

Risk factors for invasive pneumococcal disease in children in the era of conjugate vaccine use

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With this case-control study the authors evaluated risk factors for invasive pneumococcal disease (IPD) among children who were aged 3 to 59 months in the era of pneumococcal conjugate vaccine (PCV7). IPD cases were identified through routine surveillance during 2001-2004. They matched a median of 3 control subjects to each case patient by age and zip code. 782 case patients (45% vaccine-type IPD) and 2512 matched control subjects were enrolled. They calculated odds ratios for potential risk factors for vaccine-type and non-vaccine-type IPD by using multivariable conditional logistic regression. Among children who received any PCV7, there was an increased risk for vaccine-type IPD when they had underlying illnesses, were male, or had no health care coverage. Vaccination with PCV7 did not influence the risk for non-vaccine-type IPD. Presence of underlying illnesses increased the risk for non-vaccine-type IPD, particularly among children who were not exposed to household smoking. Non-vaccine-type case patients were more likely than control subjects to attend group child care, be male, live in low-income households, or have asthma; case patients were less likely than control subjects to live in households with other children.

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ECDC comment:

In recent years a large number of European countries have implemented routine PCV7 childhood immunization. After PCV7 introduction, a large impact on the epidemiology of IPD and a natural variation in pneumococcal serotype distribution has been observed. As demonstrated by the same authors in another observational study the reductions in overall IPD resulted from a 99% decrease in disease caused by the seven vaccine serotypes. Therefore, vaccination with PCV7 is an effective tool for reducing the risk for vaccine-type IPD even more among children with traditional risk factors. Since these factors are still associated with non-vaccine-type IPD risk, it is important to continue following the serotype distribution to assess the possible replacement with the new licensed conjugate vaccines.

