Purpose: Chronic periaortitis (CP) is a rare condition, characterized by a fibroinflammatory tissue surrounding the abdominal aorta and the common iliac arteries. Three main entities are included: idiopathic retroperitoneal fibrosis (IRF), inflammatory abdominal aortic aneurysms (IAAAs), and perianeurysmal retroperitoneal fibrosis (PRF). A systemic inflammatory nature of this condition is suspected by the presence of elevated acute phase reactants, constitutional symptoms and prominent adventitial inflammation. Chemokines may contribute to the inflammatory CP process through their binding to CC chemokine receptor 5 (CCR5). The aim of this study was to examine if the 32 base pair deletion allele in CCR5 (CCR5 delta 32 allele) might be associated with CP susceptibility.

Method: We enrolled 100 consecutive Italian patients with CP. As a control group we used 180 healthy blood donors from the same geographic areas. The CCR5 genotype of all CP patients and controls was studied by polymerase chain reaction amplification of the region which includes the 32 deletion (CCR5 delta 32 allele) might be associated with CP susceptibility. Results: Homozygosity for CCR5 delta 32 allele was not detected in CP patients and controls. Carriers of the CCR5 delta 32 allele were significantly more frequent among the CP patients than among the controls (15% versus 5.6%; P corr = 0.018; odds ratio [OR] 3.0 [95% confidence interval (95% CI) 1.3-7.0]). No significant associations were found for comparisons of CP patients with and those without specific manifestations. Conclusion: The presence of CCR5 delta 32 significantly influences disease susceptibility of CP in an Italian study population. Further studies are required to replicate our findings in other populations.

Keywords: polymorphism and vasculitis

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