177
NT-proBNP DIFFERENT SECRETORY PATTERNS IN MYOCARDIAL INFARCTION

S. Ferraro[1], A. Lupi[1], G. Marano[2], C. Vendramin[3], L. Rossi [1], L. Ciardi[3], G. Bellomo[3], E. Biganzoli[2], A.S. Bongo[1]

[1]*SCDO Cardiologia 2, AOU Maggiore della Carità, Novara*

[2]*Istituto di Statistica Medica e Biometria, Università degli Studi di Milano*

[3]*SCDU Laboratorio Ricerche Chimico Cliniche, AOU Maggiore della Carità, Novara*

Aim. In myocardial infarction(MI) NT-proBNP represents a reliable prognostic tool despite high variability. Study aim was to investigate in MI, the dependence of NT-proBNP levels at admission, from sympathetic activation and glomerular impairment, assessed respectively by Chromogranin A (CgA) and Cystatin C(CC) measurements; moreover we compared BNP/NT-proBNP kinetics.
Methods. We enrolled 132 patients, 90 ST elevated acute coronary syndroms (STE-ACS) and 42 non ST ACS (NSTE-ACS), admitted within 24h from symptoms with creatinine levels lower than 1.6mg/dl. In all patients NT-proBNP (DPC), CgA (CIS-BIO), CC (Dade-Bohering) were measured. In 33 STE-ACS patients, at admission and in the following 6h, 24h and 48h, the contemporary kinetics of NT-proBNP, BNP and hsTn I were evaluated. A multiple regression model was used to investigate the dependence of NT-proBNP levels from CgA, CC, time from the onset of symptoms, ACS subsets (STE-ACS/ NSTE-ACS) and gender, adjusting for the effect of LVEF and age. An analysis of interactions was performed.
Results. NT-proBNP levels showed a positive asymmetric distribution even after logarithmic conversion. NT-proBNP levels were higher in NSTE-ACS with a longer time from symptom onset. From multiple regression analysis, evidence was found of two interactions involving ACS subsets: the first with CgA levels and the second with age. The first proved the inversion of the secretory pattern of NT-proBNP in STE-ACS vs NSTE-ACS. This could be linked to the characteristic of the marker, stored in secretory vesicles, and to the different sympathetic activation in the two groups. From the second interaction, only in STE-ACS the effect of age on NT-proBNP secretion followed an increasing curve. The time release curves showed for both natriuretic peptides a rising within 11h from symptoms, NT-proBNP peaked later than 48hs, BNP within 29hs and hsTn I within 11hs.
Discussion. Our data showed in this MI population that only sympathetic activation but not glomerular impairment could affect NT-proBNP secretion yielding different secretory patterns in STE/NSTE-ACS. Furthermore the time elapsed from symptoms, carries a critical role on NT-proBNP evaluation.
Reference
Hall C. NT-proBNP: The Mechanism Behind the Marker. J Card Fail 2005;11(S):S81-S83.

178
REAL TIME PCR EVALUATION FOR C-TYPE NATRIURETIC PEPTIDE AND FOR ITS SPECIFIC RECEPTOR, NPR-B IN CARDIAC TISSUE OF NORMAL AND CHRONIC HEART FAILURE ANIMALS

S. Del Ry[1], M. Cabiati[2], V. Lionetti[2], M. Emdin[1], F. Recchia[2], D. Giannessi[1]

[1]*CNR Institute of Clinical Physiology and G. Monasterio Fondation Pisa, Italy*

[2]*Scuola Superiore Sant'Anna, Pisa, Italy*

Background. C-type natriuretic peptide (CNP) was recently found in the myocardium, but possible differences between atrium and ventricle production are so far lacking.
Aim. To evaluate the expression of transcripts coding for CNP and for its specific receptor, NPR-B, in cardiac tissue (right and left atrium and ventricle) of normal and HF animals.
Methods. Cardiac tissue was collected from male adult minipigs without (control, n=5) and with pacing-induced HF (n=5). HF was induced by rapid pacing (180 beats/min) for 3 weeks. mRNA was extracted with the method of phenol/guanidine-thiocyanate/chloroform. The expression of mRNA coding for CNP and NPR-B was determined in myocardial tissue (n=40) by Real Time-PCR with DDCt method. As overall control, a parallel Real Time-PCR assay for BNP mRNA expression was carried out in the same samples.
Results. CNP gene expression was observed in controls and at 3 weeks of pacing resulting lower than that of BNP (left ventricle: p=0.05 controls vs. HF). As expected, BNP gene expression in all the cardiac chambers resulted higher after 3 weeks of pacing compared to normal heart (right atrium and left ventricle: p=0.003 controls vs. HF). Moreover, BNP mRNA expression was higher in atrium than in ventricle. We also observed higher, but not significantly, levels of CNP mRNA expression between normal and HF animals in all chambers. The NPR-B resulted to be expressed in all cardiac regions analyzed, and a down-regulation was observed in ventricles after HF (right ventricle p=0.001 controls vs. HF).
Conclusions. In the present study, we provided the first evidence of CNP and NPR-B expression in tissue from normal and HF. The increased myocardial CNP synthesis was associated to the NPR-B down regulation in HF. The co-localization of the CNP system and its specific receptor suggests a possible role of this peptide in a complex pathology such as HF and the present results may prompt novel therapeutical strategies targeting NPR-B.
Reference
Kalra PR et al. Myocardial production of C-type natriuretic peptide in chronic heart failure. Circulation 2003;107:571-3.