**AP-199**

**Genetic variants in the RUNX3 gene and gastric cancer prognosis**

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**AIM:** To explore the association between runt related transcription factor 3 (RUNX3) gene polymorphisms and gastric cancer prognosis. **METHODS:** 10 tagging single-nucleotide polymorphisms (tSNPs) were genotyped in RUNX3 using TaqMan method in 944 gastric cancer patients. The Kaplan-Meier method with log-rank test and Cox proportional hazards model were used for survival analyses. **RESULTS:** Among the 10 tSNPs, SNP10 rs2282718 AA genotype was found to be significantly associated with a poor gastric cancer survival in a recessive model (log-rank P = 0.035), and this effect was more pronounced among subgroups with diffuse-type gastric cancer (HR = 1.45, 95% CI = 1.08-1.94), T4 depth of invasion (HR = 2.48, 95% CI = 1.04-5.92), distant metastasis (HR = 2.22, 95% CI = 1.06-4.64), and stage IV (HR = 2.30, 95% CI = 1.27-4.16). Multivariate Cox regression analysis revealed that the SNP10 rs2282718 was an independent prognostic factor to predict gastric cancer clinical outcome. Moreover, the combined genotypes of these ten tSNPs showed a locus-dosage effect on gastric cancer survival (P_trend = 0.006). **CONCLUSIONS:** Our results suggested that the genetic variation in RUNX3 may contribute to gastric cancer prognosis and the SNP10 rs2282718 could be an independent marker of survival assessment and individualized clinical therapy for gastric cancer, particularly among the diffuse-type gastric cancer in Chinese populations.

**AP-200**

**Genetic variants in microRNAs predict bladder cancer risk and recurrence**

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MicroRNAs (miRNAs) play important roles in numerous cellular processes, including development, proliferation, apoptosis, and carcinogenesis. We hypothesized that genetic variations in miRNAs are associated with bladder cancer risk and prognosis. We performed a systematic survey of single nucleotide polymorphisms (SNPs) in miRNAs and evaluated association of selected SNPs with bladder cancer risk and recurrence. The functionality of these miRNA SNPs was further examined by a series of molecular biological assays. Through bioinformatics analysis, five miRNA SNPs were selected for the association study. We found that miR-146a rs2910164 C allele was associated with a significant decreased risk of bladder cancer in both test and validation sets as well as in the combined set (P = 2.92×10⁻⁴). Furthermore, rs2910164 GC/CC genotypes conferred a significantly reduced recurrence compared with the GG genotype (P = 0.016). Functional analysis revealed that miR-146a rs2910164 C allele inhibited cell proliferation and significantly downregulated IRAK1 and TRAF6 expressions in bladder cancer cells. Additional examination of 64 bladder tissues revealed that individuals carrying the C allele had increased expression levels of miR-146a compared with those carrying the G allele (P = 0.010). Our findings demonstrate that miR-146a rs2910164 plays important roles in the risk and recurrence of bladder cancer.