ABSTRACT

Adaptation to chronic hypoxia provides myocardial protection against ischemia – reperfusion injury (IR). Cardioprotective effect of adaptation depends on the degree and duration of hypoxic exposure and daily regime of adaptation. Certain protective regimes of adaptations to hypoxia have been reported to activate proapoptotic signaling pathways and bioactive sphingolipids were recently shown to play important role in the regulation of apoptosis in the heart. We aimed to determine the mRNA level of selected genes related to apoptotic pathways and to sphingolipid metabolism in two models of hypoxic adaptation, continous normobaric hypoxia (CNH 10% O_2) with different exposures (4h, 48h, 120h, 21days) and intermitent hypobaric hypoxia (IHH 7000 m, 8h/day). Both ventricles, LV and RV, were analysed after adaptation to CNH and only LV was analysed after IHH adaptation. Our results show that both types of adaptation increased mRNA of proapoptotic genes, CNH mainly in RV and IHH in LV. Furthermore, increased expressions of proapoptotic genes were accompanied by the increase of expression of enzymes producing predominantly protective kinds of sphingolipids. The exact role of apoptosis and sphingolipid signaling molecules in endogenous myocardial protection requires further research.

Key words: Apoptosis, Sphingolipids, Hypoxia, Myocardium, Real time PCR, BioMark HD System (Fludigm), Light Cycler 480 (Roche)