O053

2-hour Oral Session

Severe infections in children

MBL2 polymorphisms do not influence the susceptibility to invasive meningococcal disease in a population of Danish children

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Background: *Neisseria meningitidis* is the cause of meningococcal bacteremia and meningitis, and colonization with this pathogen of the nasopharynx is common. Invasive meningococcal disease (IMD) has the highest incidence in infants, whereas carriage is more frequent in young adults.
Presence of specific polymorphisms regulating the innate immune system may predispose to IMD. We investigated the effect of genetic variation in the mannose-binding lectin gene, *MBL2*, and its promoter on susceptibility of IMD in children younger than 5 years.

Methods and patients: Individuals with IMD were identified through national registries from 1982 through 2006. DNA was obtained from the Danish Neonatal Screening Biobank. The association between *MBL2* haplotypes and IMD susceptibility and outcome was investigated using logistic regression analysis.

Results: Three hundred eighty-seven cases with meningitis, 263 with bacteremia and 642 age- and sex-matched controls were included. One thousand two hundred and ninety-two individuals (96%) were successfully genotyped and assigned *MBL2* diplotypes.
The median age in our combined case series was 50 months (interquartile range (IQR) 23-81 months). Children with defective *MBL2* diplotypes were not at higher risk for meningococcal meningitis than children with intermediate and normal diplotypes (odds ratio (OR) 0.69, 95% confidence interval (CI) 0.47-1.02). Similar results were found for children with bacteremia and defective diplotypes (OR 0.84, 95% CI 0.53-1.32) as well as for all cases (OR 0.75, 95% CI 0.56-1.01). There was no association between *MBL2* diplotypes and 30- or 90-day mortality.

Conclusions: Defective *MBL2* diplotypes did not predict increased IMD susceptibility in a Danish population of children under 5 years.