number of reported events. Implementation of preventive measures, such as universal precaution measures and HBV vaccination results a significant reduction in the incidence of HBV infection among healthcare workers. In many countries, the number of healthcare workers that underwent HBV vaccination usually does not exceed 65%, indicating that HBV vaccination is not applied in a sufficient number of healthcare workers.

P14-09

Trends in antibiotics prescribed for bacterial pneumonia with higher CRP in preschool children

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Objective: To estimate the incidence rates of preschool children outpatient bacterial pneumonia, examine time trends in antibiotics prescribed for bacterial pneumonia with higher CRP, and determine factors associated with broad-spectrum antibiotic prescribing for pneumonia in this population.

Materials and methods: The material consists of 902 small preschool Bosnians children aged 6 months to 6 years or half year more who took part in this retrospective study in pediatrics settings in six municipalities from nine municipalities of Canton Sarajevo. Within 72 or 96 hours after establition of diagnosis and beginning of antibiotics therapy blood samples CRP were taken for first and control analysis.

Results: The four most commonly prescribed antibiotic classes for bacterial pneumonia in preschool children were cephalosporins, macrolides, penicillins and aminoglycoside antibiotics. Cephalosporins were most commonly prescribed, ranging from 33.3% to 44.5% of all antibiotics prescribed for pneumonia in ages from 6 months to 6 years. Macrolides were the second most commonly prescribed antibiotic, ranging from 22.5% to 35.3% of all antibiotics prescribed for this diseases. There was no statistical difference in serum CRP values among the four groups with pneumonia after antibiotics therapy.

Conclusions: A strong association has been found between the level of circulating C-reactive protein (CRP) and the severity of pneumonia and success of antibiotics therapy in control laboratory data after three or four days in outpatients conditions .

P15 - Molecular diagnosis 1

P15-01

The association of postprandial triglycerides with hsCRP, TAS, ICAM-1 and APOA5 and HL gene variants

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Background: Several authors have reported the association of postprandial hypertriglyceridemia with oxidative stress, systemic inflammation and endothelial dysfunction. Our aim was to investigate the effect of postprandial hypertriglyceridemia on oxidative stress and endothelial dysfunction. We also assessed the association of APOA5 -1131T/C and -250G/A hepatic lipase polymorphisms with different response to the high-calorie meal in the group of healthy middle aged male individuals.

Materials and methods: We recruited 102 healthy male volunteers (52-68 years). All participants con-

sumed a high-calorie meal (800 calories, 50 g fat, 28 g protein, 60 g carbohydrates). Blood samples were drawn at 8 a.m., after an overnight fast and 3 hours after the meal. Glucose, total cholesterol, triglycerides, HDL-cholesterol, LDL-cholesterol, bilirubin, uric acid, hsCRP, TAS and ICAM-1 were measured at fasting state and postprandially. APOA5 -1131T/C and -250G/A hepatic lipase promoter genetic polymorphisms were determined for all participants.

Results: Postprandial triglycerides were significantly increased (1.4 (1.1 - 2.1) *vs*. 2.4 (1.9 - 3.3) mmol/L, $P < 0.001$). Average triglyceride increase was 1.0 ± 0.7 mmol/L (65%). Although concentrations of triglycerides, HDL-cholesterol, LDL-cholesterol, TAS and ICAM-1 differed significantly between fasting state and postprandial measurements ($P < 0.001$), differences were within the limits of analytical imprecision and are not considered as clinically relevant. Other parameters did not change 3 hours after the meal. Triglycerides response did not differ respective to the APOA5 and HL polymorphisms.

Conclusion: Postprandial hypertriglyceridemia is not associated with increased concentrations of hsCRP, TAS and ICAM-1. Furthermore, APOA5 and HL polymorphisms are not associated with different response of triglycerides.

P15-02

Association of three polymorphisms of scavenger receptor class BI gene in with coronary stenosis

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Background: The potential role of scavenger receptor class BI in the regulation of lipoproteins metabolism and atherosclerosis has attracted considerable interest. We tested the relationship of three *SCARB1* polymorphisms with significant coronary stenosis (SCS) and lipid profile in a coronary Tunisian population.

Materials and methods: Three *SCARB1* polymorphisms (exon8 (C/T), exon1 (G/A), intron5 (C/T)) were studied in 316 tunisians undergoing coronary angiography. SCS was defined as a luminal narrowing of ≥ 50% in at least one major coronary artery. Lipid profile was measured. Genotyping was performed using PCR-RFLP. Statistical analysis was performed by SPSS.

Results and conclusion: TT genotype of exon8 was associated with higher concentrations of HDL-C and ApoAI in the group without SCS. The T allele of exon 8 was associated with 41% lower risk of SCS. This protective effect seemed to be particularly significant in women, non diabetics and nonsmokers. The T allele of intron 5 was associated with an increased risk of SCS, particularly in smokers. AA genotype of exon1 was associated with an increased risk of SCS in diabetics and in patients with metabolic syndrome. The (CAT) haplotype was associated with an increased risk of SCS compared to the wild haplotype and had a 4-fold greater risk of SCS than patients with haplotype (TGC) which seems to be the most protective against SCS. The T allele of exon 8 in SCARB1 seemed to increase the HDL-C and ApoAI concentrations and reduce the risk of SCS. The intron 5, exon 1 polymorphisms and (CAT) haplotype seemed to have an atherogenic effect.

P15-03

Six lipoprotein lipase gene polymorphisms, lipids and coronary stenosis in a Tunisian population

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Background: Lipoprotein lipase (LPL) is the rate-limiting enzyme in the hydrolysis of triglyceride-rich lipoprotein particles. LPL polymorphisms' effects on lipids and coronary artery disease are controversial among studies and populations. Our aim was to study the association between six polymorphisms and significant coronary stenosis (SCS), disease severity and lipid parameters in Tunisian patients.

Materials and methods: LPL *PvuII*, 93 T/G, 188 G/E, *HindIII,* N291S and D9N polymorphisms were analyzed in 316 patients who underwent coronary angiography. SCS was defined as the presence of stenosis ≥ 50% in at least one major coronary artery. The stenosis severity was determined by using Gensini score (GS).

Results and conclusions: A significant association of SCS with TT and TG genotypes of the *HindIII* polymorphism was showed: OR = 2.84, 95% CI, 1.19-7.40, P = 0.017; OR = 1.77, 95% CI, 1.99-2.82, P = 0.033), respectively. The TT genotype was significantly associated with increased triglyceride level and ApoB/ApoA-I ratio and with decreased HDL-C. Haplotype analysis showed that OR of SCS associated with the CTGTAG haplotype was 2.12 (95% CI 1.05-4.25,P = 0.032) and with CGGGAA was 0.71 (95% CI 0.26-1.95, P = 0.022) compared to the CTGTAA. Significant difference in GS was observed among *HindIII* genotypes and haplotypes. A significant association between the mutated genotype of *HindIII* polymorphism with decreased HDL-C level and increased ApoB/ApoA-I ratio and triglyceride level was showed. Our results suggest that *HindIII* and D9N polymorphisms and CTGTAG haplotype seem to be considered as marker of coronary stenosis. In another hand, *HindIII* and haplotypes were related to coronary stenosis severity.

P15-04

Toll-like receptors tlr-2 and tlr-4 gene polymorphisms in patients with cerebral atherosclerosis

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Background: The innate immunity proteins TLR-2 and TLR-4 are possible connection between immune response and inflammation involved in the pathogenesis of atherosclerosis. Previous studies suggest that tlr-2 and tlr-4 gene polymorphisms could contribute to the differences in the disease development.

Materials and methods: A group of patients with cerebral atherosclerosis, evaluated by digital subtraction angiography, with > 50% stenosis of cerebral artery (N = 47) was compared to the control group (N = 27) concerning single nucleotide polymorphisms G/A753 in the tlr-2 gene and A/G299 in the tlr-4 gene, determined by the real-time PCR. Serum proinflammatory cytokines IL-6 and TNF-α, were determined by enzyme immunoassays.

Results: Examined polymorphism of tlr-2 gene was present in 3.7% and 5.3% subjects of the control and of the cerebral atherosclerosis group, respectively, while polymorphism of tlr-4 in 9.3% and 8.5% subjects, respectively. There was no difference in

proportions of the polymorphisms between the groups. The concentrations of IL-6 and TNF-α were higher in the cerebral atherosclerosis than in the control group (1.54 pg/mL, (1.04-3.50 pg/mL) *vs*. 1.21 pg/mL, (0.45-2.32 pg/mL), P = 0.048 and (0 pg/mL (0-1.8 pg/mL) *vs*. 0 pg/mL, (0-0 pg/mL), P = 0.039, respectively), presented as median (1-3 quartile).

Conclusion: Higher concentrations of IL-6 and TNF-α in the cerebral atherosclerosis group are indicators of inherent inflammation. Single nucleotide polymorphisms G/A573 of the tlr-2 and A/G299 of the tlr-4 gene had no influence on the concentrations of circulating IL-6 and TNF-α. The polymorphisms were not significant for the diagnosis of cerebral atherosclerosis with more than 50% stenosis of cerebral arteries.

P15-05

Four resistin polymorphisms, metabolic syndrome parameters and obesity risk in Tunisian volunteers

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Background: Resistin is a protein hormone produced by adipocytes. Some studies found increased circulating resistin levels and its mRNA expression in adipose tissue in patients with obesity. While other studies failed to confirm this finding. Genes encoding adipokines are important functional candidates for development of obesity. Many resistin gene polymorphisms were described and their implication in obesity and metabolic syndrome (MetS) was controversial. Our aim was to study the relationship between four resistin polymorphisms (420C/G, 44G/A, 62G/A and 394C/G) and MetS parameters and the risk of obesity in Tunisian volunteers.

Materials and methods: We have recruited 169 non obese BMI < 30 kg/m^2 (sex-ratio = 0.594, mean age 43.25 ± 13.12 years; mean BMI 24.73 ± 3.50 kg/m^2) and 160 obese BMI ≥ 30 kg/m^2 (sex-ratio = 0.221, mean age 48.41 ± 10.92 years, mean BMI 36.6 ± 4.8 kg/m^2). Genotyping was performed using PCR-RFLP. Lipids parameters were measured. BMI and HOMA-IR were calculated. MetS was defined according to IDF-2005, obesity was defined according to WHO-1995. The study was approved by the Medical Hospital Ethic Committee.

Results and conclusion: 420GG were associated with higher waist circumference and BMI. 44G/A polymorphism was associated with increased total cholesterol and LDL-C levels. The others genotypes showed no association with all MetS parameters. Concerning association between SNPs and MetS risk, only mutated genotypes at 44G/A increase the risk of MetS after adjustment to confounders parameters (OR = 1.93, P = 0.023). About obesity risk, only 420C/G seems to contribute in obesity. Adjusted ORs of obesity associated to mutated genotypes were 2.17, 95%CI [1.28-3.68]; P = 0.004.

P15-06

Simultaneous detection of mutations within genes associated with familial hypercholesterolemia

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Background: Familial Hypercholesterolemia (FH) is a genetic disorder characterised by high levels of low density lipoprotein in the cardiovascular system and early onset of cardiovascular disease. Currently in the UK, 1 in 500 people suffer from FH, with 85% of this population un-diagnosed. The genes apo-lipoprotein B, low density lipoprotein receptor, and proprotein convertase subtilisin/kexin type 9 are known to be associated with FH. This study reports the development of an assay enabling the simultaneous analysis of 20 common mutations within these genes.

Materials and methods: The assay is based on a combination of two multiplex PCRs and biochip array hybridisation. Innovative PCR priming technology permits high discrimination between multiple wild-type and mutant DNA regions, which in combination with spatially organised biochip array technology increases the multiplexing capacity of the assay. Dedicated software processes results automatically, with analysis completed within 3 hours, from template DNA.

Results: Assay specificity was confirmed using DNA from 100 FH positive patient samples. Subsequently, a further 100 blinded samples were assessed with a correlation of 98% with patient samples that had previously been sequenced. The cohort included patient samples containing the 20 common mutations.

Conclusions: Data indicates applicability of this assay for the rapid simultaneous analysis of 20 common mutations within three genes associated with FH. Treatment from adolescence age with lipid modifying drug therapy, combined with lifestyle changes, can restore normal life expectancy. Therefore, this assay can be used as an analytical tool to facilitate FH diagnosis.

P15-07

Apolipoprotein A5 genetic polymorphisms and fasting serum lipidogram in elderly subjects with MetS

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Background: Metabolic syndrome (MetS) is a cluster of metabolic abnormalities as are obesity, dyslipidemia, hyperglycemia, and hypertension. It represents a risk factor for many disorders. Apolipoprotein A5 which is located on VLDL and HDL regulates the concentration of triglycerides. Therefore, genetic isoforms might affects triglyceride concentration and contribute in pathogenesis of MetS.

Materials and methods: The cross-sectional study included 155 men and 187 women older than 70 years. Fasting serum concentration of biochemical parameters were determined by standardized methods. International Diabetes Federation criteria was used for determination of MetS. Two *Apo A5* genetics polymorphisms (c.1259T>C-SNP1 andS19W) were genotyped using PCR-RFLP method with detection of fragments with chips on Agilent 2100 bioanalyzer.

Results: SNP1 genotype frequencies for T/T, T/C and C/C genotype were 183, 41 and 1 in MetS(+), and 96, 15 and 11 in MetS(-), respectively, (P = 0.478). S19W genotype frequencies for SS, SW and WW were 184, 41 and 2 in MetS(+) and 92, 22 and O in MetS(-), (P = 0.586). Mean total-cholesterol concentration was significantly higher in SNP1-C allele carriers then in non-carriers for women in MetS(+) group (6.23 ± 1.36 and 5.58 ±1.14, respectively, P = 0.020). LDL-cholesterol was also significantly higher for same group and same allele (4.05 ± 1.04 and 3.53 ± 0.97, P = 0.026). In subjects with MetS(+), higher triglycerides concentration were observed in W-carriers than in non-carriers of S19W (median were 1.79 and 1.97, respectively, P = 0.050). Total-cholesterol were higher in men W-carriers *vs*. non-carriers (5.55 ± 1.17 and 4.97 ± 1.11 respectively, P = 0.048).

Conclusions: Apo A5 genetic polymorphisms SNP1 and S19W are associated with dislypidemia in elderly subjects with MetS.

P15-08

Adiponectin gene variants, and gene-environment interactions as predictors of early central obesity

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Background: Adiponectin is an adipose tissue-derived adipokine linked to central obesity and *ADIPOQ* variants are promising markers for understanding the genetic base of obesity. We aimed to evaluate the relation of adiponectin concentrations and *ADIPOQ* gene variants to abdominal obesity and hypertension in young subjects. In addition, influence of the gene-environment (diet) interaction was estimated.

Materials and methods: The study included 149 subjects. Clinical examination and anthropometric measurements were done. Adiponectin levels were estimated by ELISA assay. *ADIPOQ* -11377C>G and -11391G>A were genotyped by real-time PCR.

Results: Waist circumference, systolic and diastolic blood pressure showed inverse correlations with adiponectin concentrations. *ADIPOQ* -11377GG and -11391GA significantly increased the risk for the development of central obesity (OR 5.57 and OR 3.37, respectively). The test of overall association showed significant correlation of central obesity with -11377C>G and -11391G>A haplotypes ($P < 0.001$). We found a significant association of -11391G/A variants with triglycerides and BMI, with A allele more frequent in subjects with BMI ≥ 25 kg/m^2 ($P = 0.021$), while GG genotype predispose for lower concentrations of triglycerides ($P = 0.005$). A significant correlation was found for -11377GG variant with the concentration of total cholesterol (G/G *vs*. other $P = 0.043$) and hypertension ($P = 0.035$), where -11377G allele carriers have significantly higher risk for elevated blood pressure (OR 2.73). When a diet was introduced as a covariable, correlation was significant between -11391G>A and HDL-C only ($P = 0.015$).

Conclusion: Analysis of adiponectin concentration and *ADIPOQ* -11391G>A and -11377C>G promoter gene variants could be clinically meaningful for estimation of obesity and obesity-related syndrome risk in young adult population.

P15-09

Gender-specific effects of PPARG, APOE, ACE, LPL, IL-6 and AT1R gene variants on metabolic syndrome

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Background: Metabolic syndrome (MS) is a cluster of modifiable risk factors including hypertension, abdominal obesity, dyslipidemia and insulin resistance, associated with nonmodifiable risk factors, such as age, sex and genetic background. We investigated the possible role of gene polymorphisms of *PPARG* (Pro12Ala), *ApoE* (ε2, ε3, ε4), *LPL* (P+/-), *IL-6* (-174G>C), *ACE* (I/D) and *AT1R* (1166A>C) in MS.

Materials and methods: 516 individuals were investigated including 263 patients with MS and 253 subjects without MS criteria. Genotyping was performed using PCR based methods.

Results: In female group associations were found for: LPL and ACE with MS (P = 0.04); *PPARG* and *LPL* with blood pressure, (P = 0.04); LPL with cholesterol and LDL (P = 0.01 and P = 0.05, respectively). Significant gene interactions observed between: *APOE* and *PPARG*, *ACE* and *APOE* were associated with BMI (P = 0.01 and P = 0.05, respectively); *LPL* and *PPARG* were associated with triglycerides (P = 0.03). For males we found associations of: *LPL* variants with MS (P = 0.02), BMI (P = 0.002) and waist circumference (P = 0.008); *PPARG* and *APOE* with BMI (P = 0.05); *IL-6* with CRP (P = 0.02). Significant gene interactions observed between: *PPARG* and *AT1R* were associated with blood pressure (P = 0.05); *PPARG* and *APOE* with triglycerides (P = 0.02); *PPARG* and *APOE*, *PPARG* and *IL6* (P = 0.03), *ACE* and *APOE* (P < 0.001) with cholesterol; *PPARG* and *LPL* (P = 0.003), *PPARG* and *IL6* (P = 0.06) with HDL; *PPARG* and *IL6* (P = 0.01), *ACE* and *APOE* (P = 0.04); *PPARG* and *APOE*, *LPL* and *ACE* (P = 0.01), *AT1R* and *ACE* (P = 0.06) with CRP.

Conclusion: Gene variants of *PPARG*, *APOE*, *LPL*, *ACE*, *AT1R* and *IL-6* could be susceptibility factors of obesity, lipid status, and glucose intolerance.

P15-10

Contribution of 5-*HTTLPR* and *BDNF* gene variants to obesity risk

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Background: 5-Hydroxytryptamine (5-HT, serotonin) plays an important role in the central nervous control of energy balance and is involved in several biological processes including mood, appetite, sleep, libido, memory, and body weight regulation. Brain-derived neurotrophic factor (BDNF) is also currently recognized as an important participant in the regulation of food intake. The aim of this study was to evaluate whether the *5-HTTLPR* S/L and *BDNF* Val66Met gene variants are associated with obesity in a sample of adults of Croatian origin.

Materials and methods: 462 individuals were investigated including 301 obese (BMI ≥ 30 kg/m^2) and 161 lean (BMI < 25 kg/m^2) (mean age ± SD was 49 ± 8 years). Genotyping of triallelic structure of *5-HTTLPR* (LA, LG, S) and of *BDNF* Val66Met polymorphisms was performed using the RealTime-based allele specific PCR methods.

Results: In the whole group we found no associations between *5-HTTLPR* S/L and *BDNF* Val66Met polymorphisms and obesity. When we compared male and female samples, we observed statistically significant differences in the distribution of *5-HTTLPR* genotypes: *5-HTTLPR* LALA genotype was more frequent in the group of lean women comparing to the group of lean men (41% and 28% respectively, P = 0.022). The *5-HTTLPR* S and *BDNF* Met allele carriers have higher risk to develop obesity (OR 2.07) than non carriers (P = 0.038).

Discussion: Our findings indicate that *5-HTTLPR* polymorphism may be linked with obesity in adult female population, reinforcing the role of the serotonin transporter as a risk factor for the obesity phenotype. *SERTPR* and *BDNF* gene interactions could additionally predispose to obesity risk.

P15-11

ABCG2 gene variant and fluvastatin adverse drug reactions in renal transplant recipients

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Background: Polymorphisms in genes encoding drug transporters could be valuable pharmacogenetic markers. The *ABCG2* efflux transporter is expressed in multiple tissues and plays an important role in the disposition of different drugs including statins. The functional 421C>A polymorphism in the *ABCG2* that reduces transporter activity has been found to be associated with increased systemic exposures to certain statins, including fluvastatin. Although genetic variability in the *ABCG2* distinctively affects the pharmacokinetics, there are no published data that would indicate that variability can result in fluvastatin induced adverse drug reactions (ADRs). The aim of this case-control study is to show the contribution of pharmacogenetic predisposition (*ABCG2* gene variant) to the development of fluvastatin ADRs (myotoxicity, hepatotoxicity, other side effects) in renal transplant recipients.

Patients and methods: 108 renal transplant recipients were included in the study, 54 patients with ADRs to fluvastatin therapy, and 54 controls without ADRs (matched according to fluvastatin dose, age, gender, concomitant therapy, and other conditions). Genotyping of the *ABCG2* 421C>A polymorphism was performed using the TaqMan allele-specific PCR assay (AppliedBiosystems).

Results: According to the statistical analysis, *ABCG2* 421CA genotype carriers have significantly higher incidence of ADRs to fluvastatin therapy comparing to *ABCG2* 421CC genotype carriers (OR 3.77, 95%CI 1.26-11.28, P = 0.024).

Conclusion: Our data are the first to indicate there is an association between adverse drug reactions to fluvastatin therapy in renal transplant recipients with *ABCG2* 421C>A polymorphism.

P15-12

Association of soluble and -2518 A>G *CCL2* polymorphism with inflammation markers and IR

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Introduction: Insulin resistance (IR) is a disease with genetic susceptibility characterized by an abnormal inflammatory response. CCL2 is secreted by adipocytes, plays a central role in macrophage accumulation in white adipose tissue (WAT), promoting the inflammatory process, remain suggested to be involved in the progression of obesity to IR. The *CCL2* gene is overexpressed in WAT and decreases insulin-stimulated glucose uptake into adipocytes. The -2518A>G polymorphism in the regulatory region of *CCL2* may regulate gene expression. The aim was to investigate the relationship of *CCL2* -2518A>G polymorphism and sCCL2 with inflammation markers and IR.

Materials and methods: In a cross-sectional study we included 309 individuals Mexican-mestizo, classified by HOMA-IR index. Body composition, anthropometrics and inflammation markers were measured by routine methods, and -2518A>G variants by PCR-RFLP and sCCL2 by ELISA methods.

Results: In this study group we found differences in: 1) sCCL2 levels (191 ± 14.9, 280 ± 21.6 ng/mL, P = 0.001); and 2) the genotype frequencies (AA: 33%, 30%; GA: 53%, 41% and GG: 14%, 29%, P = 0.007) between healthy and IR individuals, respectively. The G allele carriers showed lower measures (101 ± 9.7 cm) of hip circumference than the A allele carriers (104 ± 11.4 cm). While in IR individuals, the GG genotype carriers showed higher levels of: CRP, WBC and triceps skin fold thickness than the GA+AA genotype carriers. The sCCL2 levels showed correlations with CRP, glucose, sInsulin, HOMA-IR, weight, BMI and hip-circumference (r = 0.190 to 0.350, P < 0.05).

Conclusions: We suggest that CCL2 allele -2518G is associated with inflammatory course and distribution of body fat in IR Mexican-mestizo.

P15-13

Association of PAI-1 5G allele with inflammation markers and body fat in Mexican with obesity

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Introduction: Comorbidity in obesity are diseases with genetic susceptibility and characterized by an inflammatory response. An association between obesity, inflammation and reduced fibrinolysis activity contributes to a higher risk of cardiovascular events. The plasminogen activator inhibitor-1 (PAI-1) is the main inhibitor of fibrinolysis, representing approximately 60%. The sources of PAI-1 are endothelium cells, platelets, adipocytes and stromal cells of adipose tissue. The gene variants of PAI-1 are associated with cardiovascular diseases. Our aim was to investigate the relationship of *PAI-1* 4G/5G polymorphism with inflammation markers and body fat distribution in obesity.

Materials and methods: In a cross-sectional study we included 179 individuals Mexican-mestizo, classified by BMI index. Body composition, anthropometrics and inflammation markers were measured by routine methods, 4G/5G polymorphism by PCR-RFLP, and insulin by ELISA methods.

Results: In this study group we found differences in hsCRP levels (1.87 ± 0.36, 4.73 ± 1.64 mg/L, P = 0.031); and body-fat-index (2.17 ± 0.07, 2.54 ± 0.18, P = 0.032) between 5G/5G and 4G/4G genotype carriers. The hsCRP levels showed correlations with distribution and body fat mass (r = 0.259 to 0.557, P < 0.05). While, the genotype frequencies were (Lean: 16%, 41%, 43%; overweight: 12%, 48%, 40%; obese: 16%, 58%, 26%) for 4G/4G, 4G/5G and 5G/5G genotype carriers, respectively. In individuals classified as obesity, we found the following differences: total body fat (43% *vs.* 34%; P = 0.015), waist-hip-ratio (0.8710 ± 0.18 *vs.* 0.9328 ± 0.18; P = 0.024) and platelet-count (237.200 ± 10.595 *vs.* 288.500 ± 15.743; P = 0.010) in 5G/5G *vs.* 4G/5G + 4G/4G genotype carriers.

Conclusions: We suggest that 4G/5G *PAI-1* polymorphism may be associated with inflammatory process and body fat distribution in Mexican-mestizo individuals with obesity.