

# INFLUENCE OF IDEALIZED VERSUS MEASURED VELOCITY PROFILES ON MASS TRANSFER IN CFD MODELS OF THORACIC AORTA

Giuseppe De Nisco (1), Peng Zhang (2), Gianpaolo Usala (1), Diego Gallo (1), Xiao Liu (2), Xiaoyan Deng (2), Giovanna Rizzo (3), Umberto Morbiducci (1)

1. Politecnico di Torino, Italy; 2. Beihang University, China; 3. IBFM-CNR, Italy

## Introduction

Hemodynamics plays an important role in the mass transport and, as a consequence, in the localization of vascular disease in areas of complex flow. In particular, the occurrence of low density lipoproteins (LDL) concentration polarization in the arterial system can affect the deposition of atherogenic particles at the luminal surface, increasing the risk of the atherogenesis [1]. In this study we analyze the influence of different possible strategies of applying PC-MRI measured data as boundary conditions (BCs) to confidently model LDL transport in image-based hemodynamic models of human aorta. The study here presented would contribute to clarify which is the impact of applied at inflow BCs on aortic LDL transport.

## Methods

The geometry of an ostensibly healthy human aorta was reconstructed from 4D PC-MRI images. PC-MRI slices were used to generate the model of aorta from PC-MRI data [2],[3]. The finite volume method was applied to perform numerical simulations under steady flow conditions. Steady state LDL transport in flowing blood was described by the convective-diffusion equation for the LDL concentration  $C$ :

$$u \cdot \nabla C - D_L \nabla^2 C = 0 \quad (1)$$

where  $u$  is the velocity vector and  $D_L$  is the diffusivity of LDL in flowing blood [1]. Steady-state flow simulations were carried by applying conditions at boundaries as measured at three different phases of the cardiac cycle: acceleration phase, systolic peak and deceleration phase (Figure 1), for a total number of nine simulations. Three different inflow conditions were applied at the inlet of the ascending aorta, for each considered instant of cardiac cycle: (1) PC-MRI measured 3D velocity profile; (2) PC-MRI measured 1D velocity profile, obtained considering the axial component of measured velocity; (3) idealized flat velocity profile, with velocity magnitude computed by averaging 1D velocity profile [3]. LDL transport in the aortic arch was computed for the three inflow condition cases and the impact of the choice of idealized rather than measured velocity profiles as inflow BCs was investigated focusing on LDL transfer to aortic wall.

## Results

As main result, we report the LDL wall concentration in aorta, normalized with respect to the initial LDL concentration  $C_0$  at the aortic inlet section. Figure 1 presents the LDL accumulation profiles at the luminal

surface obtained by imposing in silico (FLAT case) and in vivo (1D and 3D cases) velocity profiles as inflow BCs for the three simulated phases of the cardiac cycle. The surface area subjected to elevated LDL accumulation is markedly wider than the 3D and 1D cases, when flat velocity profile is prescribed at the aortic inflow section. The FLAT case presents three luminal regions at the aortic arch subjected to severe polarization of LDL, more evident during the acceleration phase of the cardiac cycle (inner lateral edge of the brachiocephalic artery, intrados of the ascending aorta and inner wall of the descending aorta), as in previous studies. Results obtained for 3D and 1D cases show a more uniform LDL distributions at the wall along the aortic arch.

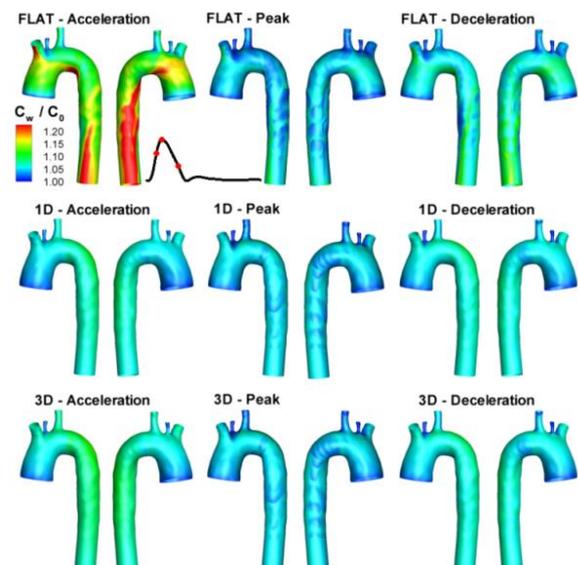


Figure 1: Comparison of the normalized LDL concentrations at the luminal surface for the simulated inflow boundary conditions.

## Discussion

The findings of this study show that the imposition of idealized velocity profile as inlet BCs in subject-specific computational hemodynamics models of mass transport in the human aorta could largely affect the location and extension of regions of LDL polarization at the luminal surface. This finding needs to be confirmed in unsteady-state simulations.

## References

1. Chen et al, *J Biomech*, 47: 544-552, 2014.
2. Gallo et al, *Ann Biomed Eng*, 40(3): 729-741, 2012.
3. Morbiducci et al, *J Biomech*, 46(1): 102-109, 2013.

