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第三十屆生物醫學聯合學術年會　投稿摘要表格（正本）

Significant Association of *Caveolin-1* Genotypes with Renal Cell Carcinoma Risk in Taiwan

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Backgrounds: Many articles have reported the *caveolin-1* gene to be down-regulated thus suggesting that it might be a candidate tumor suppressor gene in many tumors, while its involvement in renal cell carcinoma (RCC) is not clear and depending on pathological grade. **Materials and Methods:** In this case—control study, the association of *Cav-1* polymorphisms with RCC risk in a central Taiwanese population was investigated. Ninety two patients with RCC and 6.3-fold amount of age- and gender-matched healthy controls (580) recruited were genotyped. **Results:** There were significant differences between RCC and control groups in the distributions of their genotypes (p=1.3*10^{-3} and 0.323) and allelic frequencies (p=2.8*10^{-4} and 1.5*10^{-3}) in the *Cav-1* G14713A (rs3807987) and T29107A (rs7804372) polymorphisms, respectively. As for the haplotype analysis, those who had GG/AT or GG/AA at *Cav-1* G14713A/T29107A showed a decreased risk of RCC compared to those with GG/TT, while those of any other combinations were of increased risk. There were joint effects of *Cav-1* G14713A and T29107A genotype with smoking status on individual RCC susceptibility. **Conclusion:** This is the first report providing evidence that *Cav-1* being involved in RCC, the A allele of the *Cav-1* G14713A is risky, the A allele of the *Cav-1* T29107A is protective, and AA/TT on these two polymorphisms may be the most risky haplotype for the development of RCC and may be novel useful genomic markers for early detection of RCC.

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