

**HER P3****A 10-year molecular survey of herpes simplex virus type 1 in Germany demonstrates a stable and high prevalence of genotypes A and B**

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**Introduction:** Recently three different herpes simplex virus type 1 (HSV-1) genotypes (A, B and C) were described on DNA sequence data of the glycoprotein E (gE), G (gG) and I (gI) genes.

**Objective:** To type the circulating HSV-1 wild-type strains in Germany and to monitor potential changes in the molecular epidemiology over the past 10 years.

**Material and Methods:** A total of 569 clinical HSV-1 isolates from a 10-year survey in Germany were genotyped by a PCR-based restriction fragment length polymorphism analysis of gG and gI. Recombination analysis of the gE gene sequences was performed to reveal intragenic recombinants.

**Results:** Genotype A and B strains represented 76% of all strains analyzed and showed a stable distribution within all age groups investigated, independently from the gender. Intergenic gG/gI and intragenic gE recombinants were demonstrated to be less prevalent. Interestingly, for one HIV patient a gG/gI genotype switch from A/A to C/A was observed within 3 years.

**Conclusion:** The first molecular survey of clinical HSV-1 isolates from Germany demonstrated a stable distribution of 2 different genotypes and recombinants within age groups and over a period of 10 years. Moreover, homologous recombination seems to be an important feature in the evolution of the HSV-1 genome.

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