lipid-lowering treatments. Coronary artery bypass grafting (CABG) is commonly used to bypass coronary arteries diseased by atherosclerosis, routinely using the saphenous vein (SV) as a conduit. Early after grafting the SV adapts to the arterial environment through endothelialisation, and increased motility of smooth muscle cells (SMC). A clinical association between Lp(a) and coronary artery disease is evident; however, its role in vein graft failure is less clear. Endothelial cells (EC) and SMC were cultured from the SV of patients undergoing CABG. The influence of apo(a) on cellular activity was examined by proliferation (cell counting), chemotaxis (modified Boyden chamber) and chemokinesis (scratch wound) assays. Apo(a) significantly inhibited SV-EC proliferation (n=9, p<0.001). Although no effect on SV-SMC proliferation was apparent, apo(a) markedly modulated SMC motility and appeared to act as a chemorepellent. When SMC were acutely exposed to a gradient of apo(a), they consistently migrated away from the source (n=6, p<0.01). Chronic exposure to apo(a) in the scratch wound model also revealed that the speed of migration was reduced (n=5, p<0.01). Remodelling of the SV is essential for adaptation to an arterial environment, and key to its function as a successful bypass graft. Our studies show that apo(a) inhibits EC proliferation, potentially compromising endothelial repair in the grafted vein. Furthermore, the chemorepellent effect of apo(a) may also impede critical SMC migration required for effective integration. Lp(a) is therefore likely to contribute to impaired SV adaptation and inferior graft patency.

**Rationale**

Our previous studies have developed an efficient method for producing a large number of smooth muscle cells (SMCs) from embryonic stem (ES) cells. However, little is known about the underlying mechanism.

**Methodology and results**

Nuclear proteins were harvested and isolated from undifferentiated and differentiating ES cells at different time points, and subjected to proteomics analysis. Notably, the majority of upregulated nuclear proteins during SMC differentiation were differentiation markers, while enforced expression of this gene and RNA processing processes. We further focused on chromobox upregulated nuclear proteins during SMC differentiation were subjected to proteomics analysis. Notably, the majority of points, and subjected to proteomics analysis. Notably, the combination of the proteomic and transcriptomic datasets improved the statistical confidence of the pathway analysis by two orders of magnitude, with HIF—hypoxia—Akt signalling and glycolysis being the most significant.

**Conclusions**

We demonstrate how combining different ‘omics’ datasets aids in the identification of key biological pathways: chronic hypoxia resulted in a pronounced adaptive response at the transcript and the protein level to keep metabolite levels steady. This preservation of metabolic homeostasis is likely to contribute to the long-term survival of the hibernating myocardium.