

# MOLECULAR SURVEY OF HERPES SIMPLEX VIRUS TYPE 1 GENOTYPES IN GERMANY



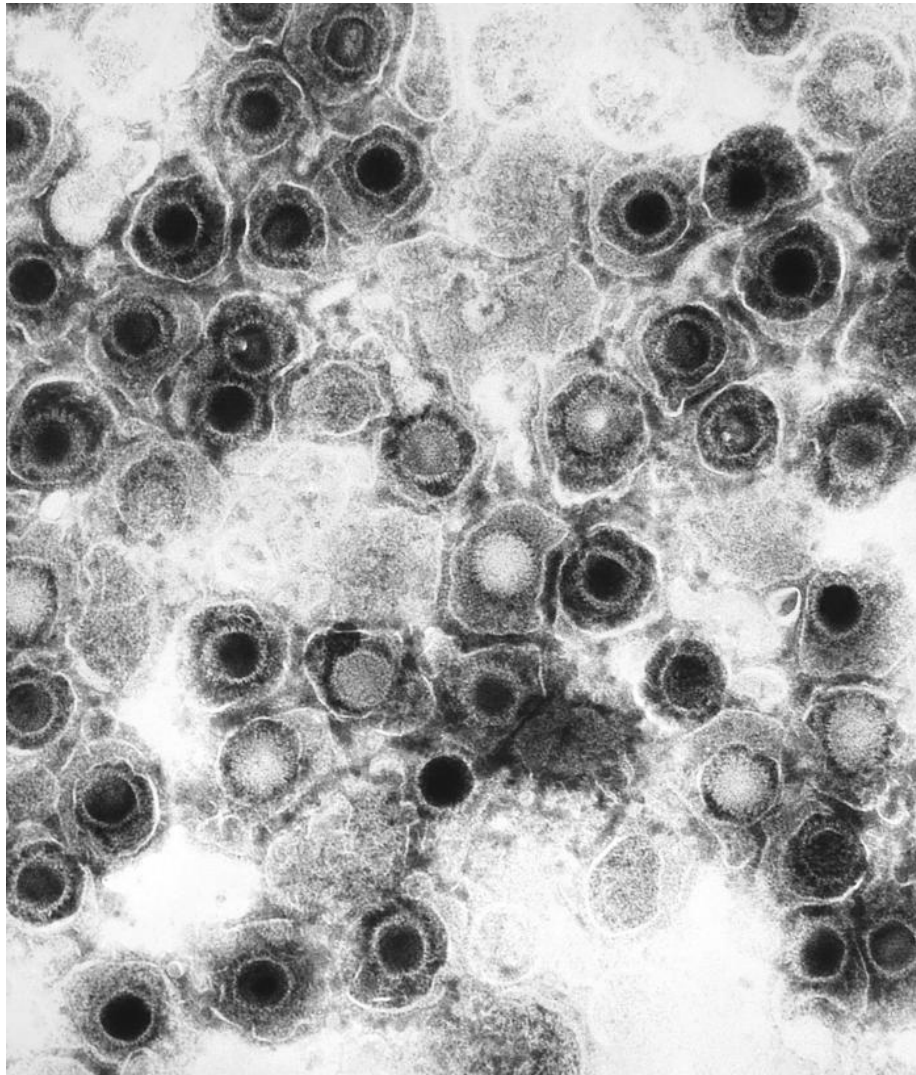
1900 - 2009

BERNHARD NOCHT INSTITUTE FOR TROPICAL MEDICINE

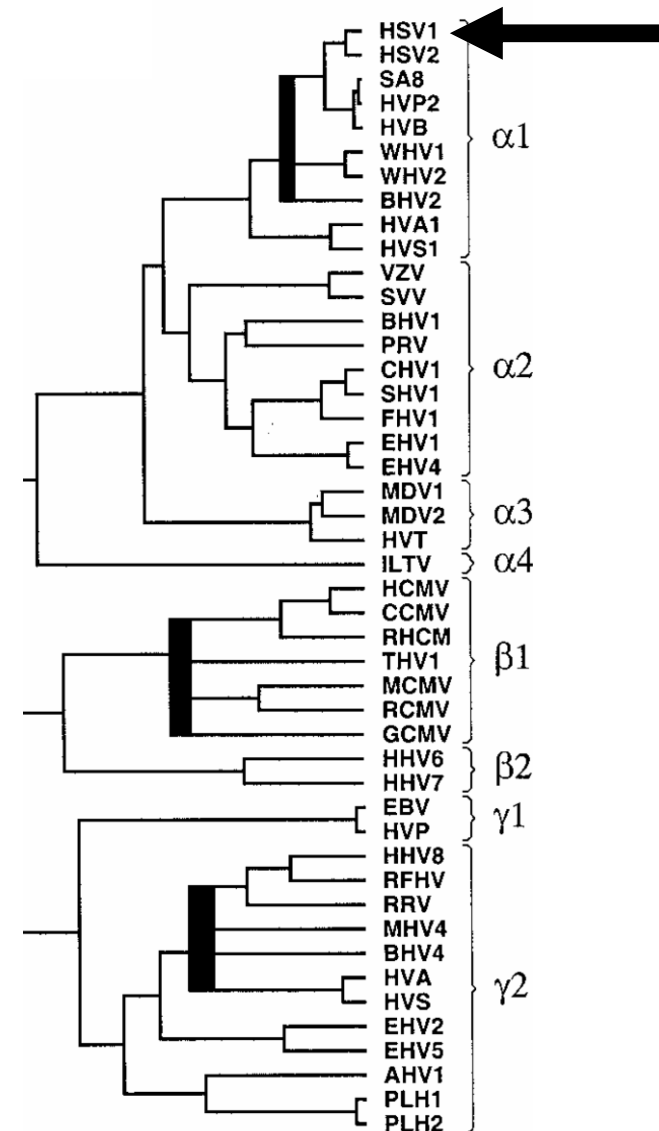
FREE AND HANSEATIC CITY OF HAMBURG

JONAS SCHMIDT-CHANASIT

# Herpes simplex virus type 1 (HSV-1) belonging to the subfamily *Alphaherpesvirinae* of the family *Herpesviridae*



HSV-1 particles (TEM)



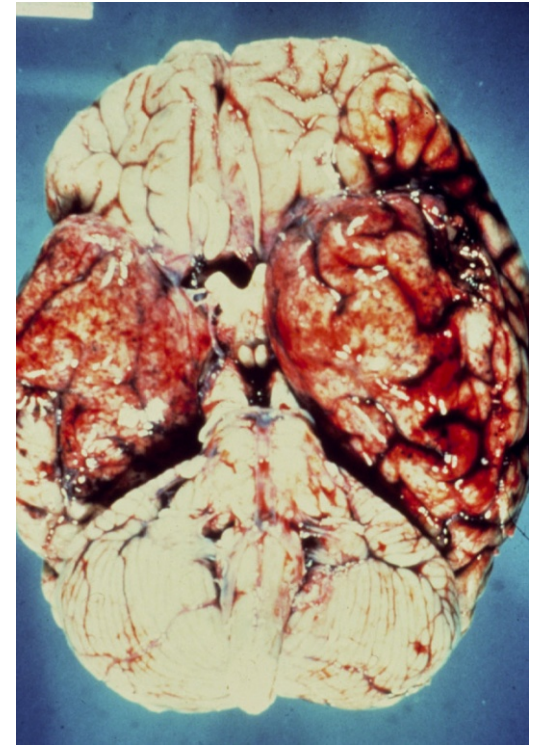
# HSV-1 causes a lifelong infection in humans



herpes labialis



herpes genitalis

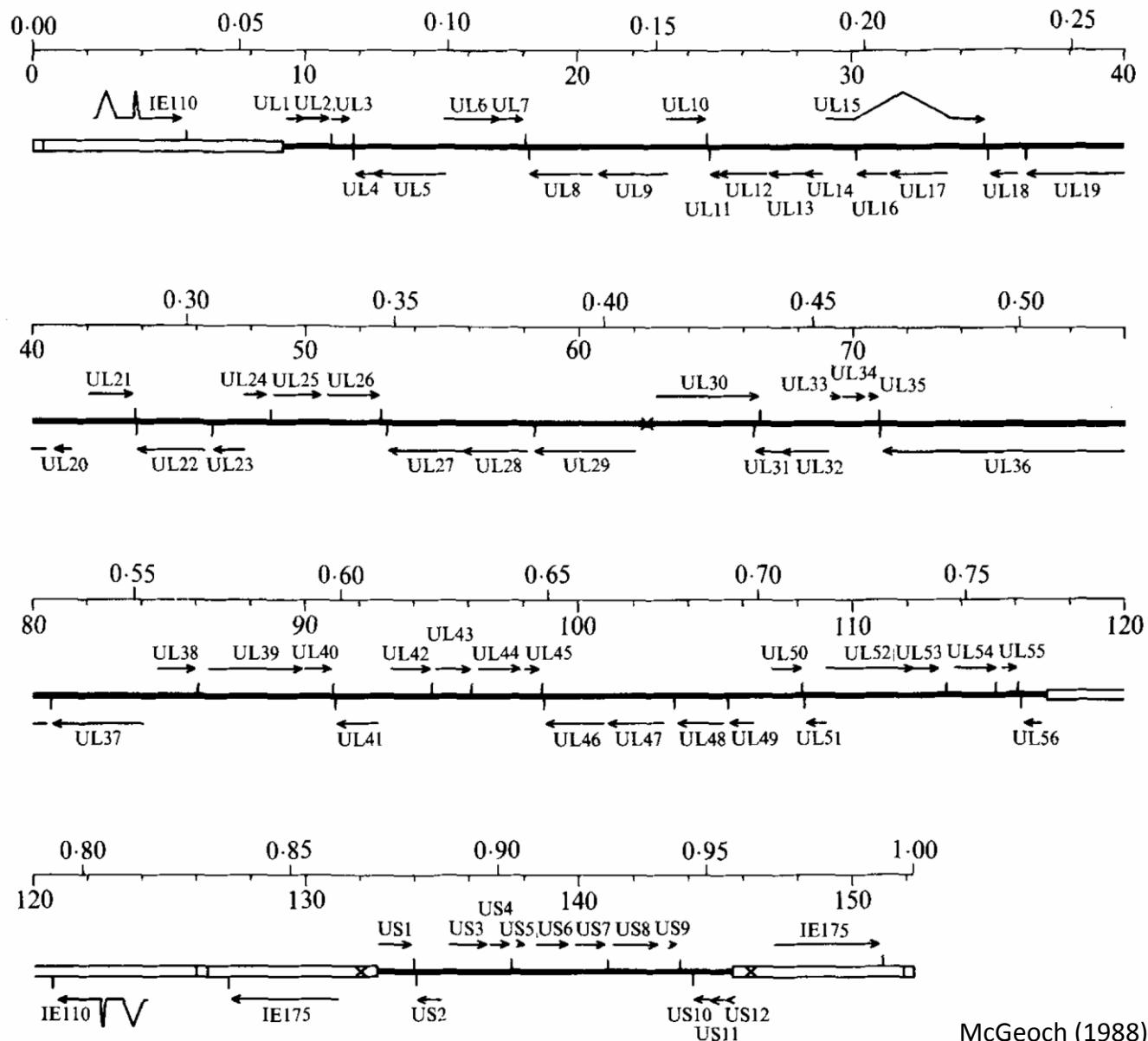


herpes encephalitis

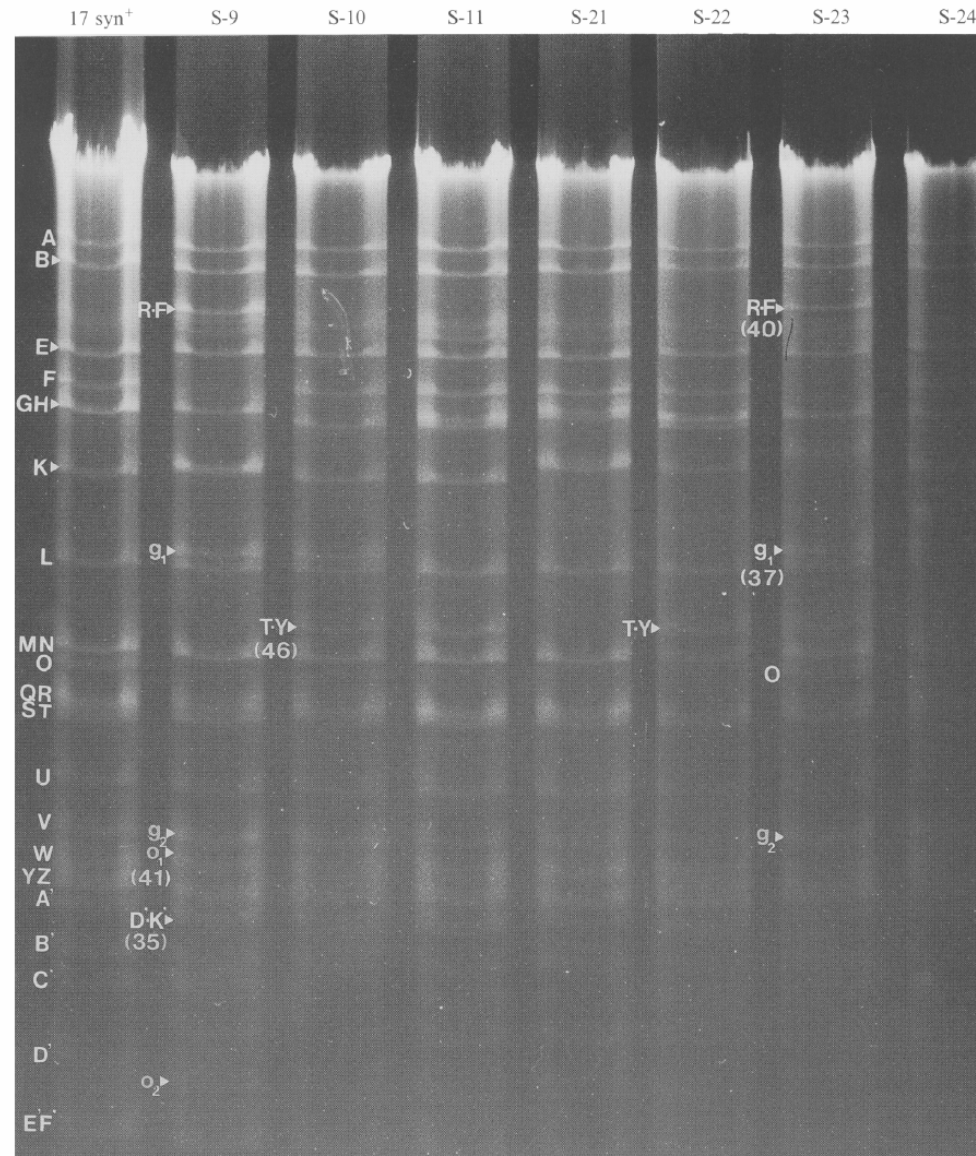
# First full-genome analysis of HSV-1 in 1988

1534

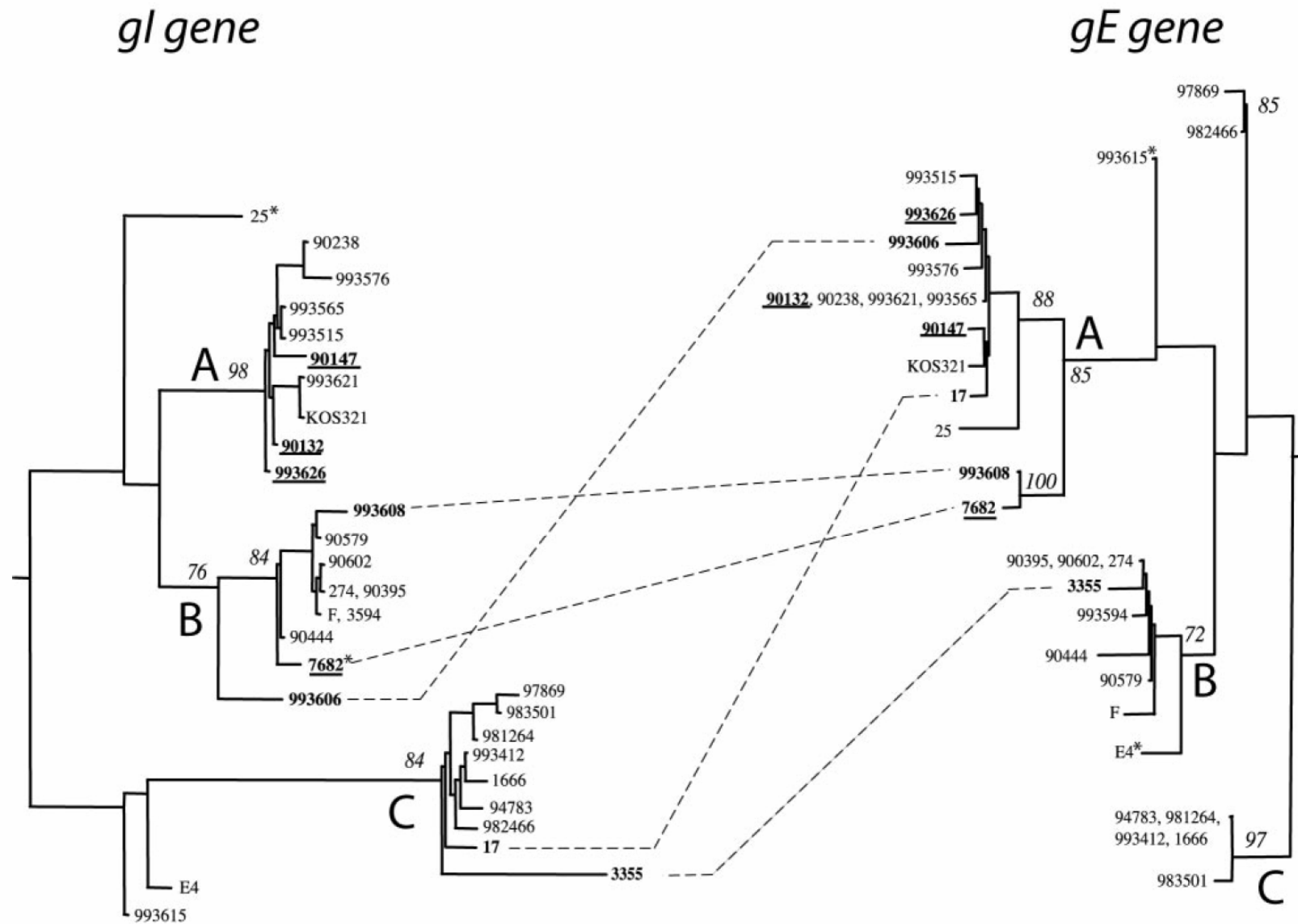
D. J. McGEEOCH AND OTHERS



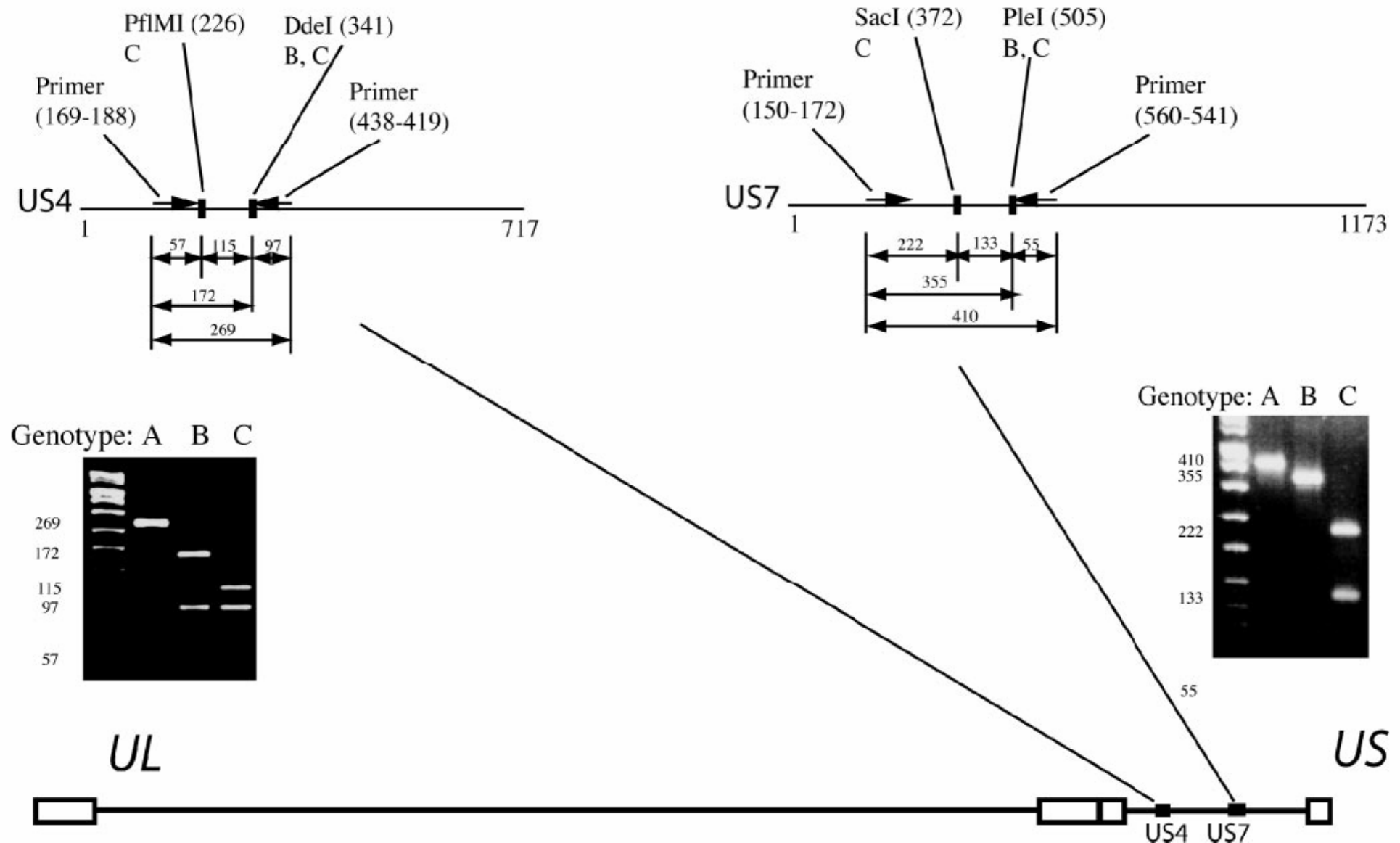
# Genetic diversity among HSV-1 strains was initially described using restriction fragment length polymorphisms (RFLP)



# Recently three different HSV-1 genotypes were described on DNA sequence data of the glycoprotein E, G and I genes



# A rapid and accurate method for high-throughput HSV-1 genotyping was developed on the basis of PCR and RFLP

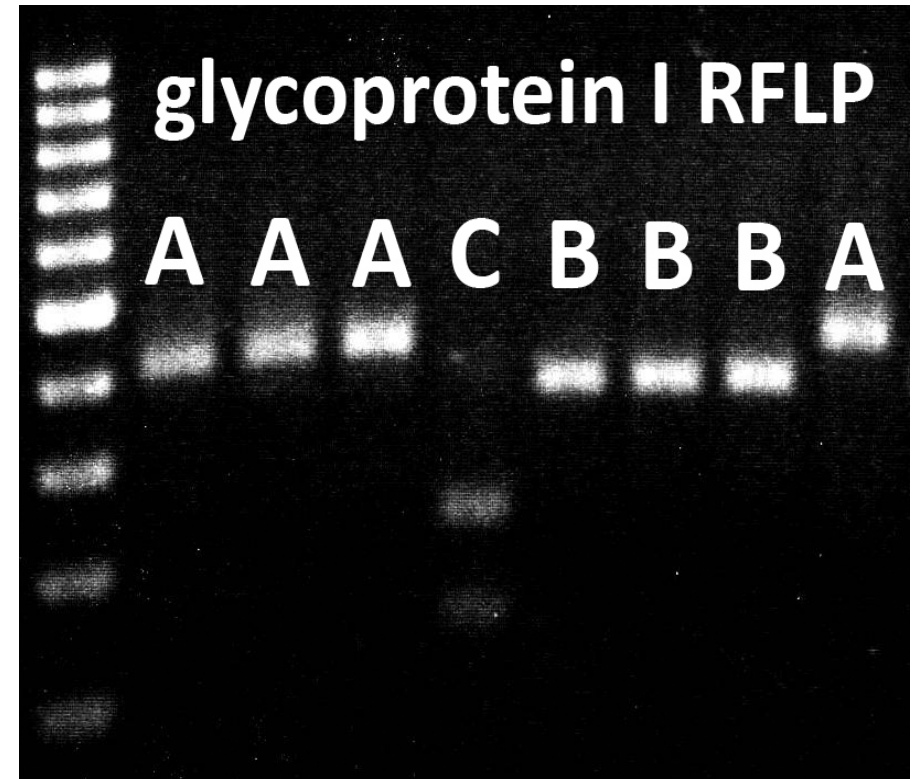
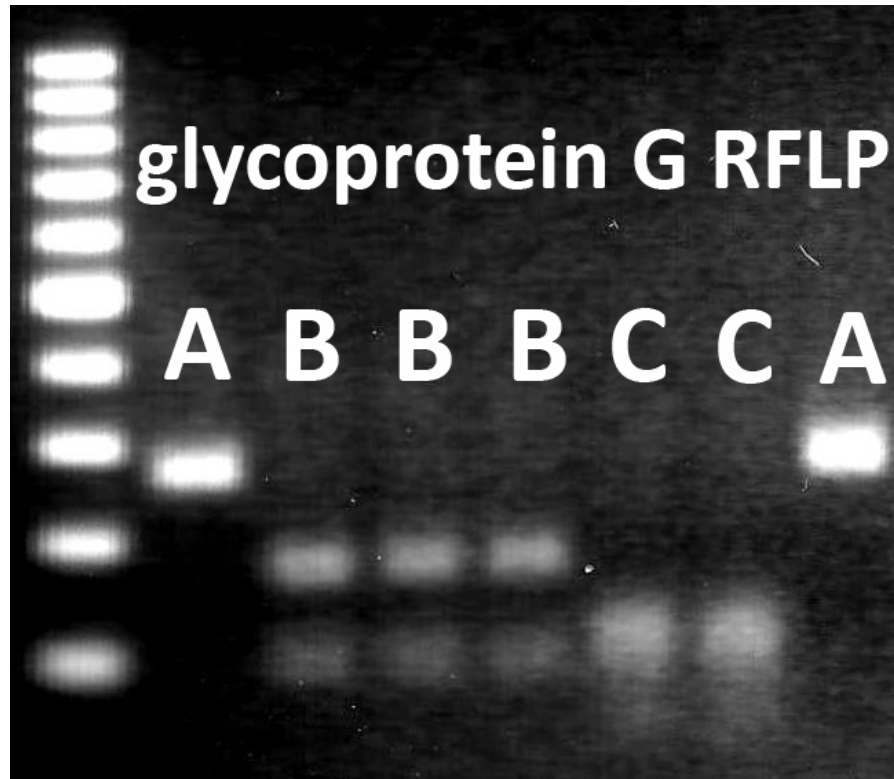


# **Objective**

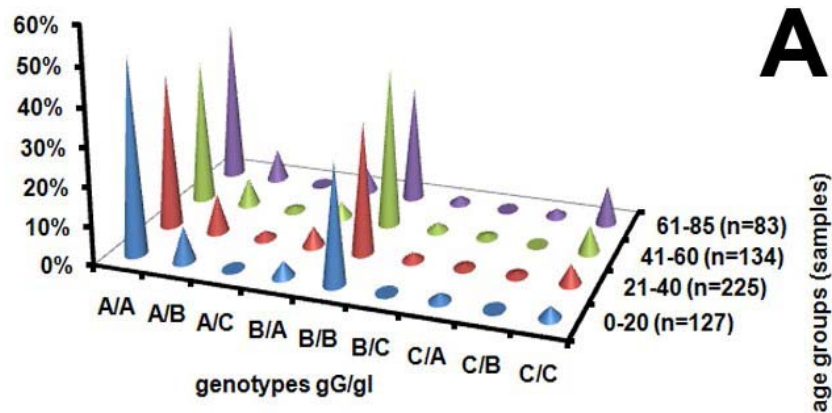
- 1. To type the circulating HSV-1 wild-type strains in  
Germany**
- 2. To monitor potential changes in the molecular  
epidemiology over the past 10 years**



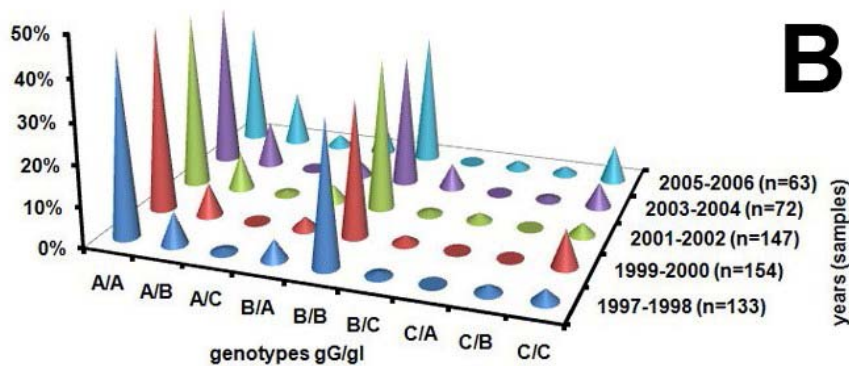
# 569 clinical HSV-1 isolates from a 10-year survey in Germany were genotyped



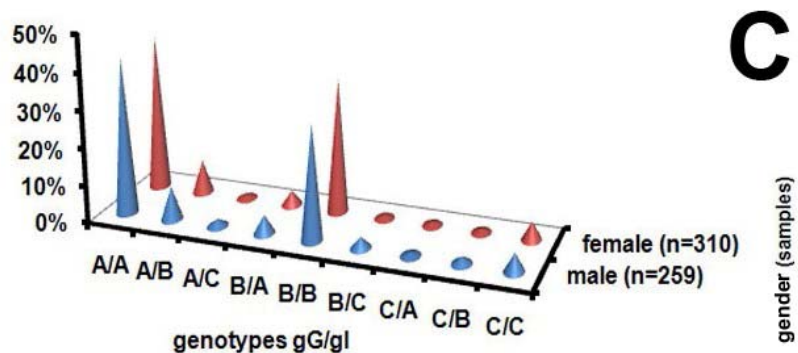
# Genotypes A and B strains represented 76% of all strains analyzed



**no association of HSV-1 genotypes and age groups**

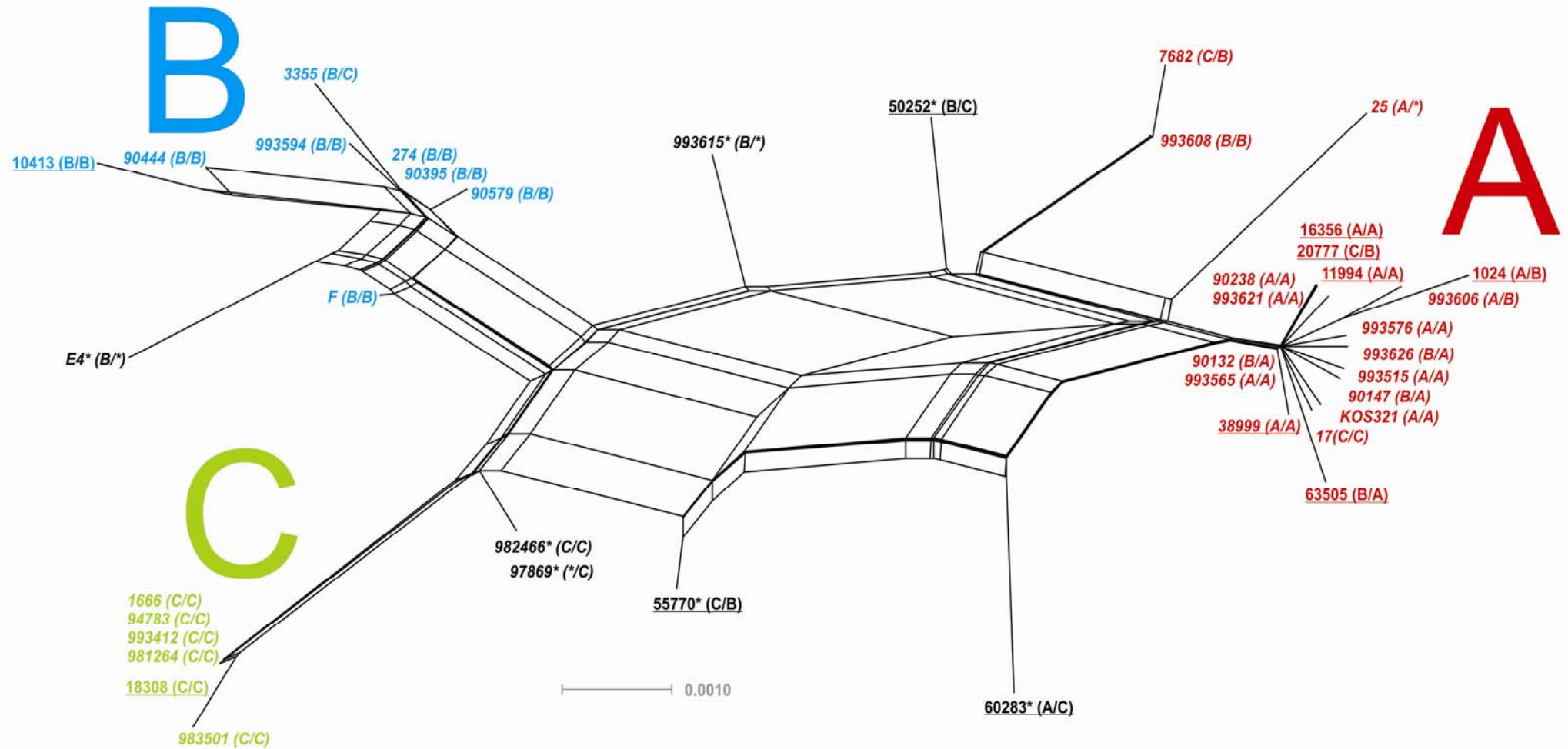


**no change of the HSV-1 genotype distribution within the last 10 years**

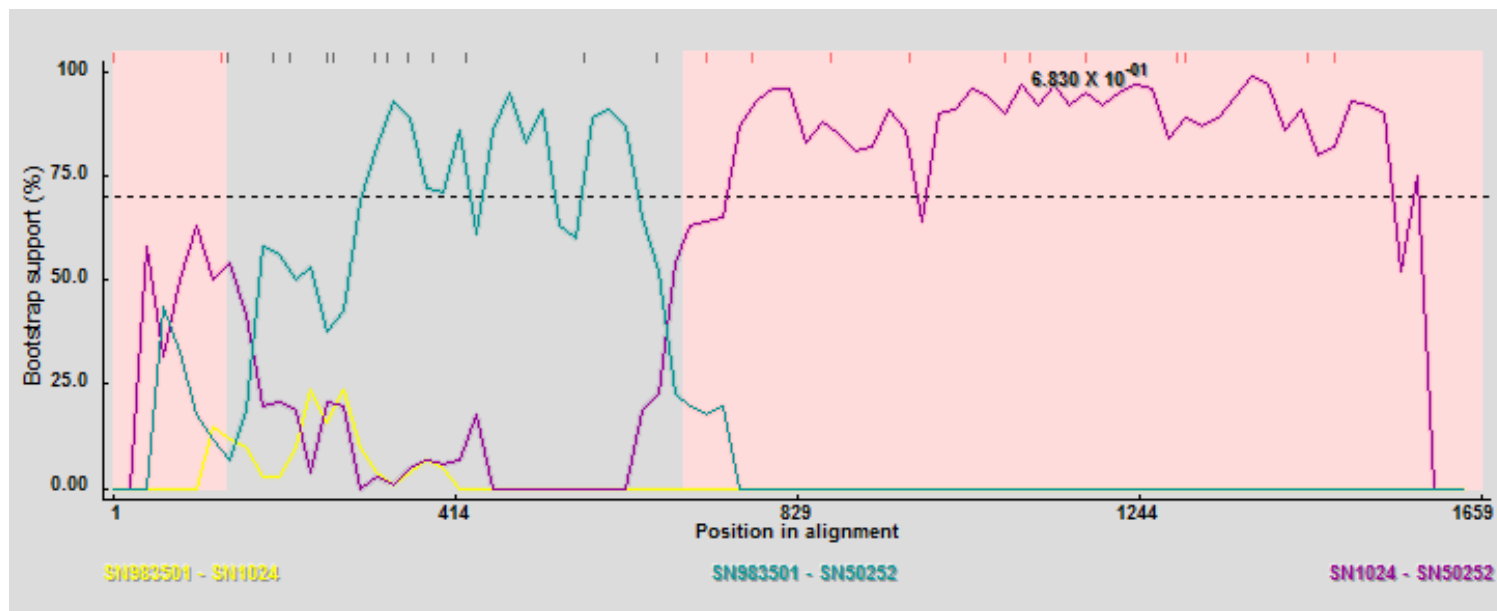
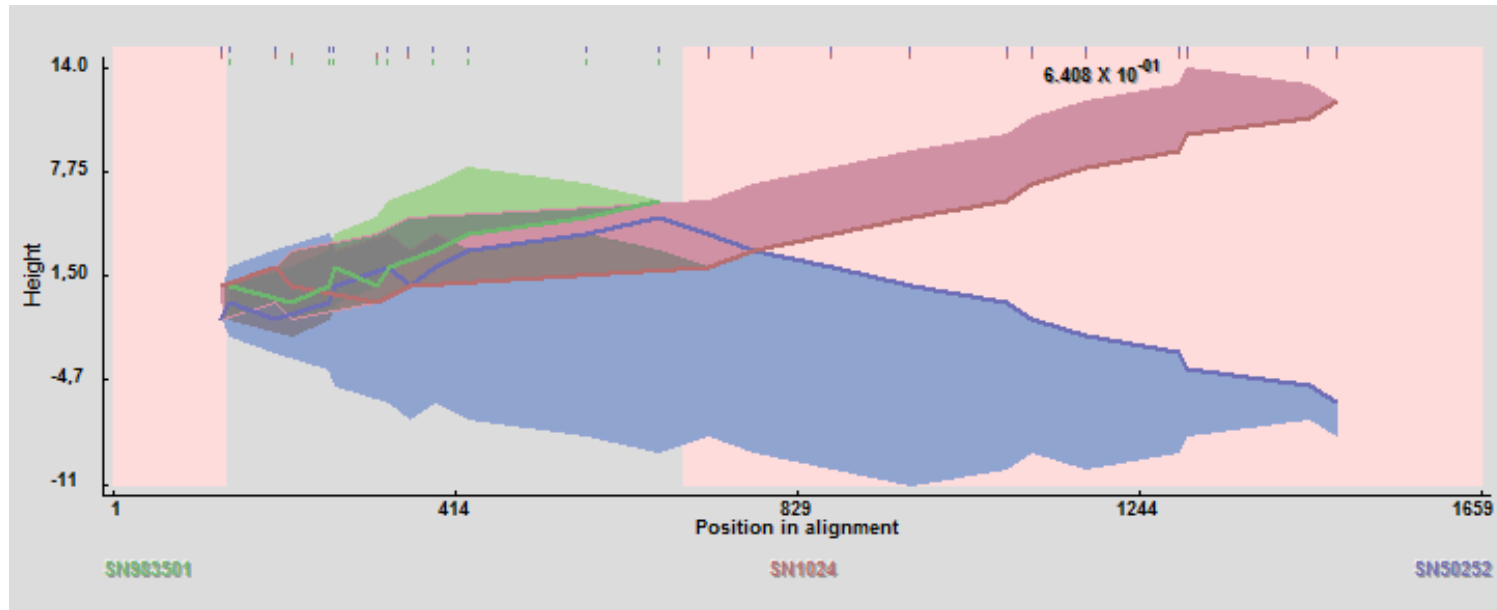


**no association of HSV-1 genotypes and gender**

# RFLP results were confirmed by phylogenetic analysis of the glycoprotein E coding DNA sequences



# Identification of gE recombination breakpoints by RDP and 3SEQ methods



# Schematic representation of a gE recombination analysis including only phylogenetically informative sites

positions and transversions		196	333	358	388	429	557	558	559	560	561	562	TV 573	660	721	726	TV 775	870	TV 891	966	TV 1000	1083	TV 1113	TV 1179	1291	1301	1449	TV 1482	
gE genotype	isolate																												
A	1024	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
	16356	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
	20777	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
	38999	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
	11994	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
	63505	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
A/C	60283*	T	A	G	C	C	-	-	-	-	-	-	C	T	A	C	G	G	G	G	G	C	C	A	C	C	A	T	
B/A	50252*	T	G	G	T	T	G	C	G	A	G	G	A	C	A	C	T	A	G	A	G	T	C	A	C	C	A	G	
B	10413	T	G	G	T	T	G	C	G	A	G	G	A	C	G	T	T	G	T	G	T	C	A	A	C	C	A	G	
C	18308	C	G	A	T	T	-	-	-	-	-	-	A	C	G	C	G	G	G	G	G	C	A	C	T	T	G	T	
A/C	55770*	T	A	G	C	C	-	-	-	-	-	-	A	C	G	C	G	G	G	G	G	C	A	A	T	C	G	T	

# Conclusions

- 1. Stable distribution of HSV-1 genotypes and recombinants within age groups and over a period of 10 years**
- 2. Homologous recombination seems to be an important feature in the evolution of the HSV-1 genome**

# Acknowledgment



**Thank you for your attention**