Bacterial DNA in non-leukocytic ascites, identification of risk factors

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Background: As culture-dependent bacterial identification methods are still limited to capture colonisation or infection of ascites fluid we established a culture-independent PCR-based method for the detection, quantification and differentiation of bacterial DNA (bactDNA). This report aims to characterize risk factors for bactDNA identification in non-leukocytic ascites fluid (nlAF) and for progression to SBP.

Methods: 299 nlAF samples of 142 patients were collected between 03/2011 and 12/2012. BactDNA was detected using real-time PCR with primers targeting the 16S-rRNA-gene and differentiated by direct sequencing. Genetic polymorphisms (SNP) of receptors recognising bacterial components such as TLR (subtypes 1,2,4,6), CD14, NOD2 and MBL2 were identified by detecting and amplifying corresponding genes. Patients’ characteristics such as liver function (bilirubin, PT, albumin, creatinine, sodium), inflammatory values (CRP-level) and underlying disease were correlated with PCR-results.

Results

BactDNA could be detected in 37 % of nlAF of indexparacentesis [fig. 1]. The risk for bactDNA in indexparacentesis was associated with genetic polymorphism of TLR2 (rs5743708 G/A, fig. 3) and TLR6 (rs5743810 C/T, fig. 4). The amount of bactDNA (copies/ml) was dependent on genetic variants of TLR1 [table 1] (rs5743618, G/T; rs4833095 T/C). Polymorphisms of CD14, NOD2 as well as MBL2 showed no association with bactDNA in ascites samples. After detection of bactDNA in nlAF 40.7% did not develop SBP (group 1) whereas 59% proceeded to SBP or received antibiotics (group 2) [fig. 2]. Group 2 had significantly decreased prothrombin time and increased CRP levels [fig. 5] Group comparison did not reveal an association with genetic polymorphisms. Etiology of cirrhosis did not influence the detection rate of bactDNA.

Conclusion

These results emphasise that the susceptibility to bacterial colonisation or ascites infection in patients with cirrhosis might be genetically determined. However, further risk factors and mechanisms favouring the progression from colonisation to overt SBP still have to be clarified.