Abstract Submitted
for the DFD12 Meeting of
The American Physical Society

Skeleton deformation of red blood cells during tank treading motions[1] QIANG ZHU, UC San Diego, ZHANGLI PENG, M.I.T. — By coupling a fluid-structure interaction algorithm with a three-level multiscale structural model, we simulate the tank treading responses of erythrocytes (red blood cells, or RBC) in shear flows. The fluid motion is depicted within the Stokes-flow framework, and is mathematically formulated with the boundary integral equations. The structural model takes into account the flexible connectivity between the lipid bilayer and the protein skeleton as well as the viscoelastic responses. The concentration of this study is on the transient process involving the development of the local area deformation of the protein skeleton. Under the assumption that the protein skeleton is stress-free in the natural biconcave configuration, our simulations indicate the following properties: (1) During tank treading motions it takes long time for significant area deformations to establish. For cells with diminished connectivity between the lipid bilayer and the protein skeleton (e.g. cells with mutations or defects), the relaxation time will be greatly reduced; (2) Deformations of the skeleton depend on the initial orientation of the cell with respect to the incoming flow; (3) The maximum area expansion occurs around the regions corresponding to the dimples in the original biconcave state; (4) Oscillations in cell geometry (breathing) and orientation (e.g. swinging) are observed.

[1] This work was supported by the National Heart, Lung, and Blood Institute under award number R01HL092793.

Qiang Zhu
UC San Diego

Date submitted: 06 Aug 2012 Electronic form version 1.4