) but not epidermal COL-19::GFP in tmem-131 mutants (Fig. 2, G and H). Knockdown of xbp-1 by RNAi in the wild-type background caused excessive ER stresses but did not apparently affect COL-19::GFP in the cuticle (Fig. 2G). In the tmem-131 mutant background, xbp-1 RNAi caused more prominent intracellular accumulation of COL-19::GFP (Fig. 2H). By Western blot analysis, we found that tm6119 decreased overall COL-19::GFP abundance irrespective of environmental temperature (Fig. S2H), although the developmental or hsp-4::GFP phenotype of tm6119 mutants worsened at 25°C compared with 15° or 20°C (fig. S1). Among 34 various reporters we examined, mcCherry-tagged EMB-9 (35), a collagen IV protein, was not affected by tmem-131 RNAi (table S2). However, we found that two other cuticle collagen reporters, COL-101::GFP and LON-3::GFP, similarly required TMEM131 for normal collagen production (Fig. 2, I to K, and fig. S2F). tm6119 decreased COL-101::GFP abundance most prominently in higher–molecular weight species (Fig. 2I). RNAi against pdi-2, which is essential for collagen folding and assembly (36), also partially decreased abundance of COL-19 (fig. S3, A and B). RNAi against cup-2, the Derlin ortholog essential for ER-associated degradation (ERAD) (37), caused synthetic lethality with tm6119 (fig. S3, C and D), consistent with the observation that abnormally accumulated COL-19::GFP as ERAD substrate decreased in overall abundance in tmem-131 mutants (Fig. 2). These results indicate that TMEM-131 is essential for mature collagen production, and its deficiency causes ER stress and UPR through abnormal accumulation of secreted proteins, including at least collagen COL-19, LON-3, and COL-101 in the ER.

Evolutionarily conserved roles of TMEM131 family proteins for collagen secretion

TMEM-131 has not been previously characterized, although it belongs to the highly evolutionarily conserved Pfam12371 (TMEM131_like) protein family (38–40). Its protein sequence is predicted by the program TOPCONS to contain two transmembrane segments, the first (i.e., signal peptide targeting to the ER) and second of which span a hydrophilic domain facing ER, endosomal lumen, or extracellular space, while the C-terminal part is predicted to localize in the cytosol (Fig. 3A) (41). We used structure homology modeling (SWISS-MODEL) (42) to search for proteins structurally similar to TMEM131 and identified many of those from bacteria that contain the PapD chaperone domain involved in the assembly and secretion of extracellular pilus components (fig. S4) (43, 44). The PapD-like domain (PapD-L domain) in the N terminus of TMEM131 is predicted to be in the ER lumen (Fig. 3A), consistent with a putative role in procollagen processing. SWISS-MODEL also predicted a second PapD-L in the N terminus of TMEM131, albeit with lower similarity score. Structural comparisons further revealed that the C. elegans PapD-L, when modeled against one of the most similar structural homolog proteins from Porphyromonas gingivalis W83, comprises a two-loped immunoglobulin fold characteristic of canonic bacterial PapD domains (fig. S4, C and E) (43, 45, 46).

To determine the physiological importance of PapD-L of TMEM-131, we generated a precise deletion of the coding sequence for the PapD-L domain (amino acids 118 to 294) in C. elegans tmem-131 (Ce-PapD) using CRISPR-Cas9 (fig. 3B). Ce-PapD deletion recapitulated the tmem-131(tm6119) or tmem-131 RNAi phenotype in strong hsp-4::GFP induction and defective COL-19::GFP secretion, although quantitative reverse transcription polymerase chain reaction (qRT-PCR) results showed that Ce-PapD deletion did not affect the overall mRNA abundance of tmem-131 (Fig. 3, C to F, and table S3). The phenotypes caused by tm6119 were rescued by the wild-type (100%, n = 20), but not the PapD-lacking (0%, n = 20), transgenes of tmem-131. We further analyzed COL-19::GFP proteins by Western blot analysis after separation of soluble versus insoluble fractions, which contain monomeric procollagens and multimerized/cross-linked collagens, respectively, from whole animal lysates. Consistent with the notion that secreted COL-19::GFP is cross-linked, thus insoluble, we found that both tm6119 and Ce-PapD deletion caused notable and robust decrease in the insoluble fractions of COL-19::GFP compared with wild type, while the abundance of soluble monomeric procollagens was less affected (Fig. 3G). These results indicate that Ce-PapD is essential for TMEM-131 to function in collagen recruitment and assembly, which is required for collagen secretion and preventing ER stress in C. elegans.

Within the evolutionarily conserved TMEM131_like protein family (Fig. 4A), the invertebrate model organisms C. elegans and Drosophila have one ortholog each, named tmem-131 and CG8370, respectively. Vertebrate genomes encode two paralogs of TMEM-131, e.g., TMEM131 and KIAA0922 (also known as TMEM131L) in humans (Fig. 4, A and B). PapD-L domains are predicted from each homolog and represent the most highly conserved parts of TMEM131_like family proteins, based on multiple sequence alignment analysis (Clustal Omega) (fig. S4A). We sought to identify conserved protein-interacting partners as the ligand or client proteins for Ce-PapD in TMEM131 and used a Y2H screen to search for human proteins that can bind to Ce-PapD (Fig. 4C). From a normalized human complementary DNA (cDNA) library with approximately 9 million yeast clones in the screen, the Ce-PapD bait cDNA yielded 34 Ce-PapD interactor-encoding prey clones, among which COL1A2 was confirmed to interact with Ce-PapD in the Y2H assay (Fig. 4D and table S4). COL1A2 constitutes the type I collagen fibril together with COL1A1 (2, 47). The library clone of human COL1A2 cDNA encodes the last 165 amino acid residues and a long 501 bp of the 3’ untranslated region (3’UTR) of full-length COL1A2. We recloned the C-propeptide domain of COL1A2 and confirmed its specific interaction with Ce-PapD (Fig. 4D). In addition to Ce-PapD, we found that the PapD-L domains from the Drosophila TMEM131 homolog CG8370 and human TMEM131, but not TMEM131L (also known as KIAA0922) (39), proteins can also interact with the C terminus of human COL1A2 by Y2H assays (Fig. 4D). These results indicate that the TMEM131_like protein family members from C. elegans, Drosophila, and humans exhibit evolutionarily conserved biochemical interactions with the type I collagen protein COL1A2 via their PapD-L domains.

To test whether TMEM131_like proteins might have evolutionarily conserved functions in collagen secretion, we examined the loss-of-function phenotype of CG8370 and TMEM131 in Drosophila and human cells, respectively. In human cells, we used lentiviral expression of small-hairpin RNAs (shRNAs) to stably knock down TMEM131 in the collagen-producing bone osteosarcoma U2OS cell line (Fig. 4, E and F, and fig. S5) (48). Immunofluorescence analysis revealed that TMEM131 depletion markedly decreased secretion of extracellular type I collagen fibers (green) (Fig. 4E), the severity of which is largely correlated
collagen accumulation but did not appear to involve further degradation.

Drosophila fat body cells in which collagen is normally secreted to the hemolymph (insect blood), measured expression and localization in TRAPPC8 mutants (Fig. 2). Fully penetrant synthetic lethality of LOFs for both tmem-131 and the Derlin gene cup-2 strongly indicates that the ERAD pathway degrades procollagens if not properly assembled and secreted (Fig. S3D).

In Drosophila, we used the Lsp2 > Col4a1:RFP transgenic fly to visualize fat body-secreted collagen and RNAi to silence expression of CG8370 in fat body cells (49, 50). We found that transgenic CG8370 RNAi, but not control animals, accumulated collagen type IV alpha 1:RFP in fat body cells, indicative of defective collagen secretion (Fig. 5). In Drosophila fat body cells in which collagen is normally secreted to the hemolymph (insect blood), tmem131 LOF caused collagen accumulation but did not appear to involve further degradation by ERAD. Nonetheless, these results collectively provide evidence that roles of TMEM131 proteins are evolutionarily conserved for collagen secretion in at least human and Drosophila cells.

**TMEM131 promotes collagen cargo secretion through cytoplasmic C-terminal interaction with TRAPP C8**

To address the mechanism by which the C-terminal domains of TMEM131 family proteins participate in collagen secretion, we used Y2H screens to identify proteins that can interact with the C terminus of human TMEM131 (Fig. 6A and table S5). Among the prey cDNA clones identified to confer interaction with human TMEM131 Ct (C-terminus) as the bait, we focused on TRAPPC8 in this study, as TRAPPC8-containing TRAPP III is critical for the ER-Golgi transport of collagen cargos. The TRAPPC8 prey clone identified encodes only part of its C-terminal region (Fig. 6, A and B). We subsequently verified interaction of the TRAPPC8 with TMEM131 Ct using coimmunoprecipitation assays (Fig. 6C). When coexpressed with the knockdown efficiency of shRNAs targeting five different coding sequences of TMEM131 (Fig. 4, E and F, and fig. S5). Decreased type I collagen in TMEM131-depleted human cells is consistent with diminished COL-19::GFP abundance of type I collagen in TMEM131-depleted human cells (Fig. 4, E and F, and fig. S5). Decreased COL-19::GFP fluorescence intensity in wild-type, tmem-131, and tmem-131∆PapD-L mutants (**P < 0.001 (n ≥ 3 biological replicates)). (G) qRT-PCR measurements of endogenous tmem-131, col-19, and hsp-4::gfp mRNA levels in wild-type and ∆PapD mutants. ***P < 0.001 (n ≥ 3 biological replicates). (G) Exemplar Western blot analysis of COL-19::GFP in different fractions from wild-type, tmem-131(tm6119), and tmem-131(∆Pap-D-L) mutants.
by its N-terminal PapD-L domain but also by its C-terminal recruitment of TRAPP III for the ER-to-Golgi transport of collagen cargo.

Interaction of TMEM131 C terminus with TRAPPC8 prompted us to determine the in vivo consequence of deleting tmem-131 C terminus on UPR and COL-19 in C. elegans. We used CRISPR-Cas9 to generate a precise deletion of the entire cytoplasmic domain (amino acids 1287 to 1808) of tmem-131 and crossed the mutant to hsp-4p::GFP and COL-19::GFP reporters (table S3). We found that C-terminal deletion mutants showed strong dumpy phenotype, activation of hsp-4p::GFP, and reduction in COL-19::GFP abundance in cuticles (Fig. 7, A and B). To identify the specific subregion of TMEM131 Ct responsible for the interaction with TRAPPC8, we generated a series of TMEM131 Ct deletion mutants and test their interaction with TRAPPC8 in Y2H assays (Fig. 7C). Among the five deletions spanning the 1142– to 1883–amino acid sequence, only the very C-terminal end deletion (amino acids 1741 to 1883) abolished interaction with TRAPPC8 (Fig. 7D). We also generated five protein-coding mutations at evolutionarily conserved sites of TMEM131 Ct but found none of the single mutation can abolish the interaction with wild-type TRAPPC8 (Fig. 7E). By contrast, the C-terminal WRD->AAA mutation in TRAPPC8 attenuated interaction with wild-type TMEM131, indicating that the interaction interface between the two may require the WRD motif and multiple residues in TMEM131. Together, these results show that the C-terminal tail domain [TRAPID (TRAPP III–interacting domain)] of TMEM131 binds to TRAPPC8 (Fig. 7F), and its C. elegans counterpart is essential for collagen production in vivo.
DISCUSSION

In this work, we identify a *C. elegans* protein, TMEM-131, which has homologs in most animals, with essential roles in collagen secretion. These roles appear evolutionarily conserved for *Drosophila* and human TMEM131 homologs. We propose that TMEM131 proteins recruit premature collagen monomers through N-terminal PapD-L domains, whereas its C-terminal TRAPIDs bind to TRAPPC8, which promotes collagen secretion as a key component of TRAPP complex during the ER-to-Golgi transport of COPII vesicles (Fig. 7F). Although we did not recognize any apparent homologous C-propeptide protein sequence in *C. elegans* COL-19 or COL-101, their normal secretion still requires TMEM-131 as *Drosophila*, or human collagen I secretion requires TMEM131 homologs. Despite the lack of obvious sequence similarity between the *C. elegans* cuticle collagens and the COLF1 domain of mammalian fibrillar collagens, TMEM131 family proteins appear to have evolved similar functions among different species. As COL-19::GFP secretion also requires *C. elegans* TRAPPC8 homolog, we propose that the interaction between the TMEM131 and TRAPPC8 family proteins and their essential roles in collagen secretion are evolutionarily conserved, while human TMEM131 evolved mechanisms to promote assembly of procollagens in the ER via direct binding of its PapD-L to procollagen. Together, these results have defined previously unknown physiological functions of conserved TMEM131 family proteins in collagen production and elucidated the underlying mechanism via TMEM131 interaction with PapD-L and TRAPPC8.

HSP47 is a collagen-specific chaperone that recognizes collagen trimers in the ER and prevents their premature aggregation during...
secretion (51). Collagen secretion also requires TANGO1, a protein that facilitates the assembly of a collagen export machine in the ER (20–22). However, no apparent HSP47 and TANGO1 orthologs can be found in C. elegans (23–25). Compared with HSP47 or TANGO1, TMEM131 family proteins are evolutionarily more ancient, consistent with their broad requirements for collagen production in animals.

In mammals, COL1A1/2 trimerization initiates from the C-propeptide domain, which can be replaced with a transmembrane domain without affecting trimer formation (10). This indicates that C-propeptide domains act by bringing procollagens close to ER membranes to facilitate procollagen assembly and secretion. Supporting this notion, we obtained evidence for direct COL1A2 binding to the ER-luminal TMEM131 PapD-L domain and notable collagen production defects of TMEM131-deficient cells. Additional PapD-L interactors identified from Y2H screens suggest possibly broader roles of TMEM131 beyond COL1A2 binding, although TMEM131 does appear to exhibit client-protein specificity as many other secreted proteins, including the type IV collagen EMB-9, were not affected by LOF of tmem-131 in C. elegans.
C. elegans (table S2). A recent CRISPR-based genetic screen identified both mammalian TEMEM131 and TRAPCC8 that affect intracellular transport of several secreted proteins (S2).

By Y2H assays, we found that TEMEM131 PapD-L domains can interact with C-terminal propeptide domains of additional members of human collagen protein families (fig. S7). With a similar intriguing function in secretion, bacterial PapD acts as a chaperone that recruits and assembles pilus components for cellular export through well-defined “donor-strand exchange” (DSE) mechanisms (44, 53, 54). DSE proceeds through a concerted β strand displacement to orderly assemble pilus subunits before export to the bacterial periplasm. Whether PapD-L in TEMEM131 acts by similar mechanisms for procolлагens awaits further studies. Given our findings, we propose that TEMEM131 family proteins play critical roles in recruiting procolлагens on ER and/or secretory vesicular membranes to promote collagen assembly en route to secretion. As multicellular organisms evolved collagen-rich extracellular matrix, which is lacking in bacteria but analogous to bacterial secretory processes, it is tempting to speculate that the role of PapD-L domains in collagen secretion originated from the homologous role of PapD in secretion of bacterial pilus components.

Our study also raises the intriguing possibility of TEMEM131 as a new therapeutic target for alleviating tissue fibrosis in human disorders, treatment of which remains a major unmet medical need (9, 55). Current antifibrotic strategies mostly leverage our knowledge on the well-characterized profibrotic mediators, including transforming growth factor–β (TGFβ), which stimulates collagen gene expression and protein biosynthesis. As TGFβ also controls gene expression involved in other biological processes than fibrosis, its inhibition can bring about many side effects, including epithelial hyperplasia, abnormal immune, and wound healing responses (56). Given the newly found role of TEMEM131 in collagen secretion, inhibition of TEMEM131 or its interfaces with collagen C-propeptide and TRAPCC8 may be therapeutically useful for treating pathological tissue fibrosis, including conditions in aging, systemic sclerosis, chronic inflammatory diseases, end-stage organ dysfunction, and heart failure (6, 57, 58). Realization of these therapeutic potentials will benefit from further studies on the mechanism of action, biological function, and regulation of TEMEM131 family proteins in broad contexts of physiology and diseases.

**MATERIALS AND METHODS**

**C. elegans** culture and strains

C. elegans strains were grown on Escherichia coli at 20°C using standard methods, unless otherwise specified (59). Synchronized worm populations were obtained by bleach mating adults. Feeding RNAi-mediated knockdown was performed, as previously described (60, 61).

The N2 Bristol strain was used as the wild type, and genotypes of strains used are as follows: zcs4 [hsp-4::GFP] V, dmasl8 [hsp-16::GFP] IV, rrf-3(pk1426) II; dmasl10 [asp-17::GFP, unc-54::mCherry] X, ire-1(zc14) II; zcs4 V, sph-1(zc12) III; zcs4 V, kals12 [col-19::GFP], dmasl40 [col-101::col-101::GFP (40 ng/µl), unc-54::mCherry (40 ng/µl)], kds55 [LON-3::GFP; unc-119(+)], and tmem-131(tm6119) III, which was further crossed with other reporters described above. Transgenic strains dmaEx151 [tmem-131::tmem-131::GFP (40 ng/µl); myo-2::mCherry (40 ng/µl)], dmaEx146 [tmem-131::tmem-131::GFP (15 ng/µl); unc-54::mCherry (10 ng/µl)], dmaEx504 [tmem-131::tmem-131::GFP (15 ng/µl); tmem-131::ER signal::mCherry::KDEL (15 ng/µl); myo-2::mCherry (10 ng/µl)], dmaEx152 [rpl-28p::F23H12.5::mCherry (45 ng/µl); unc-122p::GFP (45 ng/µl)], dmaEx153 [rpl-28p::Y73E7A.8::mCherry (45 ng/µl); unc-122p::GFP (45 ng/µl)], and dmaEx169 [rpl-28p::T19D2.1::mCherry (45 ng/µl); unc-122p::GFP (45 ng/µl)] were generated by germline transformation, as described (62). The tmem-131(dma301) PapD-L deletion and tmem-131(dma303) C-terminal (amino acids 1287 to 1808) deletion strains were generated by CRISPR-Cas9 methods to induce double-stranded breaks and subsequent homologous repair (primer sequences are listed in table S3). Other translational reporters used to identify a phenotype affected by RNAi against tmem-131 and cross with tmem-131(tm6119) include arls37 [myo-3::ssGFP + dpy-20(+)], bcs39 [lin-7p::ced-1::GFP+lin-15(+)], rme-4(b1001); bsl1 [vit-2::vit-2::GFP + rol-6(+)], cal5618 [eff-1p::eff-1::gfp], cpg-1(tn1728[mnc-3::flg::cpg-1]) III, dmaEx115 [rpl-28p::manf-1::venus (45 ng/µl), dts4 [gna-1p::GFP + Cbr-unc-119(+)] IV, unc119p [svu-1::GFP, lrp-1(ku156)eqls1 [lrp-1p::lrp-1::GFP]; rlf-3(pk1426) II, muls49 [egl-20::GFP+unc-22(+)]; nls590 [fat-7p::fat-7::GFP]; nuls26 [cat-1::GFP]; pk12386 [unc-54::alpha synuclein::YFP’ Cbr-unc-119(+)]] IV, vit-2p::vit-2::GFP + rol-6(+) I, osls66 [myo-3p::GFP:TRAM::unc-119(+)]; osls66 [myo-3p::EGFP::WRK-1], osls77 [unc-54p::RFP::SP12; unc-119(+)]; pws503 [vha-6p::mans::GFP + Cbr-unc-119(+)]; qyls44 [emb-p::EMB-9::mCherry], qyls108 [lam-1p::lam-1::dendra + unc-119(+)]; rls233 II [GFP::him-4]; qyls11 [lgl-1p::mCherry::GFP; gfp-1 + rol-6(+)]; vels13 [col-19::GFP + rol-6(+)]; V; let-7(mn122) unc-3(e151) X]; mgEx725 [lin-4::let-7 + ttx-3::RFP], vkeX1243 [nhx-2p::ubiquitin-V::mCherry + myo-2::GFP], vkeX1256 [nhx-2p::cpl-1::YFP + nhx-2p::dsRed::KDEL], vkeX1258 [nhx-2p::cpl-1(W32A Y35A):YFP + nhx-2p::DsRed::KDEL], vkeX1260 [nhx-2p::cpl-1::YFP + myo-2p::mCherry], vkeX1879 [nhx-2p::cpl-1(W32A Y35A):YFP + myo-2p::mCherry], xis196 [hmr-1p::hmr-1::GFP]. Extrachromosomal arrays were integrated using ultraviolet irradiation and backcrossed for three to six times.

**Drosophila melanogaster experiments**

Flies: UAS-Cg25C:RFP.2.1/CyO, Lsp2-Gal4/TM6B, and UAS-CG8370 dsRNA (Vienna Drosophila Resource Center ID no. 42509/GD). Lsp2-Gal4 expresses specifically in the fat body. Flies expressing collagen type IV alpha 1:RFP in fat body were crossed to either wild-type or UAS-Cg25C:RFP.2.1/CyO, Lsp2-Gal4/TM6B, and UAS-CG8370 dsRNA flies. Fat body was dissected from wandering stage third instar larvae and fixed in 4% paraformaldehyde, stained with 4',6-diamidino-2-phenylindole (DAPI), and mounted for imaging by confocal microscopy.

**Quantitative reverse transcription polymerase chain reaction**

Total RNA was extracted following the instructions of the Quick-RNA MiniPrep kit (Zymo Research, R1055) and reverse transcribed into cDNA (BioTools, B24408). Real-time PCR was performed by using SYBR Green Supermix (Thermo Fisher Scientific, FERR1081) on the Roche LightCycler96 (Roche, 05815916001) system. C values of specific genes were normalized to measurements of *act-1* (C. elegans) and RPL13 (human cell lines) levels. Results are presented as fold changes to respective references. Statistical significance was determined with unpaired Student’s *t* tests, one- or two-way analysis of variance (ANOVA) (comparisons across more than two groups), and adjusted with Bonferroni’s corrections using GraphPad Prism 7. Primer sequences are listed in table S7.

**Imaging and fluorescence quantification**

SPE confocal (Leica) and digital automated epifluorescence microscopes (EVOS, Life Technologies) were used to capture fluorescence
Western blot analysis of proteins

Stage-synchronized animals for control and experiment groups were picked (N > 40) and lysed directly into 20 μl of Laemmli sample buffer for Western blot analysis. Proteins were resolved by 15% SDS-polyacrylamide gel electrophoresis (PAGE) (Bio-Rad, 4561084) and transferred to a nitrocellulose membrane (Bio-Rad, 1620167). Proteins of interest were detected using antibodies against GFP (A02020, Abbkine), tubulin (Sigma-Aldrich), T5168), and H3 (Abcam, ab1791). All experiments were repeated for multiple times.

For subcellular fractionation, 50-ml adult-stage animal pellets were collected as the soluble part, and the pellet was resuspended in 500 μl of RIPA lysis buffer with 10 mM phenylmethylsulfonyl fluoride (PMSF) and protease inhibitor cocktail (BioTools, B14002). Then, pellet samples were disrupted by TissueRuptor (motor unit “8” 31742-250MG, Sigma-Aldrich), as well as plasmids from recloned cDNA. Lentiviral TMEM131 shRNA knockdown in cultured human U2OS cells

Human TMEM131 knockdown in osteosarcoma U2OS cells was carried out with lentiviral shRNA (Sigma-Aldrich, SHCLNG-NM_015348). The TMEM131 shRNA targeting sequences are as follows: 5′-TAG-CAGTTTCTCACCTATAAT-3′ [TRCN0000257459, CDS (coding sequence)], 5′-ATTATGCGCAAGATCTAAATT-3′ [TRCN0000246000, 3′UTR], 5′-TCCAATGTGAGTGGCTATAAA-3′ [TRCN0000246001, CDS], 5′-CTCGGACCCCTGTTCTTAATG-3′ [TRCN0000246002, CDS], 5′-CATAGATTGTGGCTATATTT-3′ [TRCN0000246003, CDS]. HEK293T was transfected by pMD2.G, psPAX2, and shRNA plasmids, following the lentivirus production methods and manuals of TurboFect Transfection Reagent (Thermo Fisher Scientific, R0531). The lentivirus-based GFP-specific shRNAs were used as negative controls (Addgene, 31849). Forty-eight hours later, the TMEM131 shRNA lentivirus-containing media were collected and filtrated by a 0.45-µm syringe filter (Millipore EMD, SLHP033RS). The osteosarcoma U2OS cells were incubated with TMEM131 shRNA lentivirus medium for 24 hours in a humidified incubator at 37°C with 5% CO2. Transduction efficacy was enhanced by adding Polybrene (Sigma-Aldrich, TR-1003-G). Lentivirus-transduced cells were enriched by the medium with puromycin selection (1.5 μg/ml) for 3 days. Ascorbates were exogenously supplemented to ensure proper collagen modification. The knockdown efficiency of TMEM131 shRNA was evaluated by qRT-PCR.

Immunofluorescence staining of type I procollagen in human U2OS cells

The human TMEM131 knockdown U2OS stable cells were seeded in 24-well plates with cover glass for 2 days, each with three replicates (Fisher Scientific, 22293232). After 1× phosphate-buffered saline (PBS) washing for once, cells were treated by 4% formaldehyde solution for 10 min. With 1× PBS washing for three times, cells were treated with 0.2% Triton X-100 in 1× PBS solution for 15 min. Then, cells were incubated in 5% bovine serum albumin in 1× PBS solution for 1 hour at 4°C after 1× PBS washing for three times. Monoclonal anti-human Procollagen Type I C-Peptide (PIP) clone PC5-5 (Takara Bio USA, M011) was incubated with the cell sample at 4°C for 12 hours then with goat anti-mouse IgG (H+L) Alexa Fluor 488 oligoclonal secondary antibody for 1 hour (Fisher Scientific, A-11001). Following 1× PBS washing for three times, the cover slide with cell samples was sealed on the microscope slide with Fluoroshield Mounting Medium with DAPI (Thermo Fisher Scientific, NC0200574). For quantification of GFP fluorescence, every cell in the captured images was outlined and quantified by measuring gray values of fluorescence intensity using the ImageJ software. The data were plotted and analyzed by using GraphPad Prism7.
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