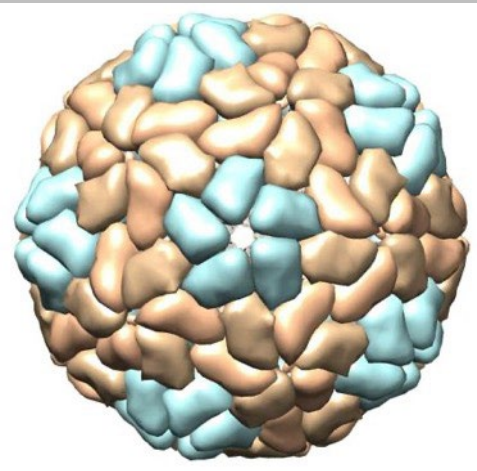


Hepatitis A outbreak in a refugee shelter in Kiel, northern Germany



**VHPB Technical Meeting: Addressing Viral Hepatitis
Among Europe's Migrant and Refugee Population,
Antwerp, Belgium**

26 March 2024 – 11:40–12:00

Prof. Jürgen Wenzel, MD

National Consultant Laboratory for HAV and HEV
University Medical Center Regensburg
Germany



Universität Regensburg

Historic Milestones HAV

1923 G. Blumer: Study on 63 outbreaks of infectious jaundice in the U.S.A (1812–1922)

1973 Electron-optical imaging (NIAID/NIH)

Feinstone et al, Science 1973; 182(116):1026–1028

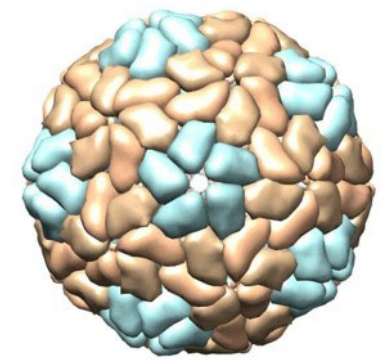
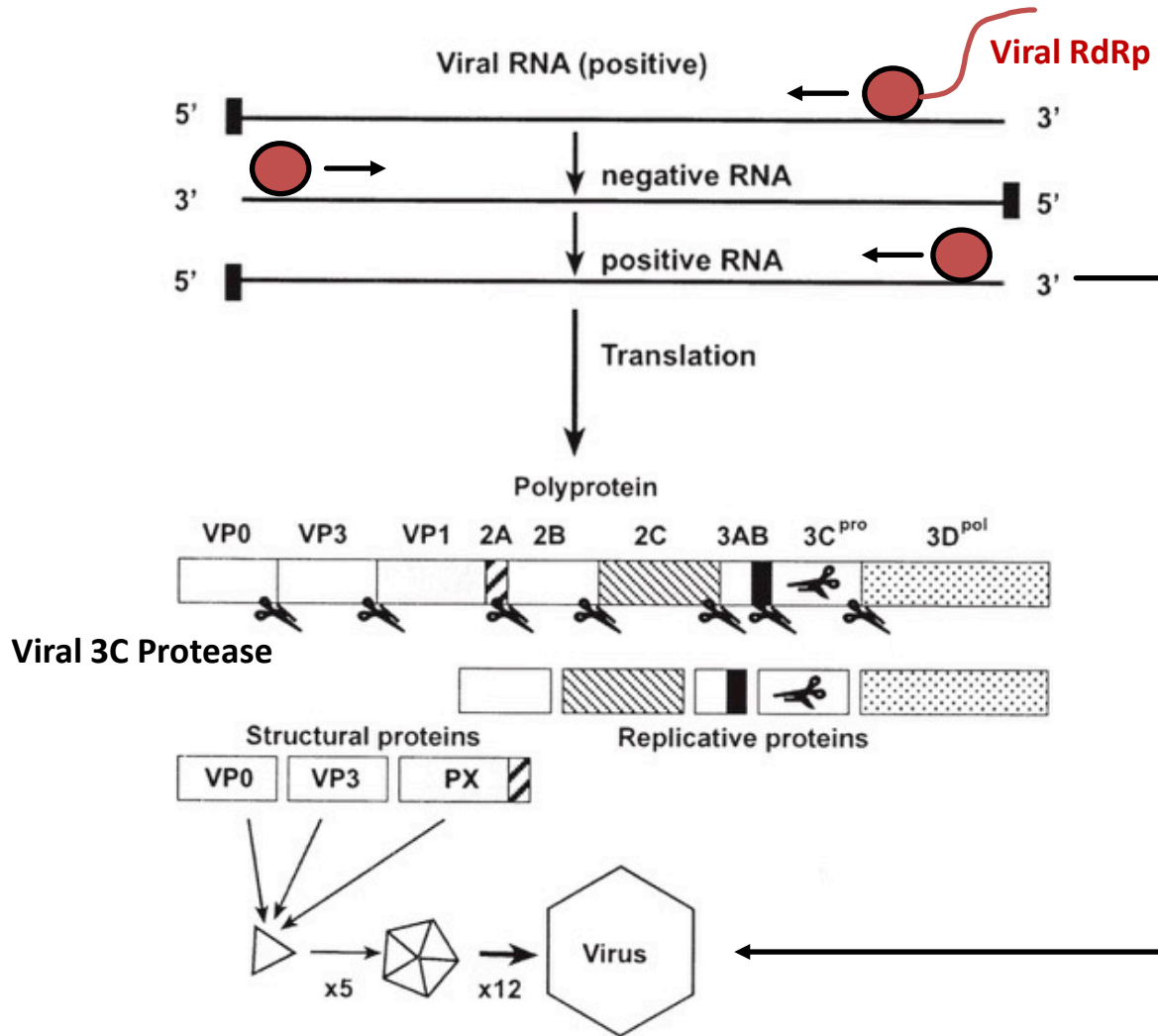
1979 P. Provost / G. Frösner: HAV-Isolation in cell culture

1996 Inactivated vaccine available

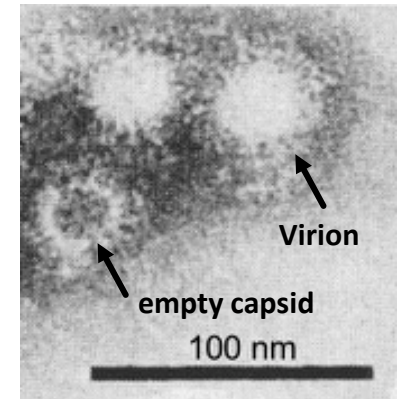


NIAID/NIH, www.niaid.nih.gov

Left to right: **Robert Purcell, M.D.**; **Albert Kapikian, M.D.**; and **Stephen Feinstone, M.D.**, first identified hepatitis A virus (HAV) in 1973. Their groundbreaking work led to development of the first licensed HAV vaccine



www.rcsb.org/structure/5WTE



Feinstone et al, Science 1973

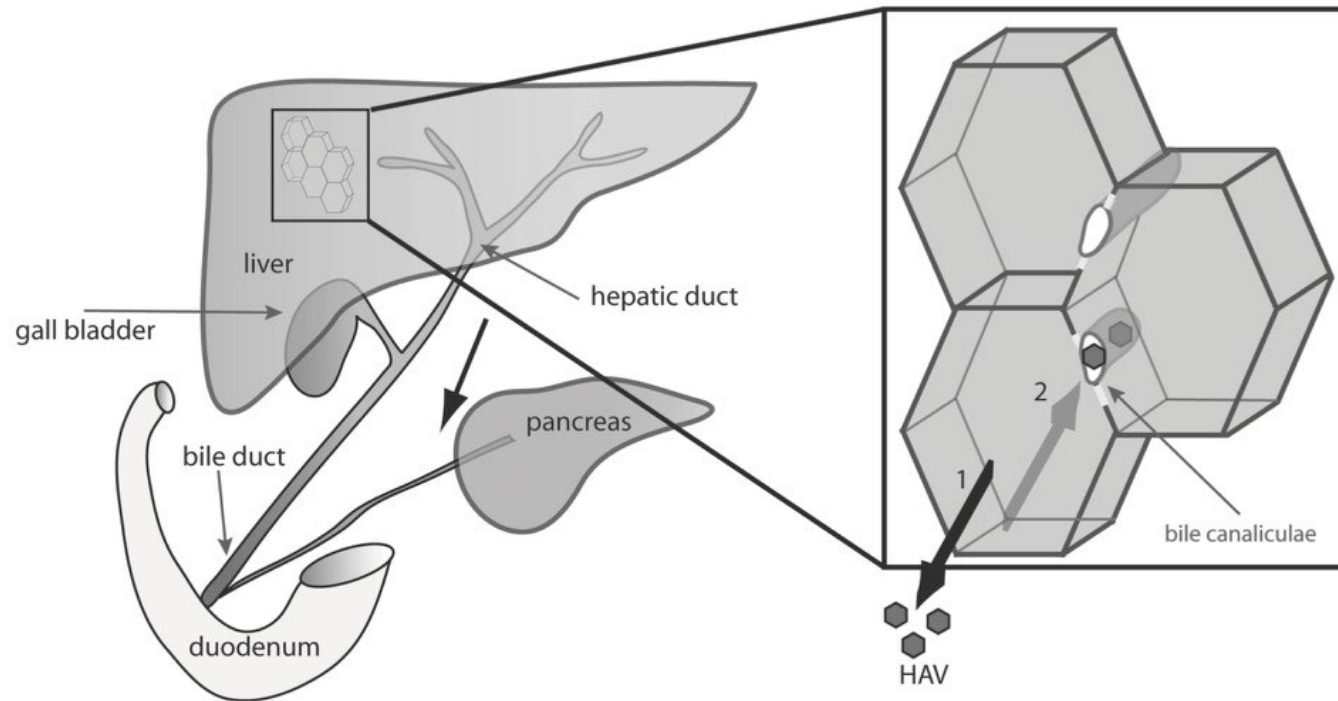
Monomer

Pentamer

HAV-capsid

Receptor: TIM-1/TIM-3 or IgA-receptor

Export of HAV from hepatocytes

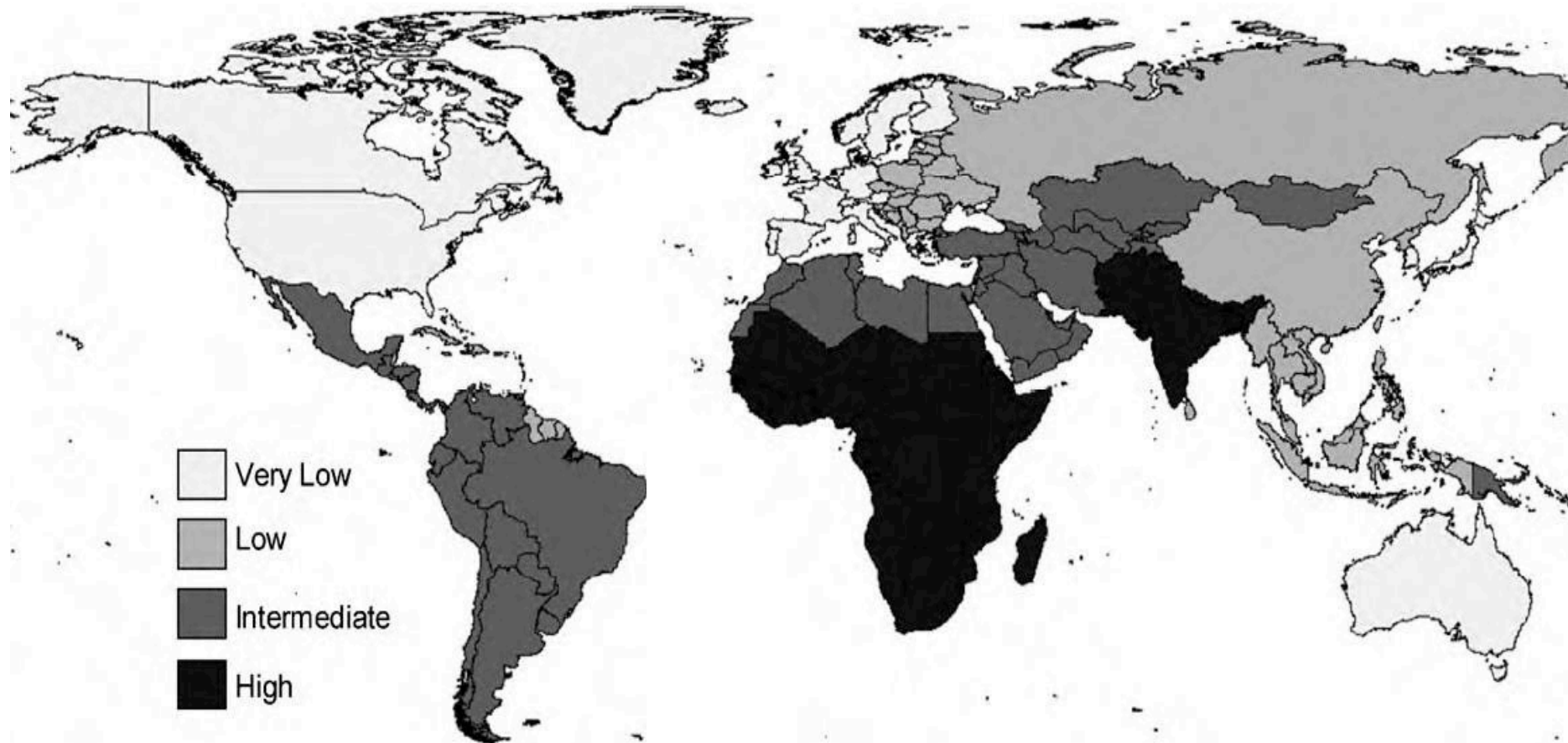


- 1) HAV is exported into the blood via the basolateral membrane of the hepatocytes
- 2) and probably travels by "transcytosis" to the apical surface and finally into the bile duct system => stool („faecal-oral-infection route“)

Liver cells are destroyed by cytotoxic CD8+ T lymphocytes, and not by the lytic activity of the virus

Hepatitis A prevalence

K.H. Jacobsen, S.T. Wiersma / Vaccine 28 (2010) 6653–6657



HAV sero-prevalence

K.H. Jacobsen, S.T. Wiersma / Vaccine 28 (2010) 6653–6657

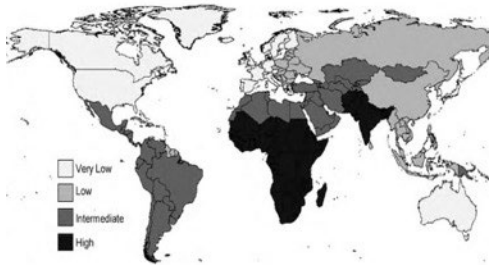


Figure 70. Plot of Estimated Seroprevalence by Age in **North Africa and the Middle East.**

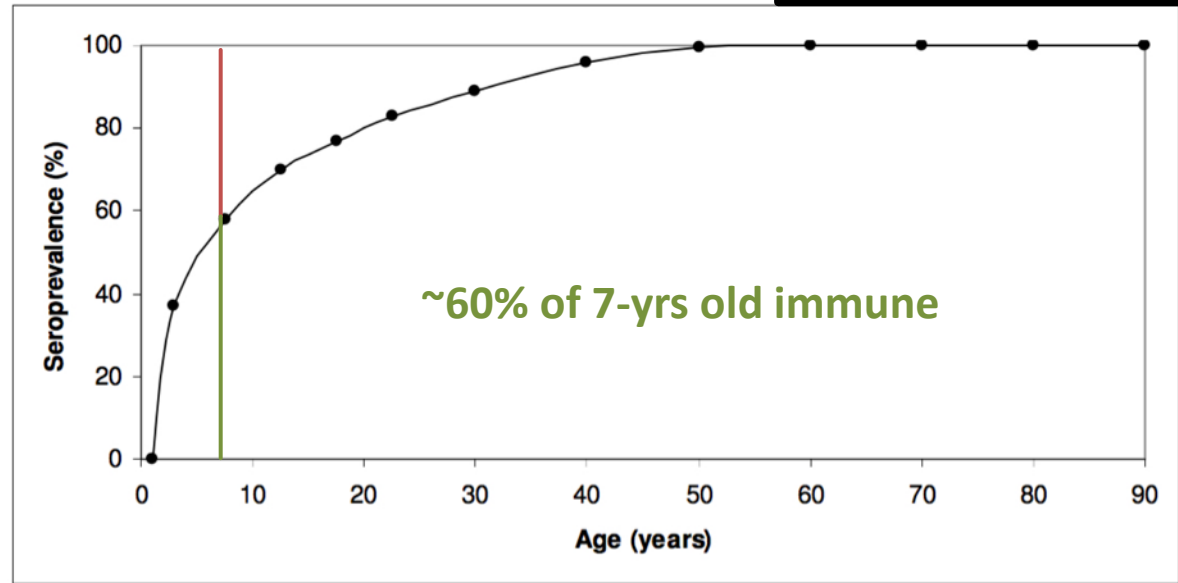
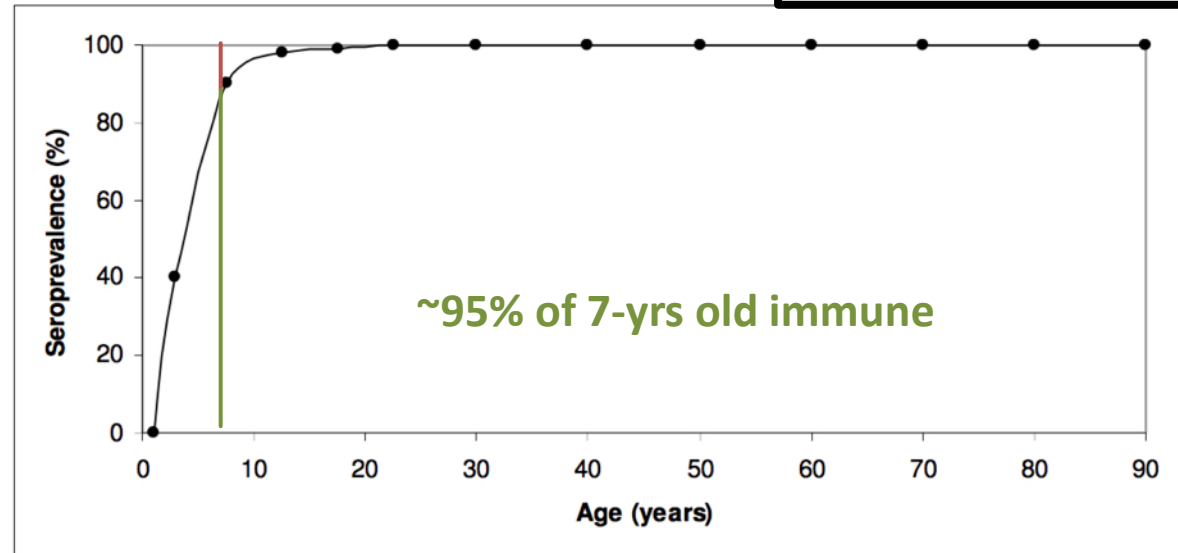


Figure 78. Plot of Estimated Seroprevalence by Age in **Central sub-Saharan Africa.**



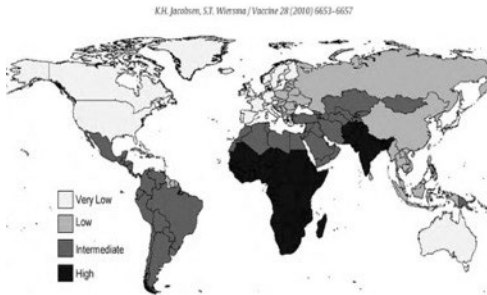
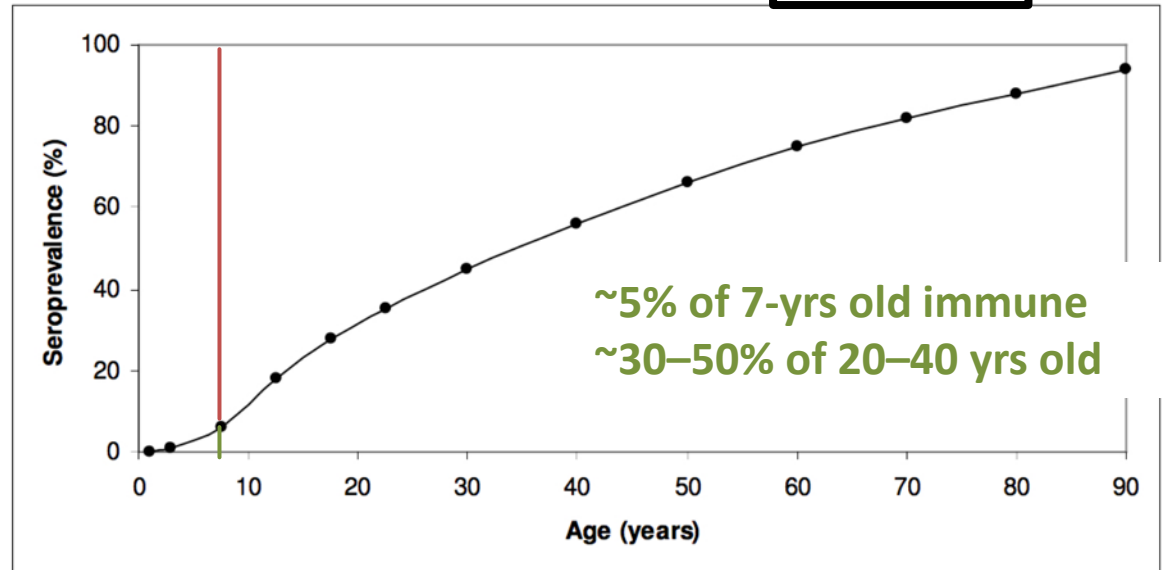
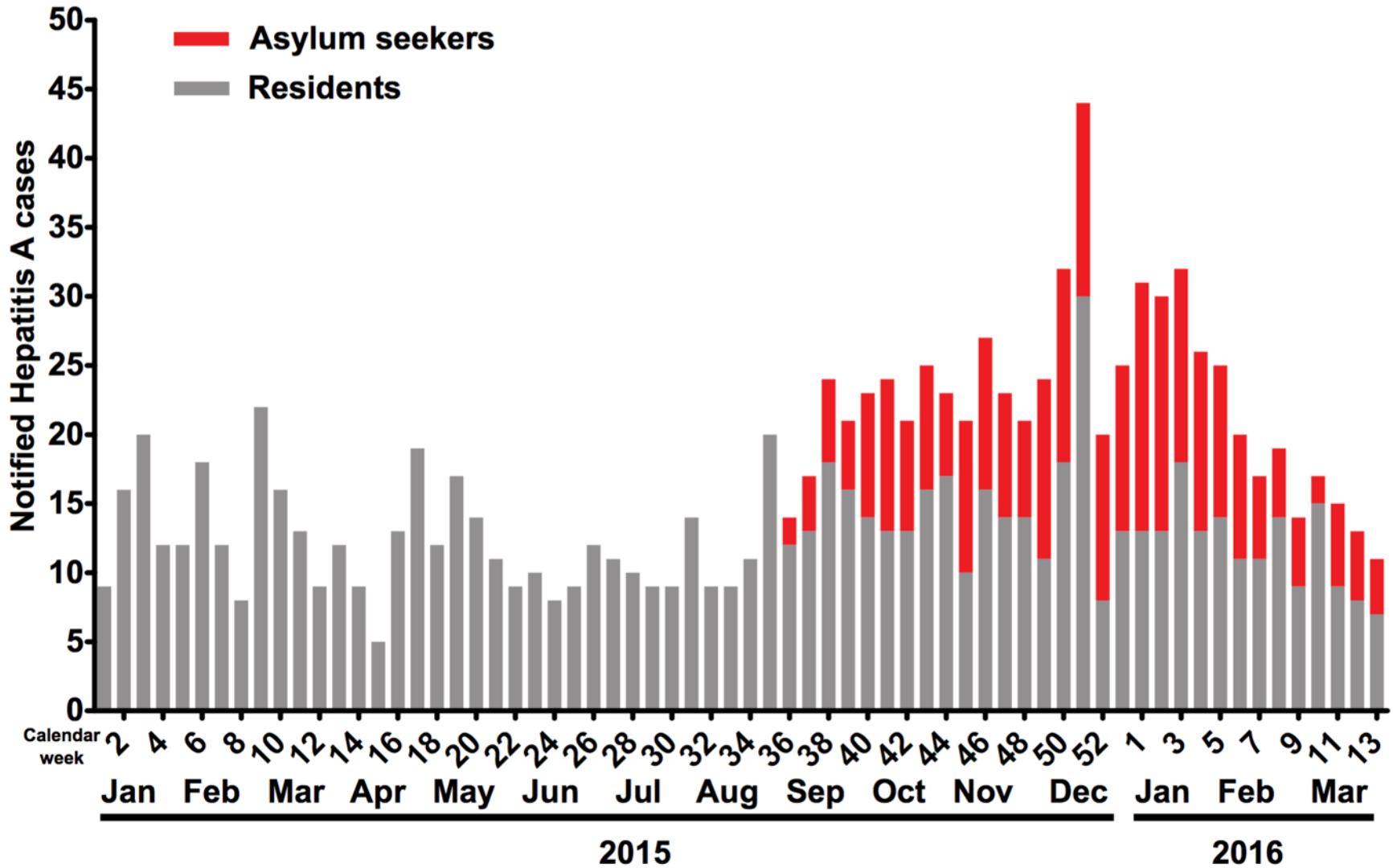


Figure 59. Plot of Estimated Seroprevalence by Age in **Western Europe.**

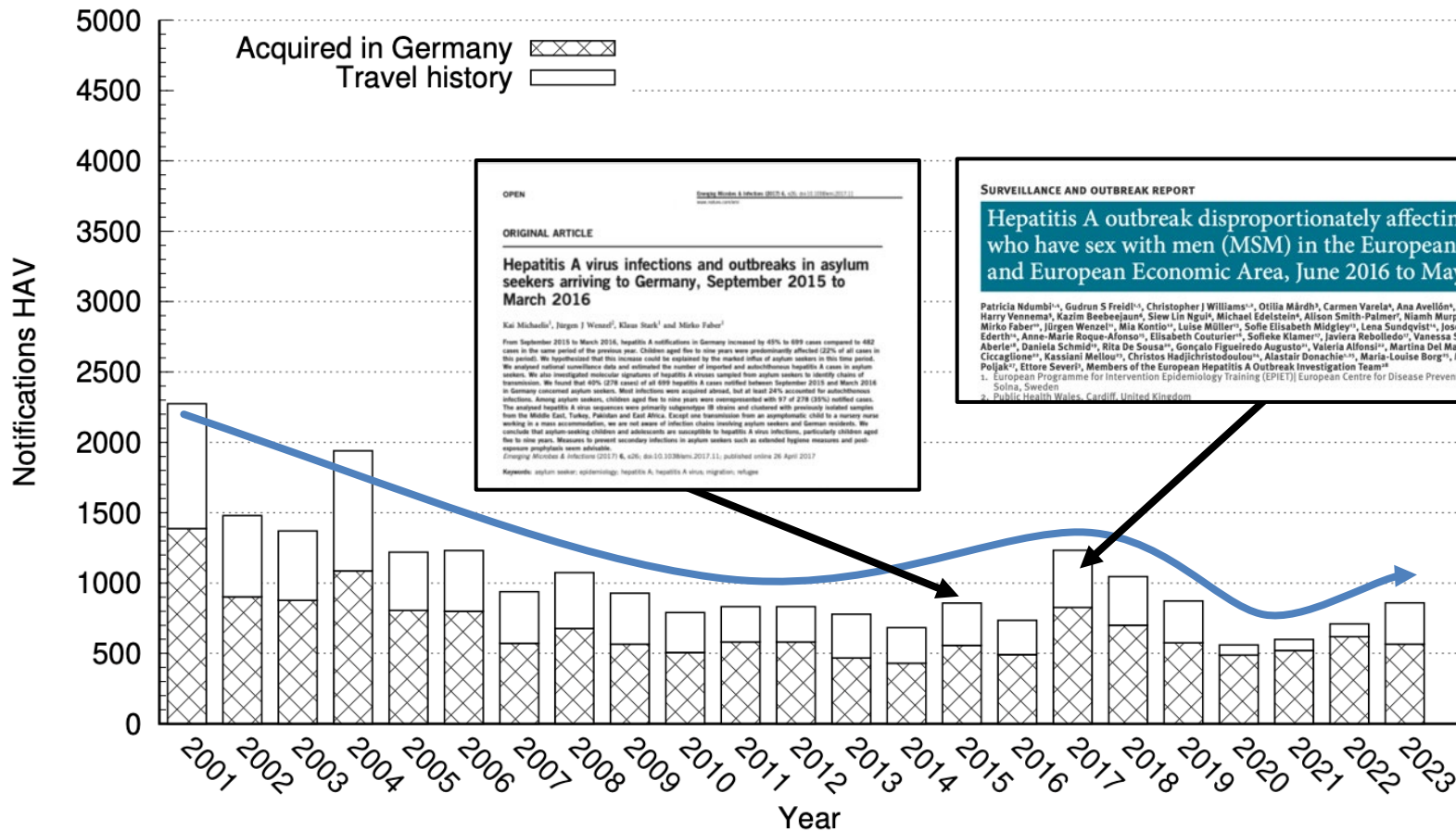


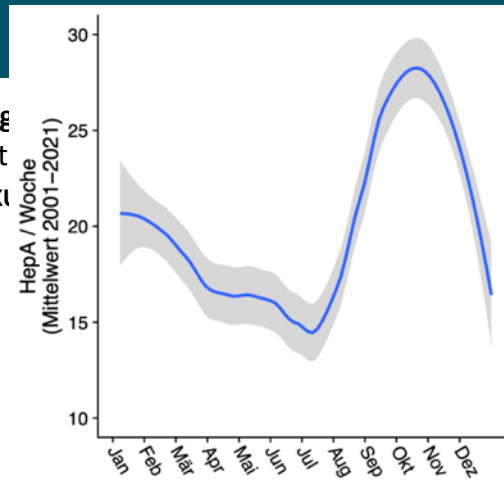
People greet refugees as they arrive at the main train station in Munich, Germany, 2015





HAV-Notifications, Germany, 2001–2023





Current HAV-"risk factors" in Western countries

- **Travel** to HAV endemic areas without vaccination (or contact to travellers)
- Contaminated **imported food** (e.g. frozen berries, dates)
- Contaminated food due to **infected food handlers**
- Transmission from **person to person** (e.g. MSM-outbreak 2017)

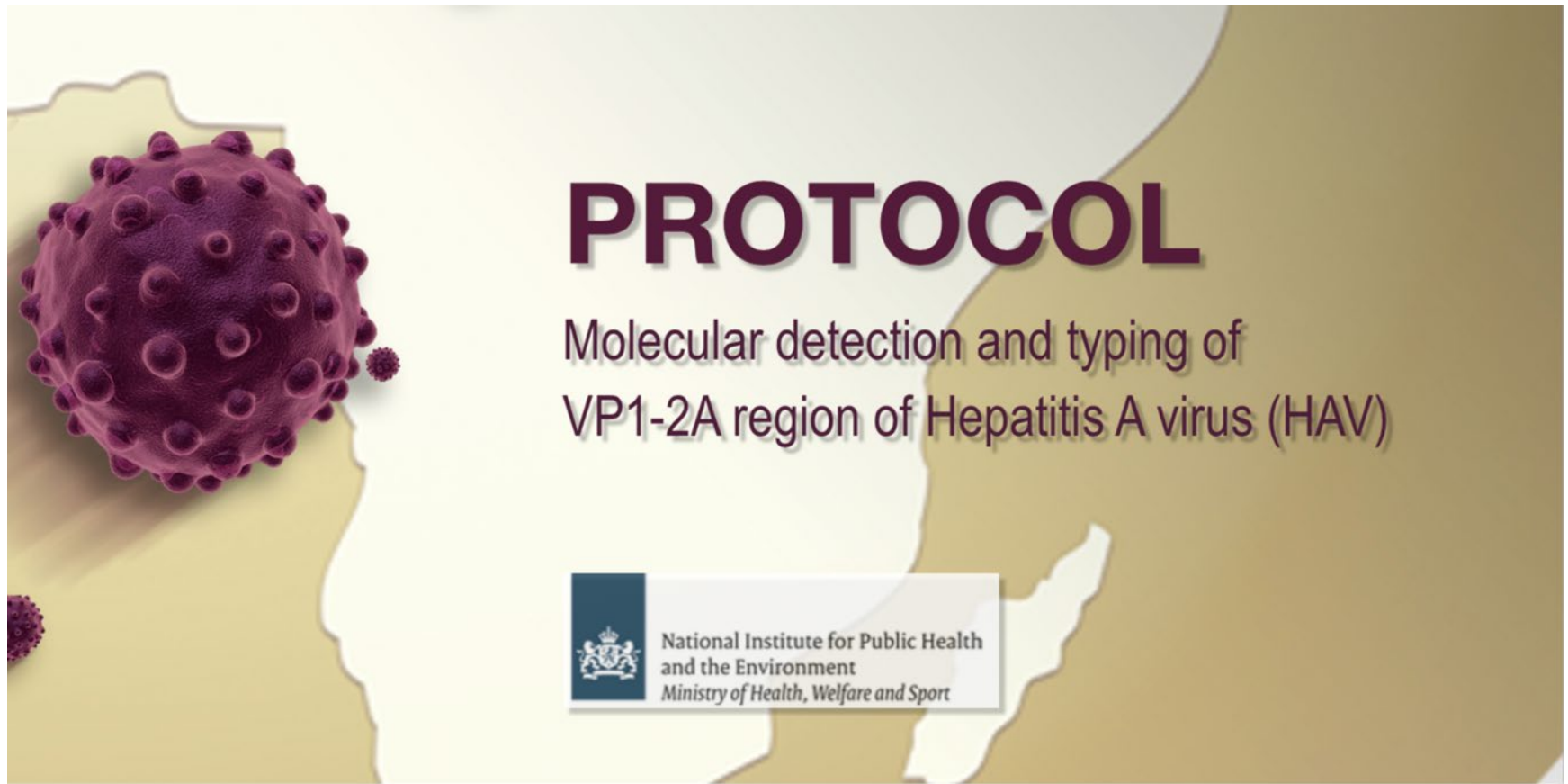


Amit Bhargava/Associated Press
A sewage pipe in Varanasi, India, in 2001 that moves waste to the Ganges River.



What tools do we have to identify HAV outbreak-strains in the lab?

HAVnet Typing Protocol



Sequencing of the VP1-2A-region

```

2821 attccttattt atatgctgtg tctggagcac tggatggttt gggtgacaag acagattcta
2881 catttggatt ggtttctatt cagattgcaa attacaatca ttctgatgaa tacttgtctt
2941 ttagttgt ttttcccaga gctccattga
3001 actcaaat aattgcagct ggagacttgg
3061 agtcatca atttgagagt catatagaat
3121 gcaggaag acaaagactc aagtatgctc
3181 aggaagaatt gtcaaataaa gtacttccac ccctaggaa aatgaaggga ctgttttcac
3241 aagccaaaat ttctcttttt tatactgagg agcatgaaat aatgaagttt tcttgagag
3301 gtgtgactgc tgatactaga gctttaagga ggtttggatt ctctttggcc gcaggcagaa
3361 gtgtgtggac tcttgaaatg gatgctgggg ttcttactgg gagactgatt agattgaatg
  
```

Unique genetic fingerprints of HAV outbreak-strains

349 nt *Grinde et al 1997 (VP1 inw)*

460 nt *HAVNet*

349 nt *CDC*

VP1-2A



Hepatitis A outbreak in a refugee shelter in Kiel, northern Germany

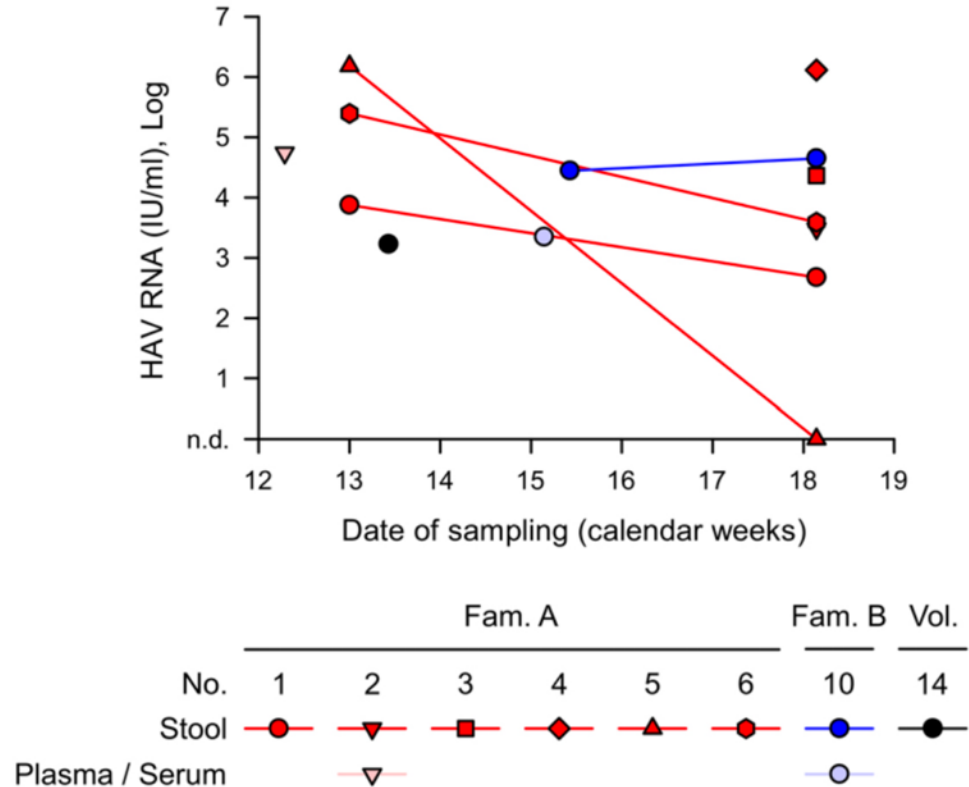


FIGURE 1 Hepatitis A virus (HAV) ribonucleic acid (RNA) concentration quantified by one-step reverse transcription and quantitative PCR in plasma/serum and stool of affected individuals

Hepatitis A outbreak in a refugee shelter in Kiel, northern Germany

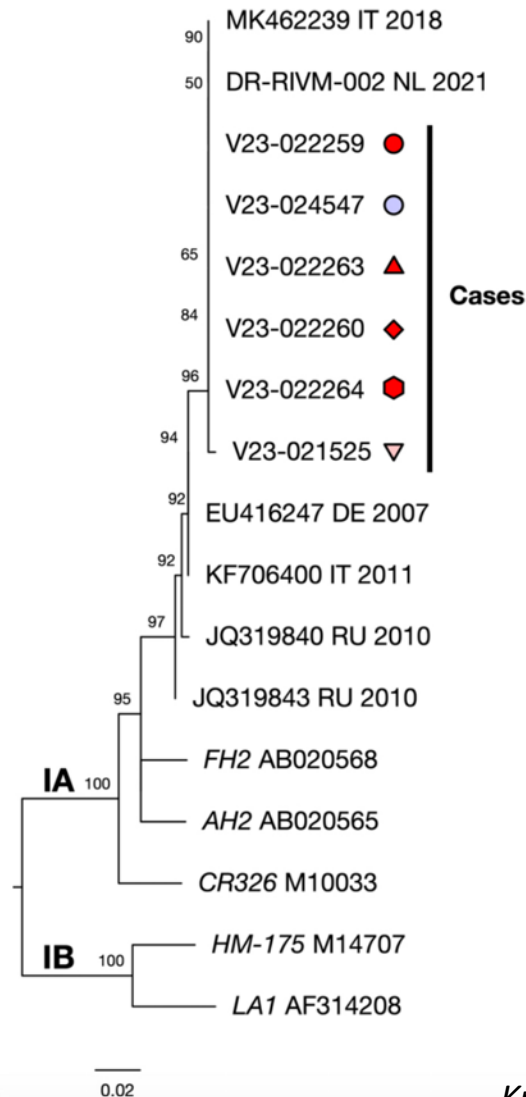


FIGURE 2 Rooted maximum likelihood phylogenetic consensus tree for viral protein 1 and protease 2A partial nucleotide sequences of hepatitis A virus (HAV) strains, hepatitis A outbreak Kiel, February–May 2023. All sequences of the outbreak-related strains cluster in HAV subgenotype IA. Sequences from five cases are 100% similar to a recent European outbreak sequence (strain HAV/Netherlands/DR-RIVM-002/2021). The sequence of case V23-021525 is 99.7% similar (one nucleotide difference in a 349-nt