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Contribution for the Genotypes of Cell Cycle Regulator Genes *p53* and *CDKN1A* to Leiomyoma

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Backgrounds: Genetically speaking, polymorphic variants of *p53* codon 72 and *CDKN1A* codon 31 have been found to be associated with cancer susceptibility, but no study has investigated their effect on the risk of uterine leiomyoma. **Materials and Methods:** In this study, a total of 130 patients with leiomyoma, and 520 age-matched controls were recruited and genotyped. **Results:** We found an association of *CDKN1A* codon 31genotype with leiomyoma susceptibility. Individuals carrying the C allele at *p21* codon 31 had a 1.58-fold increased odds ratio of leiomyoma (95% confidence interval=1.20-2.09, p=0.0011), and those with Arg/Ser and Ser/Ser genotypes for *p21* codon 31 had a 3.03- and 4.11-fold (95% confidence interval=1.52-6.05 and 1.94-8.72) increased risk of leiomyoma compared to those with Arg/Arg, respectively. No significant difference in the distribution of *p53* codon 72 genotypes was found among the leiomyoma patients and controls. The distribution of haplotype combinations of *p53* codon 72 and *CDKN1A* codon 31 was statistically different in the leiomyoma and control groups. **Conclusion:** Our findings suggested that the C allele of *CDKN1A* codon 31 associated with higher leiomyoma risk, and could serve as a potential early predictor for leiomyoma.