Gene	Hibernating LAD/normal

	3 Months	5 Months
Collagen Type I	2.8 ± 0.7*	1.3 ± 0.2†
Collagen Type III	2.2 ± 0.5*	1.4 ±0.2
Collagen Type VI	1.5 ± 0.2*	0.9 ± 0.1†
Fibronectin	4.9 ± 2.7*	1.3 ± 0.2
Vimentin	1.8 ± 0.3*	1.2 ± 0.1†
GAPDH	0.9 ± 0.2	0.9 ± 0.1

*LAD vs. normal p<0.05; mean ± SEM

† 5 vs. 3 Months p< 0.05, Statistical Analysis of Microarray

1136-85 **Ischemic Preconditioning Increases Heat Shock Protein-72 Protein Expression and Reduces Elevation of Creatine Kinase-MB Following Coronary Artery Bypass Graft in Humans**

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Background: Ischemic preconditioning, ie, the reduction of infarct size development during prolonged and severe myocardial ischemia by one or more preceding short episodes of ischemia and reperfusion, is the most powerful endogenous cardioprotective effect. We investigated whether a stress activated signal-transduction via heat shock protein 72 (HSP-72) mediated phopshorylation of p38 Mitogen activated protein kinase (MAPK) is involved in the creatine kinase-MB (CKMB) release reducing effect of ischemic preconditioning in patients undergoing CABG.
Methods: According to the ischemic episodes within 24-48 hours before CABG patients with angina CCS III or IV were classified as preconditioned (IP, n=9), whereas patients with angina CCS I or II formed the control group (CON, n=10). The effect of IP on the CABG induced maximal CKMB-release was examined. Biopsies from ischemic and control regions in each patient were processed to analyse protein expression of HSP-72 and the calcium handling proteins phospholamban (PL), sarcoendoplasmic Ca-ATPase 2a (SERCA), calsequestrin (CSQ), the inhibitory subunit of troponin (TnI) and phosphorylation of MAPK.
Results: IP reduced CKMB (18.7±1.3 vs. 13.8±1.5 U/L, CON vs. IP, mean±SD, p=0.02). Results of biopsy specimens are depicted in table 1 (relative changes of *protein expression and #MAPK-phosphorylation).
Conclusion: Cardioprotection during CABG can be improved with IP. Possible mechanisms are the induced expression of HSP-72 and/or SERCA.

Table 1: Biopsy specimens

mean±SD	PL*	SERCA*	CSQ*	TnI*	HSP-72*	MAPK#
CON	0.24±0.12	-0.26±0.07	-0.09±0.04	-0.12±0.07	0.09±0.12	0.05±0.28
IP	0.06±0.35	0.33±0.19	-0.02±0.07	0.12±0.18	0.44±0.11	0.84±0.43
t-test: P	0.626	0.008	0.354	0.212	0.045	0.141

1136-86 **Protein Kinase C Epsilon Is Upstream and Protein Kinase C Alpha Is Downstream of MitoKATP Channels in the Signaling of Ischemic Preconditioning in the Human Myocardium**

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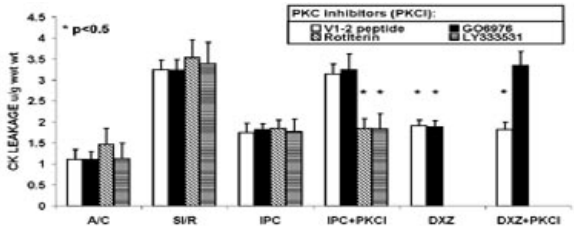
Background: PKC is part of the signal transduction of ischemic preconditioning (IPC) but the PKC isoforms involved and their relation to mitoK_{ATP} channels is unclear. **Methods:** Right atrial muscles from patients undergoing cardiac surgery were sectioned and after equilibration were randomized to receive one of the following protocols: aerobic control (A/C), simulated ischemia for 90 min and reoxygenation for 120 min (SI/R), IPC using 5 min SI/ 5 min R and the following inhibitors were added 10 min before and during IPC: V1-2 peptide [10 μM], GO6976 [100 nM], Rottlerin [100 μM], and LY333531 [100 nM] for PKCε, α, δ, β respectively. To investigate the location of the PKC isoforms involved in IPC in relation to mitoK_{ATP} channels, PKC α and ε inhibitors were added 10 min before and during preconditioning by Diazoxide (DXZ)[100 μM] in a second experiment. CK leakage and MTT cell viability were measured. Phosphorylation of PKC isoforms were measured using immunoblots after treatment with IPC or DXZ. **Results:** In Fig, PKCε and α inhibitors blocked IPC whereas PKCδ and β inhibitor did not. The protection elicited by mitoK_{ATP} channels opening with DXZ was blocked by the inhibition by PKCα but not by inhibition of PKCε isoforms. The MTT values mirrored the CK results. In addition, DXZ caused increased phosphorylation of PKCα similar to IPC but failed to cause significant increase of PKCε phosphorylation. **Conclusion:** Both PKCε and α are involved in IPC of the human myocardium with PKCε upstream and PKCα downstream of mitoK_{ATP} channels.



1136-87 **Remote Preconditioning by Infrarenal Occlusion of the Aorta Protects the Rat Heart From Infarction by a Molecular Mechanism Involving Free Radicals and a p38 Mitogen Activated Protein Kinase Activation**

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Background: Ischemic preconditioning (PC) is a powerful mechanism in reducing the infarct size of the heart. Protection can be provided either by an ischemic stimulus of the heart itself (classical or orthotopic PC) or by ischemia of an organ distant to the heart (remote or heterotopic PC).
Objective and methods: To address the question whether remote PC is dependent on endogenously released free radicals and/or on an activation of p38 MAPK, infarct size was determined in an in situ model of infrarenal occlusion of the aorta (IOA) in the rat after pharmacological inhibition of free radicals or p38 MAPK.
Results: Control hearts (30 min regional ischemia followed by 30 min of reperfusion) had an infarct size of 50±2%, whereas classical PC with one ischemia/reperfusion cycle (I/R) reduced it to 21±4% and with three I/R cycles to 14±1% of the risk zone (p<0.001). 15 min IOA followed by a 10 min reperfusion period reduced the infarct size to 20±3% (p<0.001 vs. control; p=0.051 vs. PC three I/R cycles).
20 mg/kg body weight MPG, a free radical scavenger, completely blocked the protection obtained by IOA (46±3%, p<0.001 vs. IOA no MPG) as well as the one obtained by classical PC with one I/R cycle (43±4%, p<0.01 vs. PC one I/R cycle no MPG). Protection of classical PC with three I/R cycles could, however, not be blocked (13±4%). MPG itself had no influence on infarct size in control hearts (53±5%).
Using SB203580, a selective p38 MAPK-inhibitor, at a dose of 2 mg/kg body weight, protection by remote PC was blocked (46±3%, p<0.001 vs. IOA no SB) as well as by classical PC with three I/R cycles (42±4%, p<0.001 vs. PC no SB). Again SB itself had no influence on infarct size in control hearts (47±3%).
Conclusion: Protection of the heart by heterotopic PC using IOA is nearly as powerful as orthotopic preconditioning. Both protection methods share as common elements in their signal transduction pathways free radicals and p38 MAPK. Since orthotopic PC by one I/R cycle but not by three I/R cycles could be blocked by MPG, protection by orthotopic PC is more robust than protection by heterotopic PC. The protecting substances, which are located upstream of p38 MAPK, could be free radicals but remain to be characterized further.

1136-88 **The Polymorphisms C (-260) T in the Promoter Region of CD14 Receptor Gene and G (-174) C of Interleukin-6 Gene Are Not Related to the Immune Response to Chlamydia Pneumoniae Infection and Heat Shock Protein-60 in Ischaemic Heart Disease**

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Background: The conflicting results on the role of Chlamydia pneumoniae (Cp) in ischaemic heart disease might be related to modulation of individual response to Cp-infection by genetic polymorphisms. The CD14 membrane receptor is a mediator for monocyte activation by bacterial products, as lypopolysaccharide and Chlamydial Heat Shock Protein 60 (HSP60Cp). Interleukin 6 is a pro-inflammatory cytokine stimulating B-lymphocytes differentiation and antibody production. The aim of this study was to evaluate if two functional genetic polymorphisms, the C (-260) T polymorphism in the promoter region of the CD14 receptor gene and the G (-174) C polymorphism of interleukin 6 gene, are related to immune response to Cp in patients with IHD. Methods: we studied 51 patients with IHD. In all patients we measured serum levels of Antibody anti-HSP60Cp (AbHSP60) (ELISA) and IgG anti Cp. The polymorphisms C (-260) T of CD14 receptor gene and G (-174) C of Interleukin 6 gene were detected by polymerase chain reaction and restriction analysis. Results: We did not find significant differences in AbHSP60 serum SD) among the C (-260) T polymorphisms of the CD14 receptor ± levels (AU; mean 0.42, 0.63 ± gene: CC homozygotes, CT heterozygotes, and TT homozygotes (0.66 0.46, respectively; p=ns). No differences were also found among the ± 0.37, 0.77 ± three genotypes of G (-174) C Interleukin 6 gene polymorphism: GG homozygotes, 0.37, ± 0.42, 0.58 ± 0.37, 0.74 ± GC heterozygotes and CC homozygotes (0.62 respectively; p=ns). IgG anti Cp levels (median, range), were not significantly different between the three genotypes of C (-260) T CD14 receptor gene polymorphism, CC homozygotes, CT heterozygotes and TT homozygotes (24, 0-128; 48, 0-256; 8, 0-32, respectively; p=ns) and between the three genotypes of G (-174) C Interleukin 6 gene polymorphism: GG