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J. R. Soc. Interface 2010 7, 839-850 first published online 6 November 2009

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Deformation micromechanisms of collagen fibrils under uniaxial tension

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Collagen, an essential building block of connective tissues, possesses useful mechanical properties due to its hierarchical structure. However, little is known about the mechanical properties of collagen fibril, an intermediate structure between the collagen molecule and connective tissue. Here, we report the results of systematic molecular dynamics simulations to probe the mechanical response of initially unflawed finite size collagen fibrils subjected to uniaxial tension. The observed deformation mechanisms, associated with rupture and sliding of tropocollagen molecules, are strongly influenced by fibril length, width and cross-linking density. Fibrils containing more than approximately 10 molecules along their length and across their width behave as representative volume elements and exhibit brittle fracture. Shorter fibrils experience a more graceful ductile-like failure. An analytical model is constructed and the results of the molecular modelling are used to find curve-fitted expressions for yield stress, yield strain and fracture strain as functions of fibril structural parameters. Our results for the first time elucidate the size dependence of mechanical failure properties of collagen fibrils. The associated molecular deformation mechanisms allow the full power of traditional material and structural engineering theory to be applied to our understanding of the normal and pathological mechanical behaviours of collagenous tissues under load.

Keywords: collagen mechanics; collagen fibril; mesoscopic model; failure micromechanism; size effect

1. INTRODUCTION

Fibril-forming collagens, the most abundant proteins in mammals, are found in tissues such as skin, tendon and bone. The superstructures into which these molecules self-assemble possess useful mechanical properties including high tensile strength around 1 GPa and great extensibility reaching up to 100 per cent strain before fracture (Shen et al. 2008). Exploring how molecular-level interactions conspire to produce tissue-level mechanical response of collagenous materials provides a promising avenue for advancing medical diagnosis/treatment and tissue engineering.

The structure of collagen extends over several length scales, as sketched in figure 1. The fundamental elements of collagen are amino acid sequences arranged in the pattern (–Gly–X–Y–), where in approximately 20 per cent of all cases, X and Y are Pro and Hyp, respectively (Parry 1988; Kadler et al. 1996). The amino acid sequences constitute a left-handed polypeptide helix, three of which assemble in parallel into a right-handed supercoil producing the tropocollagen (TC) molecule. A TC molecule is approximately 300 nm long, 1–2 nm in diameter and weighs 300 kDa (Rice et al. 1964; Parry 1988; Kadler et al. 1996; Ottani et al. 2002; Buehler 2006b). The detailed molecular topography of short peptide fragments that model certain aspects of the naturally occurring fibrillar collagen molecules has been determined from X-ray diffraction experiments (Bella et al. 1994; Kramer et al. 2000). The molecular structure of such a model peptide is shown in figure 1 as an example (protein data bank code 1QSU; Kramer et al. 2000). TC molecules aggregate into fibrils and are stabilized via intermolecular adhesion and covalent cross-links at their ends (through lysine, allysine, hydroxylysine and hydroxyalysine residues; Lodish et al. 1999; Bailey 2001; Alberts et al. 2002). The two-dimensional collagen fibril considered in this study follows the Hodge–Petruska arrangement (Hodge & Petruska 1963) depicted in figure 1. TC molecules are grouped into staggered structure with an axial offset distance \(D\) = 67 nm and an equilibrium centre-to-centre distance of 1.5 nm between nearest neighbour molecules. The total length of a TC molecule is approximately 4.34D, and the gap between amino and carboxy termini of two molecules in the same row is approximately 0.6D. This D period was determined through transmission electron microscopy (Schmitt...
et al. 1942). Important extensions of the Hodge–Petruska scheme to a three-dimensional generalized packing model were achieved in the mid-1980s (Lees et al. 1984a,b; Bonar et al. 1985; Lees 1986, 1987) based on pioneering neutron diffraction studies on mineralized and non-mineralized collagenous tissue. More recent efforts include the work of Gutsmann et al. (2003) and Bozec et al. (2007). While recent experimental evidence (Orgel et al. 2006) revealed a three-dimensional twisted right-handed crystallographic structure of collagen microfibrils, we have not included this in the model presented below. Finally, collagen fibrils assemble into distinct types of biological tissues through larger scale structural assemblies.


Challenges in computational mechanics modelling of collagenous assemblies lie in the numerous distinct length scales involved in their structural makeup and in the intimate coupling between chemistry, biology and mechanical deformation. Fully atomistic simulation of macroscopic collagenous tissues is currently impossible, and therefore multi-scale analysis has been developed into a promising tool that relies on a hierarchically coupled treatment of each of the scales. For example, molecular dynamics (MD) simulations of stretching, bending and shearing of TC molecules and small fibrillar assemblies thereof (Buehler 2006a; Buehler & Wong 2007) relied on potentials constructed from the results of quantum chemistry calculations and reactive force fields. This bottom-up approach was used to investigate entropic effects on the mechanical behaviours of long contorted TC molecules (Buehler 2006a; Buehler & Wong 2007) as well as collagen fibrils assembled using the Hodge–Petruska scheme (Buehler 2006b, 2008).

What has not yet been explored in a systematic fashion using MD modelling is the complex interaction among collagen fibril length, width and cross-linking density. For example, earlier simulations based on a two-dimensional mesoscopic model showed that the uniaxial stress–strain responses of collagen fibrils containing two molecules along their length and with periodicity in the width direction are greatly affected by the cross-linking density (Buehler 2008). Highly cross-linked fibrils demonstrated higher yield strength and brittle failure. Fibrils with low cross-linking exhibited a graceful failure involving a strain softening (decreasing stress with increasing strain) post-peak region. The study did not, however, consider whether the computational experiment was performed on a representative volume element (RVE). (The model behaves as an RVE if the mechanical behaviour is independent of the size of a sample.) Here, we use the same two-dimensional mesoscopic model to study the effects of fibril dimensions and cross-linking density on mechanical response, with particular attention on whether a collagen fibril of a given size can be considered an RVE (and at what scale), and whether graceful failure can be achieved in fibrils containing more than a few molecules along their length or width. The computed responses are used to construct a continuum strength model and curve-fitted equations for fibril yield stress, yield strain and fracture strain.

2. MESOSCOPIC SIMULATIONS

2.1. Model and methods

To overcome the limitations imposed by the enormous number of degrees of freedom that would be required for an all-atom simulation of a collagen fibril, the mesoscopic model (figure 2a) serves as the primary simulation tool used here (Buehler 2006a,b, 2008). The coarse-grained model describes TC molecules as chains of interacting beads (i.e. point masses) that represent the atomistic structure, which enables a sufficiently accurate treatment of long-range responses of collagen fibrils under mechanical stress. The intramolecular properties of individual TC molecules (i.e. the bond potential and angle potential among beads) and the interaction between TC molecules (i.e. the non-bonded potential among beads) are determined from the results of atomistic simulation using reactive force fields with a pure water phase (Buehler 2006a). Inter-molecular cross-links are formed in the highlighted regions shown in figure 2a. Cross-linking is incorporated in the model by locally enhancing the adhesion forces between molecules $\beta$-fold, with $\beta = 1$ corresponding to
Definition of possible slip systems in the collagen structure. (b–d) Definition of possible slip systems in the collagen structure. $m^{(a)}$ and $s^{(a)}$ represent the normal of slip plane and slip direction.

no cross-linking. Varying $\beta$ enables us to model different cross-link densities. The coarse-grained simulations were carried out using the MD simulator LAMMPS (Plimpton 1995).

We note that a molecular-level model of the cross-link structure (with atomistic resolution) is being developed, based on experimental data on the chemistry and location of cross-links in the fibril arrangement. Once developed, this model will enable us to probe the effects of cross-links on the mechanical behaviour of collagen fibrils from a more fundamental perspective than what is done in this paper.

A detailed description of the two-dimensional mesoscopic model of collagen fibrils is included in earlier publications (Buehler 2006a; Buehler & Wong 2007). Regarding the effect of water (and other solvents), the full atomistic simulations that are used to extract parameters for the coarse-grained model are carried out in explicit water solvent (see earlier papers by Buehler et al.). As such, they directly include the effect of water solvent. For any larger scale effects of water (e.g. nano/microfluidic mechanisms that occur at the fibril scale), the mesoscale model could in principle be reformulated to include explicit water as well; however, this is beyond the scope of current studies. Initial attempts by the authors have been made by using the coarse-grained MARTINI force field, based on which we are currently building a microscale model of a fibril with explicit water.

As shown in figure 2a, the dimensions of the fibril are defined by the number of TC molecules along the length, $m = 2–10$, and across the width, $n = 2–20$. In subsequent discussion, the fibril size is thus defined as $m \times n$, and $\beta$ is varied from 1 to 50. The nominal strain $\epsilon_{nm}$, defined as the extension, $u$, divided by the initial length of the fibril, $L_0$, and nominal stress, $\sigma_{nm}$, determined by dividing the virial stress by the initial volume of the collagen fibril (i.e. $D_0 L_0 d$, where $D_0$ and $d$ are the initial width and thickness of the specimen), are tracked throughout the simulation.

Visualization of the molecular deformation mechanisms within the fibril is facilitated by using the slip vector approach (Zimmerman et al. 2001), with the slip vector $\delta^i$ defined as

$$\delta^i = -\frac{1}{\xi_{ij}} \sum_{j \neq i} \left( x^{(i)} - X^{(ij)} \right),$$

where $x^{(i)}$ and $X^{(ij)}$ are the vector differences between the coordinates of beads $i$ and $j$ in the current and reference states, respectively, $\xi$ is the number of nearest neighbours (the beads spatially closest) to bead $i$ in the reference state and $\zeta$ is the number of slipped neighbours (neighbour beads that slip along a slip plane adjacent) to bead $i$ in the current state. The reference state is taken as the zero mechanical stress configuration at the beginning of the simulation.

2.2. Results

2.2.1. Short fibrils with varying cross-linking density. The first example involves a $2 \times 5$ fibril. The same structure, but with periodic boundary conditions across its width, was considered in a previous study focused on the effects of varying cross-linking density (Buehler 2008). Here, we consider a finite geometry to remove the periodicity constraints and present the results in figure 3.

The stress–strain curves for cross-linking in the range $1 \leq \beta < 20$ are linear elastic and exhibit a small strain modulus of approximately 5 GPa. For higher levels of cross-linking, $\beta \geq 20$, the curves are approximately bilinear with an elastic modulus of approximately 35 GPa activated at a strain of approximately 0.32. After yielding at strains in the range of 0.06–0.42, except for $\beta = 40$ the fibrils display a graceful failure as evidenced by either post-peak yielding at constant stress or strain softening. The most highly cross-linked fibril fails in a brittle fashion at a failure strain, $\epsilon_f$, approximately equal to 0.42, whereas the graceful failures are associated with $\epsilon_f = 0.64–1.03$. These results are consistent with those of the periodic structure (Buehler 2008).

The stress–strain curves result from the competition between fracture of TC molecules and fracture of cross-links as well as sliding of TC molecules thereafter (Buehler 2006b, 2008). For high-density cross-links, TC molecules rupture at a critical force, leading to the brittle failure of the collagen fibril. The breaking
Thus an extension of TC molecules. Concomitantly, the tangential moduli in these plots are similar. Because the collagen fibrils, which typically contain large numbers of molecules along their lengths, are expected to fail in a brittle manner (results for other values of \( n \) and varying \( m \) are presented in §3.2). As will be discussed in §2.4, this transition from stable to unstable structural behaviour is analogous to that of a fibre-shaped continuum that contains (or develops) a propagating crack.

Figure 5 shows the results for \( n = 5 \) and varying \( m \). The undeformed structure is shown in figure 6a. A full atomistic simulation of tropocollagen molecules shows that the deformation from a to b can be fully explained by molecular stretching and uncoiling of the triple helical protein structures (Buehler & Wong 2007). The configuration corresponding to point b indicates an increase in distance between material points \( \mathcal{T} \) and \( \mathcal{T} \) thus an extension of TC molecules. Concomitantly, intermolecular interactions result in the bending of TC molecules at the gap regions. Further loading from point b to point c leads to stretching of the covalent bonds in the collagen structure and is met by a slight increase in stiffness (Buehler & Wong 2006b, 2008). At point c, the collagen structure begins to yield, and the structural configuration at this critical moment is depicted in figure 6c.

The failure of the collagen fibril is caused by rupturing of TC molecules or breaking of cross-links, and relative slip between TC molecules. In this specific example, the loads do not exceed the elastic limit of any single TC molecule. Instead, cross-links reach their maximum fracture stress, and slip motions take place at the most vulnerable positions of the collagen structure, resulting in the whole fibril experiencing unloading (the drops in the post-peak region in figure 5). Although the fibril did not contain pre-existing defects, dislocation-type slip of TC molecules occurs due to the staggered nature of the fibril (figure 2a), using a previously described mechanism (Buehler 2006b). Three slip systems, I, II and III, are
described by the arrangement of molecules shown in figure 2b–d, where \( m^{(a)} \) and \( s^{(a)} \) represent the normal to the slip plane and the slip direction, respectively. Development of these slip systems provides a molecular scale mechanism that describes the post-peak softening behaviour of the fibril.

To quantify the slip motions in the collagen fibril, the magnitude of the slip vectors is computed for each bead in the structure and the resulting contours superimposed on the fibril in figure 6. By tracking the trajectories of selected beads, we observe type I slips along the fibril surface all through the post-peak deformation. However, only the relative movements of beads 1–6 lead to softening. The collagen fibril initiates type II slips in figure 6c. Points 1, 3, and 5 switch their orders with 2, 4, and 6, respectively. This results in a steep reduction in stress at point d and the localized deformation shown in figure 6d. Subsequently, type II slip occurs again only at positions 3 and 5, leading to a further stress drop at point e. In figure 6e, two TC molecules remain where the deformation localizes. Finally, type III slip occurs at the new positions 1 and 5, resulting in fracture at point f.

### 2.4. Plausible explanation of the brittle-to-ductile transition

The results in §2.2.2 clearly illustrate that fibril length and width determine whether the structural response after the peak stress is stable (i.e. the stress–strain curve is associated with a gradual decrease in stress with increasing strain) or unstable (i.e. the stress–strain curve terminates at the peak stress). One way of thinking about the transition from stable to unstable response involves an analogy between the hierarchical fibril and a continuum beam containing a crack (figure 7) whose equilibrium length is dictated by the Griffith condition (the applied energy release rate, defined as the change with respect to crack length of the work of the applied force minus the strain energy, is equal to the critical energy release rate that is required to propagate the crack). Consider the normalized stress–displacement response of a tension-loaded edge-cracked beam. The edge crack in this continuum represents the numerous crack-like regions that develop as bonds break and molecules slide, and the cross-sectional area is reduced in the MD simulation of the fibril. The response before the initial crack starts to propagate is linear up to the stress that renders the applied energy release rate equal to the critical energy release rate. For relatively small aspect ratios \( (L_0/D_b = 0.2–1.0) \), Griffith equilibrium is maintained by a decreasing stress and a concomitant increase in displacement. For relatively large aspect ratios \( (L_0/D_b = 2–4) \), however, a balance between the applied energy release rate and the critical energy release rate requires a negative increment in the work of the applied load. This results in a post-peak response involving snap-back instability. The snap-back cannot be captured in a displacement-controlled experiment or simulation such as the ones performed in this study; for those specimens that may be associated with such unstable structural response, displacement control forces the post-peak response to jump vertically to the equilibrium path (which approaches zero stress for increasing aspect ratios).

Furthermore, the transition can also be understood by considering the deformation mechanisms. The MD simulations suggest that failure of a collagen fibril is localized within several specific slip planes. During the softening stage, if the elastic strain decreases faster than the accumulation of plastic strain in the localization region(s), snap-back is found in the stress–strain curve (Jirasek & Bazant 2001). Otherwise, the fibril fracture is caused by a type II slip between two contacting TC molecules.
The softening response of the $2 \times 5$ fibril, decomposed and illustrated in §2.3, involves multiple slips of types I–III. For fibrils with larger width ($2 \times 10$ and $2 \times 20$), more slip motions are observed at different positions in figure 8. The increasing number and magnitude of slips indicate that more plastic strain accumulates while unloading. Hence, fibrils with larger widths dissipate more energy as a result of a graceful post-peak region terminating at larger fracture strains. Figure 9 presents snapshots of the $5 \times 5$ collagen fibril corresponding to the points marked in figure 5. The sequence and magnitudes of the slip motions of this fibril are similar to those of the $2 \times 5$ fibril. This implies that a smaller amount of plastic strain accumulates in the $5 \times 5$ fibril, resulting in more brittle behaviour. Because our simulations are displacement controlled, the snap-back instability that may be associated with a relatively long fibril ($m \geq 10$ in this example) is not captured, and the fibril fails catastrophically at the onset of yielding.

It is clear that the variation of the stress–strain curve with fibril size is structurally describable using relative slip between the collagen molecules. These observations provide the basis for the simple analytical model presented next.

3. MODELS

3.1. Analytical model

A model for the yield stress and fracture strain capable of transitioning from brittle to graceful failure can be constructed according to the $m \times n$ staggered collagen fibril structure shown in figure 2a. The left end of the fibril is fixed and its right end is loaded by a force $F$. The molecules are assumed to be linear elastic. For the rising portion of the stress–strain we assume that the total extension $u$ equals the elastic extension $u_e$. The force is thus

$$ F = E u_e \frac{A_0}{L_0} = E u_0 \frac{A_0}{L_0}, \quad (3.1) $$

where $A_0$ and $L_0$ are, respectively, the initial cross-sectional area and the initial length of the staggered fibril structure. For the plane stress model considered here, $A_0$ equals $D_0 d$. The equilibrium distance between rows of TC molecules, $d$ (shown in figure 2a), can be regarded as the thickness of the fibril, $D_0 = nd$ is the initial width of the structure and $E$ is the effective elastic modulus of the cross-linked TC molecules.

In the range $1 < \beta < 40$, cross-links break at a critical force $F^{cr}$. Consider the simplest case involving only type II slip (figure 2a). At the onset of yielding, $n-1$ pairs of TC molecules are in contact. $F^{cr}$ is related to the maximum intermolecular adhesion line force $\tau^{cr}$ through

$$ F^{cr} = (n - 1) \tau^{cr} b_0 = \left( \frac{D_0}{d} - 1 \right) \tau^{cr} b_0, \quad (3.2) $$

where $b_0$ is the initial contact length between two TC molecules at ends illustrated in figure 2a. We define the normalized width $\tilde{D} = n = D_0/d$ and the normalized maximum adhesion force $\tilde{\tau} = \tau^{cr} b_0/(E\tilde{d}^2)$. The corresponding critical nominal stress $\sigma^{cr}_e$ (i.e. yield strength) becomes

$$ \sigma^{cr}_e = \frac{F^{cr}}{A_0} = \tilde{\tau} \left( 1 - \frac{1}{\tilde{D}} \right), \quad (3.3) $$

The total force applied after yielding can be written as

$$ F = \left( \frac{d}{\tilde{D}} - 1 \right) \tau^{cr} b_0 = \left( \frac{D_0 - \Delta D}{d} - 1 \right) \tau^{cr} b_0, \quad (3.4) $$

where $D$ and $\Delta D$ are, respectively, the diameter and its change at the section experiencing localization. Defining $\alpha$ as the angle of the slip plane in the deformed coordinates for large deformation, $\Delta D = u_\alpha \tan \alpha$ (figure 2a). The plastic deformation after yielding, $u_{p\alpha}$, equals the total extension minus the elastic deformation of the fibril, $u_p = u - u_e = u - F L_0/(A_0 \tilde{E})$. Substituting these last two relations into equation (3.4), the relationship between external force and total extension after yielding becomes

$$ F = \frac{(D_0 - d) - u \tan \alpha}{d/(b_0 \tilde{E})} - L_0 \tan \alpha/(D_0 d \tilde{E}). \quad (3.5) $$
The associated fracture strain is

\[ \varepsilon^f = \frac{D_0 - d}{L_0 \tan \alpha} = \frac{(n-1)s}{L_0} \]

\[ = \frac{(D - 1) + \bar{\tau}(\bar{D} + 1/D - 2)}{L}. \] (3.8)

The model captures the transition from brittle to graceful failure, as evidenced by the inverse-length dependence of the fracture strain. Qualitatively, \( \sigma^\varepsilon^f \) increases with increasing \( \bar{\tau} \) and \( D \), and \( \varepsilon^f \) decreases with decreasing \( D \) and \( \bar{\tau} \) or increasing \( L \). The predictions can be assessed by using the parameters developed previously through MD simulation of a 2 \( \times \) 5 collagen fibril with \( \beta = 1 \): \( \sigma^\varepsilon^f \approx 5.55 \text{ pN} \cdot \text{Å}^{-1} \), \( E = 5 \text{ GPa} \), \( L_0 = 6200 \text{ Å} \), \( d = 16.3 \text{ Å} \), \( b_0 = 300 \text{ Å} \) and \( s_0 = 630 \text{ Å} \) (Buehler 2006a; Buehler & Wong 2007). The bilinear stress–strain curve predicted by the model, plotted in figure 3, is defined by \( \sigma^\varepsilon^f = 0.5 \text{ GPa} \) and \( s_0 = 0.45 \). The peak stress is reasonably captured, while the fracture strain is underestimated because the model does not include the multiple slips of types I–III observed in the MD simulation.

### 3.2. Phenomenological model

Extensive numerical analyses were performed involving \( \beta = 1–50 \), \( m = 2–10 \) and \( n = 2–20 \) in order to train the phenomenological model based on the molecular simulation results. The average run time of one serial simulation on the IBM Blade Cluster at the University of Minnesota Supercomputer Institute is approximately 50 h. Performing parameter studies on larger values of \( m \) and \( n \) will be one of our future directions. Data-fitting equations for the normalized yield strength \( \sigma^y/YTC \), yield strain \( \varepsilon^y \) and fracture stress \( \varepsilon^f \) are presented and discussed next. These expressions reflect the overall trends of the characteristic properties and can be useful to those researchers who do not have the resources to perform MD simulations. The results suggest that \( \sigma^y/YTC \) is a strong function of \( \beta \), a weak function of \( n \) and insensitive to \( m \) and can be written as

\[ \frac{\sigma^y}{YTC} = \frac{1}{1 + \frac{1}{\beta}} \left( 1 + \frac{1}{\beta} \right) \]

\[ \times \left( 0.01435 + 0.012663 \ln \beta + 0.01041 \ln \beta^2 + 0.00961 \ln \beta^3 \right) \]

\[ + 0.084903 \ln \beta + 0.01435 \ln \beta^2 + 0.00961 \ln \beta^3 \]

\[ + 0.01435 \ln \beta^4 + 0.00961 \ln \beta^5 \] (3.9)

Yield strain \( \varepsilon^y \) depends on \( \beta \) according to

\[ \varepsilon^y = q_1 + q_2 \exp \left( -\frac{\beta}{q_3} \right). \] (3.10)

The coefficients that enter equations (3.9) and (3.10) are listed in table 1.

![Table 1. Coefficients of the phenomenological model.](image)

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The results of the simulations and their associated fitting curves are shown in figure 10. While \( \sigma^y/YTC \) increases slightly with increasing small values of \( n \) (figure 10a), it is a strong function of cross-linking density. The inset in the figure shows that the yield strength increases monotonically with increasing cross-linking density and approaches a constant value. The nonlinear transition from small to large \( \beta \) is due to the nonlinear stress–strain behaviour of individual TC molecules. The curves reflect two failure mechanisms of
For $\beta \sim 40$, the maximum adhesion forces transferred by the cross-links account for the maximum tensile strength of approximately 8.3 GPa of a single TC molecule (Buehler & Wong 2007). For $\beta < 40$, a graceful softening behaviour results from intermolecular shear (i.e. breaking cross-links and plastic slips of TC molecules). For $\beta \geq 40$, collagen fibrils fail in a brittle manner as a result of rupture of TC molecules.

Figure 10b shows the simulation results and the fitting curve for $\varepsilon^y$. Because the simulation results have a weak dependence on $n$, the data were fitted using the average over $n$ at all values of cross-linking density. The non-linearity of the curve is again due to the nonlinear mechanical responses of individual TC molecules. For $\beta \sim 40$, the dominant failure mechanism transitions from intermolecular shear to molecular fracture.

Cross-sections of the contour plot of $\varepsilon^y$ calculated from the MD simulations, whose trends are more complex, are shown in figure 10c. A constant contour is observed for $\beta \geq 40$, since for those brittle fracture cases the fracture strain is equal to the yield strain. For $1 < \beta < 40$, $\varepsilon^y$ is a function of $m$, $n$ and $\beta$ that increases with $n$ and approaches $\varepsilon^y$ for large $m$. As shown in figure 10d, the fracture strain–cross-linking density plot is bell shaped. The fitting equation describing these trends is

$$
\varepsilon^y = \begin{cases}
q_1 + q_2 \exp \left( \frac{-\beta}{q_3} \right) & \beta \geq 40 \\
\left( \frac{1 - t_1}{m^5} \right) + \frac{t_3}{m^n b^2} \left( 1 + t_4 \exp \left( -2 \ln \left( \frac{\beta + t_5 m^2}{t_0(1 + t_1 n + t_2 n^2) + t_3 n^2} \right) \right) \right) \times (1 + t_4 \ln(n)) + t_5 (\ln(n))^2) & 1 < \beta < 40
\end{cases}
$$

with the best-fit coefficients listed in table 1.

---

Figure 10. Results of MD and phenomenological model of collagen fibrils. (a) Yield strength $\sigma^y/E_{TC}$ ($\beta = 1$: unfilled pentagon (MD), dashed grey line (phenomenological model); $\beta = 10$: star (MD), dotted dashed grey line (phenomenological model); $\beta = 20$: unfilled square (MD), dotted dashed black line (phenomenological model); $\beta = 30$: inverted triangle (MD), dotted grey line (phenomenological model); $\beta = 40$: open circle (MD), dashed black line (phenomenological model); $\beta = 50$: filled pentagon (MD), grey line (phenomenological model)); (b) yield strain $\varepsilon^y$ (open circle, $n = 2$; pentagon, $n = 5$; inverted triangle, $n = 10$; star, $n = 20$; black line, phenomenological model); (c) fracture strain $\varepsilon^f$ of MD simulations; (d) comparison of fracture strain $\varepsilon^f$ of collagen fibrils with sample sizes ($n = 20$ and $m = 2$, black line (phenomenological model), unfilled square (MD); $n = 10$ and $m = 5$, dashed grey line (phenomenological model), grey circle (MD)). The parameters $m$ and $n$ are the number of TC molecules in length and width direction, and $\beta$ is the cross-linking density factor.
4. COMPARISON WITH EXPERIMENTAL RESULTS

Our computed small-strain and large-strain elastic moduli of collagen fibrils are approximately 5 and 35 GPa, respectively. The moduli slightly increase as the cross-linking density or the fibril width assumes larger values (figures 3 and 4). These computational results are close to a recent atomic force microscope nanoindentation experiment in air (Wenger et al. 2007), which found that the upper and lower limits of modulus were 5 and 11.5 GPa for collagen fibrils whose diameters ranged from 50 to 100 nm. However, this may be a coincidental agreement, since Wenger et al. computed the moduli by assuming the fibrils possess isotropic mechanical properties. The stiffness measured by applying tensile strain along the axial direction of type I collagen fibrils was smaller (Gupta et al. 2004; Shen et al. 2008).

The higher moduli in our simulations may result from an overestimation of mechanical stiffness properties at the molecular level, since the modulus of a single collagen molecule was found to form the upper limit of the modulus obtained from experiments (Buehler 2008). When considering the simplifications used to construct our molecular-level model (multiple repeats of 1QSU), it is not surprising to find that we arrived at a modulus that was too stiff. Ninety per cent of our model’s amino acid triplets are Gly–Pro–Pro while only approximately 10 per cent of type I or type II collagen triplets have this sequence. This means that the helical stability of our model is probably much higher than that of the actual collagen molecule. The deeper minima of the model molecule’s energy landscape would be expected to lead to a stiffer response of the model compared with the actual molecule. Recent MD simulations have shown that even small genetically based variations in the amino acid sequence can have a profound effect on the protein’s biomechanical properties (Uzel & Buehler 2009). Furthermore, it is well known that when the prolines are hydroxylated, the secondary structure of each alpha helix while the unmodified prolines form a 10/3 helix (Brodsky & Persikov 2005). Real collagen molecules are thought to have stretches of both types of helices. The transition regions between these two helical forms may well be less tightly wound than the helices on either side. These would provide sections of the molecule with a lower stiffness than the flanking helices. Finally, it is thought that fibril-forming collagenagens have more than a dozen ‘kink’ regions where no helix is clearly defined (Shattuck 1994). These could also provide a softening mechanism for the overall molecule. The incorporation of more molecular-level details into the model might help to resolve the apparent discrepancies between experiment and simulation.

Other potential reasons for our stiffer modelled moduli include the presence of substantially higher deformation rates in simulation compared with experiment, which has been shown to lead to an overestimation of the molecular stiffness by a factor of approximately 1.75 (Gautieri et al. 2009a). Incorporating this effect, the modulus of collagen fibrils approaches a value around 2.9 GPa, closer to the tensile strain experimental results (Gupta et al. 2004; Shen et al. 2008). Furthermore, the computational setup considers perfectly two-dimensional staggered TC molecules, neglecting the influence from the more realistic three-dimensional woven configuration of collagen fibrils and the presence of molecular defects such as kinks and inclusions or free volume that exist in experimental specimens (Misof et al. 1997). Other reasons may include the difference in geometries and boundary conditions between simulation and experiments. For example, the maximum size of the specimen is 3 μm in length and 32 nm in width. While the gauge lengths of measured fibrils are of the same order of magnitude as our model, our maximum fibril width is substantially smaller than any of the experimentally tested fibrils (Gupta et al. 2004; Shen et al. 2008). Based on our results, this latter point is not expected to describe the theoretical/experimental discrepancy since we did not find any strong change in modulus with fibril width.

The yield strain of collagen fibrils is in the range 0.06–0.42 for different cross-link densities and sizes (figure 5), which is of the same order as corresponding experimental results (Shen et al. 2008). The yield strength predicted by the mesoscopic model is beyond 0.4 GPa, falling in the upper range of experimental findings (Shen et al. 2008). This suggests that mechanisms for yield which are at play in the experimental system have not been captured by our model. In our simulation, the yield strength increases when cross-linking density or width of the collagen fibril increases. However, experimental studies (Shen et al. 2008) showed that the yield strain decreases for specimens with larger volume. The experimental observations and the simulation results are not necessarily contradictory since our model ignored the existence of initial defects, which usually increases with volume in real specimens. In addition, the cross-linking density is uniform in the current model, while it could be a distributed function in experimentally tested specimens.

Owing to the complexity of the cross-linking densities and existing defects of real specimens, it is difficult to verify the trends of fracture strains presented in this study using available experimental results. We expect that new experiments will be stimulated to confirm the findings put forth based on the multi-scale simulations reported here. On the other hand, to simulate the mechanical responses of real collagen fibrils, the numerical model needs to be further improved to capture the distribution of cross-linking density and defects and to consider the varying amino acid sequence along the molecular axis. Current efforts are under way to incorporate these effects in molecular modelling (Uzel & Buehler 2009).

5. CONCLUSION

We applied a mesoscopic reactive molecular model to study the responses of collagen fibrils upon uniaxial tension, focusing specifically on the effect of fibril width and length on the mechanical behaviour. Dependence of post-peak behaviour of the stress–strain curve of a finite size relatively short fibril on cross-linking density is consistent with the results obtained previously using
periodic boundary conditions across the width. This study showed, however, that the post-peak stress behaviour is highly dependent on fibril length, width and cross-linking density. These size effects appear to reach asymptotic values in the range of a few tens of molecules in the length and width directions. All fibril-forming collagens produce fibrils that are much longer than this. In addition, most normal type I collagen fibrils are much wider than this. Thus, we would not expect to see length dependence effects in tissue fibrils that possess no defects. However, if the defect distribution in tissue fibrils presents in such a way that the fibrils display stress concentrations over lengths of a few micrometres or less, then the size dependence effects we show are expected to be seen in experimental data. Moreover, non-type I collagen fibrils with diameters of a few tens of molecules are often present in tissues (e.g. type XI/II heterofibrils in cartilage). Thus, it is possible to experimentally measure such thin fibril samples, we would expect strong size effects to govern the mechanical response of collagen fibrils in these tissues. Visualization of the deformation of the finite size collagen fibrils up to fracture, presented here for the first time by using the slip vector approach, demonstrated that the underlying micromechanisms could be explained by extension of and relative sliding between TC molecules. The results were used to construct a simple analytical model and curve-fitting expressions for yield stress, yield strain and fracture strain. Our phenomenological model is expected to be of use to researchers who do not have the resources to implement the full hierarchical model used to fit the functions described in the phenomenological model.

Our study illustrates the use of a multi-scale approach, in which a hierarchy of simulation techniques is used to derive the macroscale constitutive behaviour of collagen fibrils. Future work could also include a study of the effect of structural defects, sequence variations and a more detailed modelling of intermolecular cross-links. Applications of this hierarchical approach could be found in the study of genetic diseases or tissue injuries, where deformation mechanisms and associated mechanical properties are crucial to understand physiologically relevant materials phenomena (Gautieri et al. 2009b).

R.B. and S.J.E. acknowledge support from the National Science Foundation (grant no. 0532320) and the National Institutes of Health (grant no. 1 R21 EB004985-01A1). M.J.B. acknowledges support through a National Science Foundation CAREER award (CMMI-0642545) and the Army Research Office (W911NF-06-1-0291). Y.T. and R.B. acknowledge support from the James L. Record Chair Army Research Office (W911NF-06-1-0291). Y.T. and R.B. also acknowledge support from the James L. Record Chair and the computing resources provided by the Minnesota Supercomputer Institute (MSI).

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