Introduction:
Shock is the most common cause of death in the postsurgical ICU, including septic shock and hypovolemic shock, reaching the 50–60% mortality in septic shock. The inadequate response of the immune system to the infection triggers a potent inflammatory cascade, where the C-Reactive Protein (CRP) is an essential key in the amplification and maintenance of this cascade.

The gene encoding to CRP is located on the proximal long arm of human chromosome 1 (1q32). The GT polymorphism in the promoter sequence of CRP gene (rs2794521) has been associated with invasive pneumococcal disease. Thus, we analyze the relationship between rs279451 polymorphism and the risk of developing septic shock in postsurgical patients.

Methods:
An observational, retrospective and single-center study was conducted on a sample of Caucasian patients undergoing major abdominal surgery, of which one part developed septic shock and another part developed systemic inflammatory response syndrome, who were used as control. The rs2794521 polymorphism was analyzed by the Sequenom’s MassARRAY platform and a recessive inheritance model was selected (CC vs TT/CT).

Results:
The possible association between the CC recessive form of the rs279451 polymorphism and the septic shock risk was analyzed, demonstrating a statistically significant relationship (p=0.02) between both conditions. Among patients who developed septic shock, 79.2% presented a recessive inheritance pattern while 54.5% showed the CT/TT genotype. On the other hand, those patients with the recessive form of the rs279451 polymorphism were selected and a statistical analysis was performed comparing those patients who developed septic shock from those who did not develop it, obtaining a statistically significant relationship (p=0.036) between the presence of the recessive form of polymorphism and the likelihood of developing septic shock.

Conclusion:
The recessive form of rs279451 polymorphism is a risk factor for septic shock in post-operative patients of major abdominal surgery.