

# P037

## To Examine the Role of *Caveolin-1* in Taiwanese Hepatocellular Carcinoma at DNA, RNA, and Protein Levels

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**Backgrounds:** Hepatocellular carcinoma (HCC) is one of the most common types of malignant tumor worldwide, for which the prevalence and mortality rates are very high in Taiwan. Caveolin-1 (CAV-1) is a main structural protein of caveolae and plays a regulatory role in signaling pathways and tumorigenesis. High expression of Cav-1 in mouse HCC is positively correlated with higher cell invasive capacity, but the contribution of CAV-1 genetic variants during HCC progression is still largely unknown. In this study, we investigated the contribution of CAV-1 variant to the risk of HCC from the analyses of DNA, RNA and protein. **Materials and Methods:** We enrolled 298 patients with HCC patients and 298 cancer-free controls frequency matched by age and gender in this case—control study. Firstly, the associations of six single nucleotide polymorphisms (SNPs) of the *Cav-1* gene at C521A (rs1997623), G14713A (rs3807987), G21985A (12672038), T28608A (rs3757733), T29107A (rs7804372), and G32124A (rs3807992) with HCC risk in a Taiwanese population were evaluated. Secondly, thirty HCC tissue samples with variant genotypes were tested to estimate CAV-1 mRNA expression by real-time quantitative reverse transcription. Finally, the HCC tissue samples of variant genotypes were examined by western blotting to estimate their CAV-1 protein expression patterns. **Results:** There were significant differences between the HCC and control groups in the distributions of the CAV-1 G14713A genotypes ( $p=0.0124$ ), and these carrying AG and AA genotypes had a higher risk for HCC, compared with those with the GG genotype (odds ratio=1.51 and 1.94, respectively). Patients with CAV-1 G14713A AG or AA genotype had higher levels of mRNA ( $p=0.0001$ ) and protein ( $p=0.0019$ ) than those with GG genotype. **Conclusion:** Our multi-approach findings at the DNA, RNA and protein levels suggest that CAV-1 may play a critical role in HCC carcinogenesis, and serve as a target for HCC therapy.