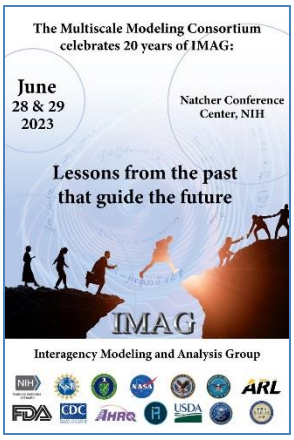

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ABSTRACT FACE PAGE

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DIRECT NUMERICAL SIMULATION OF BLOOD FLOW WITH CELLS IN A PATIENT-SPECIFIC RETINA VASCULAR NETWORK

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BACKGROUND: Blood flow in capillary network is important for delivery of oxygen, water, nutrients, and removal of waste substance. Modeling the blood flow in capillary network is important for both fundamental understanding of the multiphase flow and clinic applications. However, it is challenging because of the complex network structure with branches and loops and deformable cells whose size is comparable to capillary vessel. Previous simulations have modeled blood flow with cell suspensions in physiologically realistic microvascular networks [1] and cancer vascular network [2]. This paper tried to study the transport of cells in the complex vascular network and with stenosis. To the best of authors' knowledge, this is the first time to simulate blood cell transport in a patient-specific vascular network with stenosis [3].

METHODS: The flow in a patient-specific retina capillary network was simulated by the lattice Boltzmann method (LBM) coupled with particle-based cell membrane models[4] through the immersed boundary method[5]. The flow solver was based on open source code Palabos[6] and the cell membrane model was implemented in LAMMPS[7]. The patient-specific geometry of the retina network was obtained from National Institute of Health (NIH) 3D print database. The model had 81,095,168 lattices among which 13,658,289 (about 16.8%) were fluid nodes with a lattice size of 400 nm. There were 1,466,863 vessel wall particles, and 2,432,760 membrane particles for 1,843 red blood cells (RBCs), with a hematocrit of 18.4%. The Reynolds number defined with RBC diameter and the maximum flow velocity was 0.0052.

RESULTS: The overall simulation is shown in Fig. 1(c). The complex retina geometry and bifurcations can lead to cells temporarily being stuck at the vessel wall near flow stagnation regions, as seen in Fig. 1(a). The size of the blockage varied over time and eventually stabilized during the simulation. At its largest, the local flow was significantly reduced at the bifurcation region, as shown in Fig. 1(b). In addition, RBC transport in the network with a 50% stenosis in one blood vessel was simulated, as shown in Fig. 1(d). Interestingly, oscillatory flow was observed in an adjacent vessel near the stenosis. The cells oscillating in the vessel were shown in different colors in the dashed box in Fig. 1(d) with a time history for the center of mass plotted in Fig. 1(e).

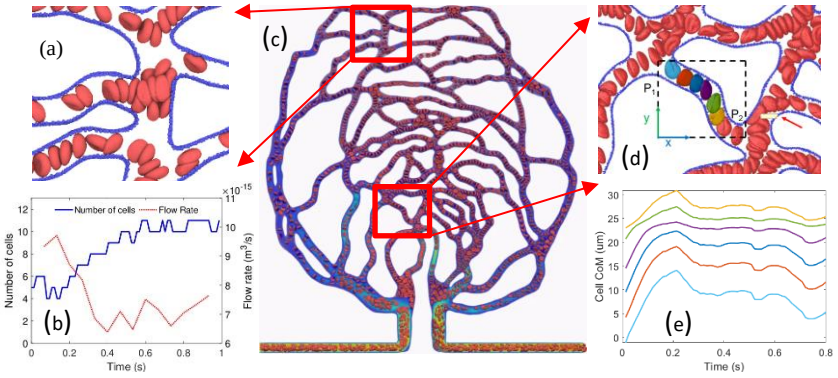

Figure 1. (a) the accumulation of cells in the T-junction of the retina network; (b) the growth of cell accumulation and decrease of flow rate at the T-junction; (c) the overview of the simulation in the retina network; (d) cells trapped and oscillating in one blood vessel; (e) the time history of the center of mass (CoM) of the oscillating cells.

CONCLUSIONS: Blood flow simulation showed interesting behaviors in capillaries. Cells can accumulate in a T-shaped bifurcation and oscillate in an adjacent blood vessel to stenosis. Direct simulation of blood flow with cell suspensions can provide more insights on the flow physics and explain events such as dynamic stalling in capillary pathologies.

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