Lipoprotein-Associated Phospholipase A2 Mass and Activity and PLA2G7 Gene Polymorphisms as Markers for Cardiovascular Risk Stratification In High Risk Coronary Artery Disease Patients

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Background:
Lipoprotein-associated phospholipase A2 (Lp-PLA2), which is secreted by different cell types (e.g. monocytes, macrophages and T lymphocytes) and in plasma is associated with low-density lipoprotein (LDL). As it remains controversial if Lp-PLA2 it plays a pathogenic role in atherogenesis we aimed at testing the hypothesis that the PLA2G7 gene Arg92His SNP predicts cardiovascular (CV) events.

Methods:
The titer of Lp-PLA2 was measured in 749 randomly selected Caucasian patients of the GENICA Study, who underwent coronary angiography and has been followed-up for incident CV events. Patients were classified including the last and the first three quartiles, respectively by Lp-pLA2 and after we determined the best cut-off value in predicting CV deaths and MACE with ROC curves and into a high and a low titer group. Patients were grouped in two groups, assuming the effect of the His92Arg mutant allele to be dominant (AA and AG vs. GG). Propensity score matching analysis was used to compare the two groups for CV event-free survival.

Results:
Patients in the high Lp-PLA2 activity group again showed a significantly worse CV events-free survival (33.3% vs. 20.5%, respectively, p=0.023) than those in the low Lp-PLA2 activity group. Patients carrying the mutant allele showed a better ACS-free survival (88.3% vs. 78.6%, respectively, p = 0.043) and AMI-free survival (94.4% vs. 82.6%, respectively, p = 0.003) compared to the patients with a homozygous wild type genotype.

Conclusions:
The analysis performed to correct for the imbalance of variables distribution confirm the role of Lp-PLA2 activity in CV events-free survival. Our study demonstrates for the first time in a prospective cohort High-risk Caucasian patients referred for coronary angiography carrying the His92Arg mutant allele have a better CV prognosis.