P4732 : Pharmacogenetically determined treatment' influence on Left Ventricular Mass Index (LVMI) in relation to polymorphisms of ACE, AGTR1, eNOS, PPAR-G2, ADRB1 genes in essential hypertensive (EAH) patient

Authors:
L. Sydorchuk (Bukovinian State Medical University, Chernivtsi /Ukraine), **K. Amosova** (National State Medical University, Kiev /Ukraine), **R. Sydorchuk** (Bukovinian State Medical University, Chernivtsi /Ukraine), **J. Ursuliak** (Bukovinian State Medical University, Chernivtsi /Ukraine), **I. Sydorchuk** (Bukovinian State Medical University, Chernivtsi /Ukraine)

Topic(s):
Haemodynamics, heart and hypertension

Citation:
European Heart Journal (2010) 31 (Abstract Supplement), 820-821

Purpose: To evaluate LVMI changes in EAH patients under the treatment depending on I/D polymorphism in ACE gene, A1166C in AGTR1 gene, T894G in eNOS gene, Pro12Ala in PPAR-G2, Arg389Gly in ADRB1 gene.

Methods: 249 patients (EAH I – 26.5%; EAH II – 45.8%; EAH III – 27.7%; women – 48.2%, men – 51.8%, age 50.5±10.4) underwent pharmacogenetic therapy (hydrochlorothiazide (HCTZ)+angiotensin II receptor (ARB) blocker), HCTZ+beta1-blockers (BB), HCTZ+ACE inhibitor (ACEI), calcium antagonists (CA)+ARB, CA+BB, CA+ACEI). Left ventricular mass index (LVMI) and wall thickness/radius ratio (T/R) were detected with EchoCG. Efficacy criteria: ESC/ESH 2007.

Results: The number of patients with target LVMI and T/R increased by 8.0% and 6.0% ($p \leq .005$). HCTZ+ARB lead to growth of target LVMI and T/R patients' number by 6.7% ($p=.038$) and 11.6% ($p>.05$): reliable only in II (ACE) carriers ($p=.034$). HCTZ+BB caused normal LVMI increase by 8.8% ($p=.035$) reliable only in I/D-genotype (ACE), target T/R ratio increased by 5.6%: significantly in I/D-genotype (ACE) ($p=.003$), A-allele (AGTR1) ($p=.046$-$.026$) and ProPro-genotype (PPAR-G2) ($p=.026$). HCTZ+ACEI didn't influence target LVMI and T/R share ($p>.05$). CA+ARB are better according to "target" LVMI and T/R, than combinations with HCTZ ($p<.05$). Target LVMI and T/R patients' number increased by 13.3% ($p<.001$) and 6.7% ($p<.01$), accordingly: authentically in DD (ACE) ($p<.001$), AA (AGTR1) ($p=.024$), ArgArg (ADRB1) ($p=.024$-0.052) and TG (eNOS) ($p=.002$). CA+BB lead to normal LVMI patients' increase by 20.0% ($p<.001$), less target T/R – by 6.7% ($p<.01$): reliable in DD (ACE) ($p<.001$), AA (AGTR1) ($p=.002$), GG (eNOS) ($p<.002$), ProPro (PPAR-G2) ($p<.001$) and ArgGly (ADRB1) ($p<.001$) EAH patients. CA+ACEI caused target LVMI patients' amount increase by 7.4% (reliable in DD (ACE), $p=.007$, TT (eNOS), $p=.009$, CC (AGTR1), ProAla (PPAR-G2) and GlyGly (ADRB1), $p \leq .044$), without authentic changes of T/R threshold patients number. In generall, after the number of patients with normal LV myocardium geometry increased by 6.6% ($p=.002$): reliable in II (ACE), $p=.02$, AlaAla (PPAR-G2) and GlyGly (ADRB1) ($p<.001$). The number of patients with hypertrophic LV models decreased towards concentric remodeling ($p \leq .046$-$.001$).

Conclusions: Pharmacogenetic treatment with CA combinations in EAH patients – DD-genotype (ACE gene) carriers caused more effective decrease of LVMI and T/R ratio, than treatment of I-allele carriers (ACE) with HCTZ combo ($p<.05$), without reliable differences (after drugs combinations) on polymorphisms of AGTR1 (A1166C), eNOS (T894G), PPAR-G2 (Pro12Ala) and ADRB1 (Arg389Gly) genes.