**ASSOCIATION OF H558R POLYMORPHISM IN SCN5A GENE WITH FAMILIAL DILATED CARDIOMYOPATHY**

C. Mazzaccara[1], A. Fusco[2], A. Redi[2], D. Bonaduce[3], G. Limongelli[4], F. Salvatore[5], G. Frisso[1]

[1]*CEINGE-Biotecnologie Avanzate s.c.ar.l., Napoli, Italia; Dip. di Medicina Molecolare e Biotecnologie Mediche, Università Federico II, Napoli, Italia*

[2]*Dip. di Medicina Molecolare e Biotecnologie Mediche, Università Federico II, Napoli, Italia*

[3]*Dip. di Scienze Mediche Traslazionali, Università Federico II, Napoli, Italia*

[4]*U.O.C. di Cardiologia A.O. Monaldi, Seconda Università degli Studi di Napoli, Napoli, Italia*

[5]*CEINGE-Biotecnologie Avanzate s.c.ar.l., Napoli, Italia; IRCCS – Fondazione SDN, Napoli, Italia*

Dilated cardiomyopathy (DCM) is a cardiomyopathy caused, frequently, by ischemic heart disease. Less common causes include structural heart disease, inflammation, infections and genetically-mediated forms (i.e. familial DCM; FDC) [Fazio G. Open Medicine 2014].

Approximately 40-50% of DCM cases are classified as Idiopathic Dilated Cardiomyopathy (IDC), after detectable causes have been excluded. Up to 35% of IDC has a genetic basis. To date several genes have been identified associated to DCM, among which SCN5A gene, encoding the cardiac sodium channel $\alpha$ subunit. The SNP rs1805124 (c.1673A>G; p.H558R) in SCN5A gene is associated with different cardiac disorders. However no studies have evaluated the prevalence of rs1805124 in DCM patients.

We examined the association between the rs1805124 and the risk of DCM in 185 DCM cases and 251 age and sex matched controls. By family history screening and by evidence of coronary artery disease and/or myocardial infarction, we identified 56/185 FDC and 50/185 post-ischemic patients (pi-DC) respectively. Seventy-nine IDC patients, were also recognized according the known criteria. We valuated the allele and genotype frequencies of rs1805124, in FDC, IDC, pi-DC patients and controls and their association with DCM risk.

In FDC (OR=7.39, 95% CI=2.88-18.96; p<0.0001) and DCM (OR=2.78, 95% CI=1.26-6.13; p=0.011) patients, the GG genotype was associated with increased risk of disease compared to the AA genotype.

When we pooled the FDC and the IDC patients in the single ni-DC group, the association was still significant (OR=2.73, 95% CI=1.70-8.55; p=0.001), instead no difference was found comparing rs1805124 genotype frequencies in the pi-DC and IDC patients vs controls.

Moreover logistic regression analysis, showed that GG carriers had a higher risk of DCM than AA + AG carriers, particularly in FDC subjects (OR=5.45, 95% CI=2.23-13.35; p<0.001) and ni-DC group (OR=3.14, 95% CI=1.43-6.92; p=0.006) but also in the whole DCM population (OR 2.21, CI=1.0-4.83; p=0.05. These results indicate that the GG genotype was significantly associated with DCM risk in non ischemic dilated cardiomyopathy, and particularly in familial cases. Further studies are needed to replicate our results in other ethnic groups with larger sample size.