

PROBING THE TWISTED STRUCTURE OF SICKLE HEMOGLOBIN FIBERS VIA PARTICLE SIMULATIONS Lu Lu,¹ Xuejin Li,¹ Peter G. Vekilov,² and George Em Karniadakis¹

Introduction

Sickle cell disease (SCD) is an inherited anemia that arises from a single point mutation, from glutamate to valine, in the hemoglobin molecule. The primary pathophysiological event in SCD is that sickle hemoglobin (HbS) polymerizes into long fibers under deoxygenated conditions. The fibers distort the morphologies of red blood cells (RBCs) and dramatically alter their mechanical and rheological properties.

HbS molecule model

Hemoglobin (Hb) contains two a- and two b-globin subunits. Three types of contacts:

- intra-double-strand axial contacts (blue);
- intra-double-strand lateral contacts (green);
- inter-double-strand contacts (red).



HbS fiber nucleus

In this study we focus on the growth dynamics of HbS molecules and the polymerized structure of HbS polymer fiber, so we assume that a sickle hemoglobin fiber nucleus already exists.



Interactions

- How do two HbS molecules combine to form a molecular contact?
- -Two HbS molecules interact through their patches, which are divided into two types (active and inactive) depending on whether the HbS molecule is attached to a site or not.
- -If an active site and an inactive site come into a close contact, i.e., less than a constant δ , an axial bond is built between the two HbS molecules.

¹Division of Applied Mathematics, Brown University; and ²Departments of Chemical and Biomolecular Engineering and Chemistry, University of Houston



Interactions

- Why is the HbS polymer fiber helically twisted? -Angle-bending potentials between axial vectors \mathbf{p}_i and \mathbf{p}_i , and lateral vectors \mathbf{q}_i and \mathbf{q}_i of two neighboring HbS molecules in the same strand.
- The inter-double-strand contact holds the seven double strands together and stabilizes the HbS polymer fiber. There are three hypotheses for the possible interdouble-strand contact:





Dykes-Rodgers' model

Carragher's model

Simulation method

$$m_i rac{doldsymbol{v}_i}{dt} = -m_i \zeta_i^T oldsymbol{v}_i + oldsymbol{F}_i$$
 $I_i rac{doldsymbol{\omega}_i}{dt} = -I_i \zeta_i^R oldsymbol{\omega}_i + oldsymbol{T}_i$ -

where \boldsymbol{v}_i and $\boldsymbol{\omega}_i$ are center-of-mass linear velocity and angular velocity of particle *i*. F_i and T_i are force and torque exerted on particle i, and ξ_i^T and ξ_i^R are random force and torque, respectively. ζ_i^T and ζ_i^R are friction coefficients.

Formation dynamics of HbS polymer fiber



Dykes-Rodgers' model or Roufberg-Ferrone's model



Roufberg-Ferrone's model

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Roufberg-Ferrone's model

$$+ oldsymbol{\xi}_i^T$$

$$+ oldsymbol{\xi}_i^R$$



the growth rate of HbS fiber

The growth rate j is expected to be a linear function of HbS activity a, which, in turn, is the product of the activity coefficient γ , and HbS concentration $C, a = \gamma C$. The coefficient γ is determined by the volume fraction of all Hb species in the growth medium.

Structural and mechanical properties of HbS polymer fibe

Pitch length $s = \frac{2\pi}{\sum \phi} l \approx 270$ nm



of the HbS fibe

$$\kappa = \frac{k_B T L^3}{3 \langle \delta u(L)^2 \rangle}$$
$$l_p = \frac{\kappa}{k_B T}$$

References

Lu, Lu, et al. "Probing the Twisted Structure of Sickle Hemoglobin Fibers via Particle Simulations." Biophysical journal 110.9 (2016): 2085-2093.







The mean value of ϕ is ~7.4° with a standard derivation (SD) about 3.5°