SY10-1 Genetic Risks of Atrial Fibrillation in Japan

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Introduction: Recent genome wide association study (GWAS) in Caucasian found association of SNPs in chromosome 4q25 and ZFHX3 with AF. We examined association of these SNPs with AF in Japanese, and tested potential use for risk-stratify of AF. Methods: 2500 AF and 2500 control were enrolled in this study. Genotyping was carried out using PCR/invader assay. Correlation with AF, the age of AF onset, and the recurrence after catheter pulmonary vein isolation (PVI) was analyzed retrospectively. Results: Both SNPs in 4q25 and ZFHX3 were significantly associated with AF (p=2.1x10^-54 and p=4.6x10^-8, respectively). Odd ratio for AF was more than 5 times higher in those with homozygous risk allele in both 4q25 and ZFHX3 than those with homozygous protective allele in both SNPs. The onset of AF was significantly younger in those with homozygous 4q25 risk allele than those without. The recurrent rate of AF after PVI was more in those with 4q25 risk allele than those without by about 20%. Conclusion: SNPs in 4q25 and ZFHX3 are associated with AF also in Japanese, which could be utilized to risk-stratify AF. Keywords: atrial fibrillation, SNP