Table 7. Genotype frequency distribution of rs3219175, rs34861192 in CI group and control group for LAA and SAO

SNP	Case (SAO)	Control	*P*
rs3219175			
AA	7 (2.70)	3 (1.10)	
AG	55 (21.5)	83 (31.0)	
GG	194 (75.8)	182 (67.9)	0.025*
rs34861192			
AA	7 (2.70)	3 (1.10)	
AG	56 (21.9)	83 (31.0)	
GG	193 (75.4)	182 (67.9)	0.032*
SNP	Case (LAA)	Control	*P*
rs3219175			
AA	1 (0.10)	3 (1.10)	
AG	25 (22.9)	83 (31.0)	
GG	83 (76.1)	182 (67.9)	0.283
rs34861192			
AA	1 (0.10)	3 (1.10)	
AG	25 (22.9)	83 (31.0)	
GG	83 (76.1)	182 (67.9)	0.283

P value: assessed by SHESIS Software.

Some limitations certainly exist in our study. First, the sample was relatively small. Second, the selected subjects were all between 45 and 75 years old, which means our study was targeting mainly the susceptibility of CI in a middle-aged population. Thus, there were not enough elder control subjects, and the research on the elder group was therefore impacted. Third, when collecting the information on the ailing and healthy subjects, with the difficulty of and limitations on blood sample collecting, the serum resistin level was not detected. Thus, we were unable to judge the influence from the resistin gene polymorphism on the serum resistin level of the CI patients. In conclusion, the major discovery of the current study first discovered in the Chinese Han middle-aged population, the GG gene type carriers of the resistin gene sites rs3219175 and rs34861192 had a high risk for CI onset, especially in middle-aged male patients and SAO CI in all middle-aged patients. In middle-aged population, the occurrence rate of the haplotype AGGCAGC (rs34124816, rs3219175, rs34861192, rs1862513, rs3745367, 180C/G and rs3745369) was 1.97 times ($P<0.05$) higher in the patient group than in the control group. To further make the relationship between the gene bands, the middle-aged male CI patients, and the SAO middle aged CI patients clear, we need to understand the relevance of the functions of sites rs3219175 and rs34861192 for the population, and explain the similarity of the sites rs3219175 and rs34861192 in the population. The study of these functions will require large samples, multiple locations and multiple races of subjects. To sum up, our study laid the foundation for early prevention, personal treatment and research on the related genetic mechanisms of CI with clinical significance.

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