

# THE IMPACT OF HCV DIVERSITY ON DIAGNOSIS TOOLS FOR HCV INFECTION

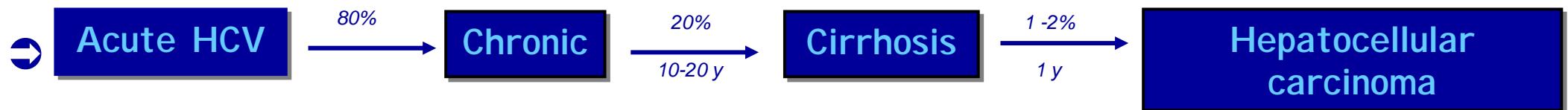
P. Mavromara, A. Sall, O. Kalinina, V. Horm, A. Budkowska and HCV Collaborative Team of the International Network of Pasteur Institutes



# HCV-INFECTION IS A MAJOR HEALTH PROBLEM WORLDWIDE

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- ⇒ HCV is a hepatotropic RNA virus and it is a major causative agent of human liver disease

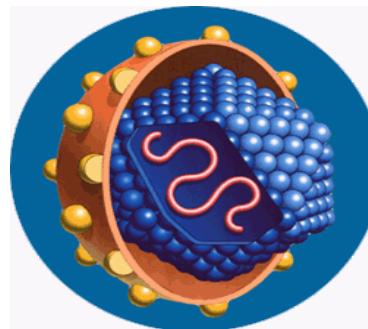


- ⇒ HCV infects over 170 million people worldwide and causes 476.000 deaths per year
- ⇒ Blood borne virus transmitted mainly parenterally
- ⇒ Current therapies for HCV infection (combination of pegylated IFN-α and ribavirin) show only limited efficacy and the development of a vaccine remains a major challenge

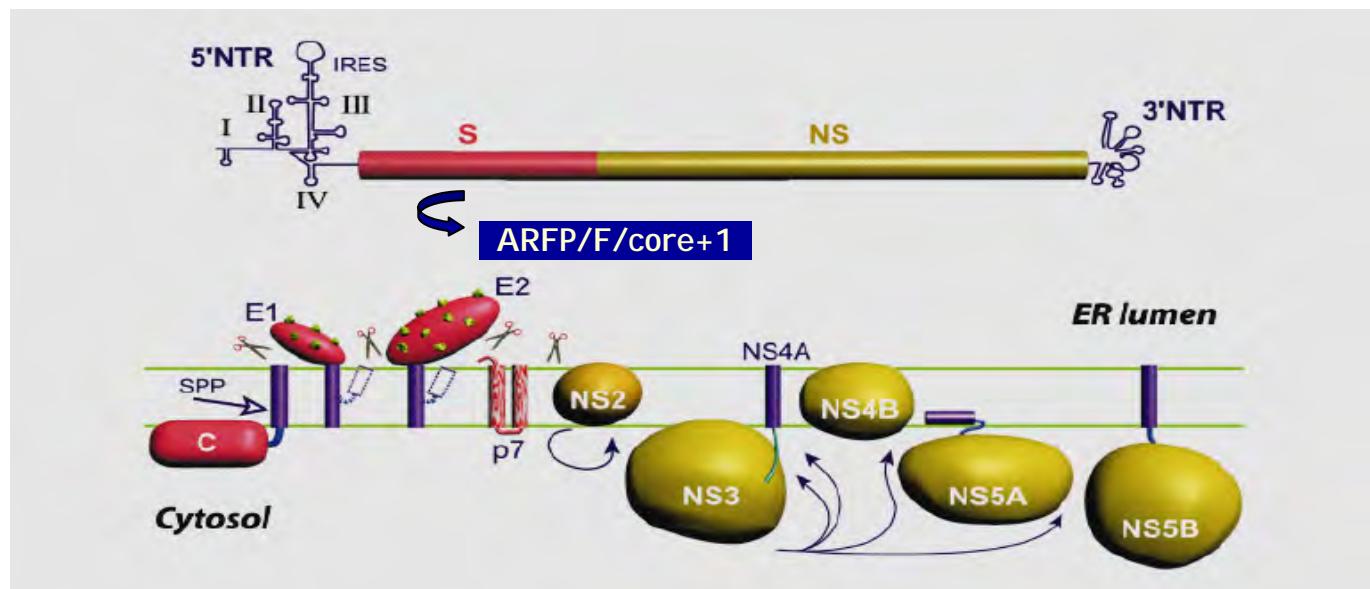
# HCV: THE VIRUS

HCV is a small enveloped RNA virus that is classified within the flaviviridae family

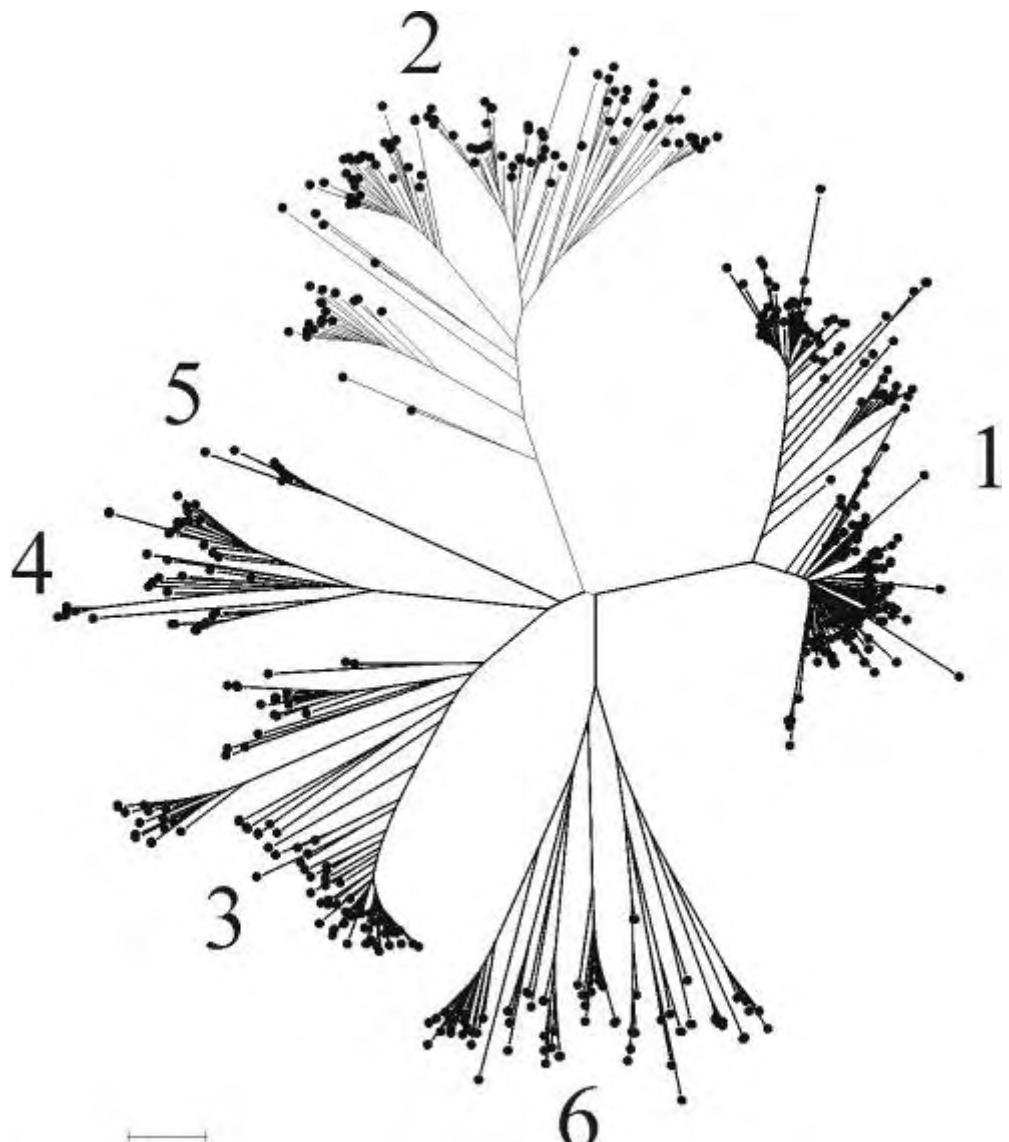
Exceptional degree of genetic heterogeneity



High propensity to establish chronic infection



# HCV GENETIC VARIABILITY



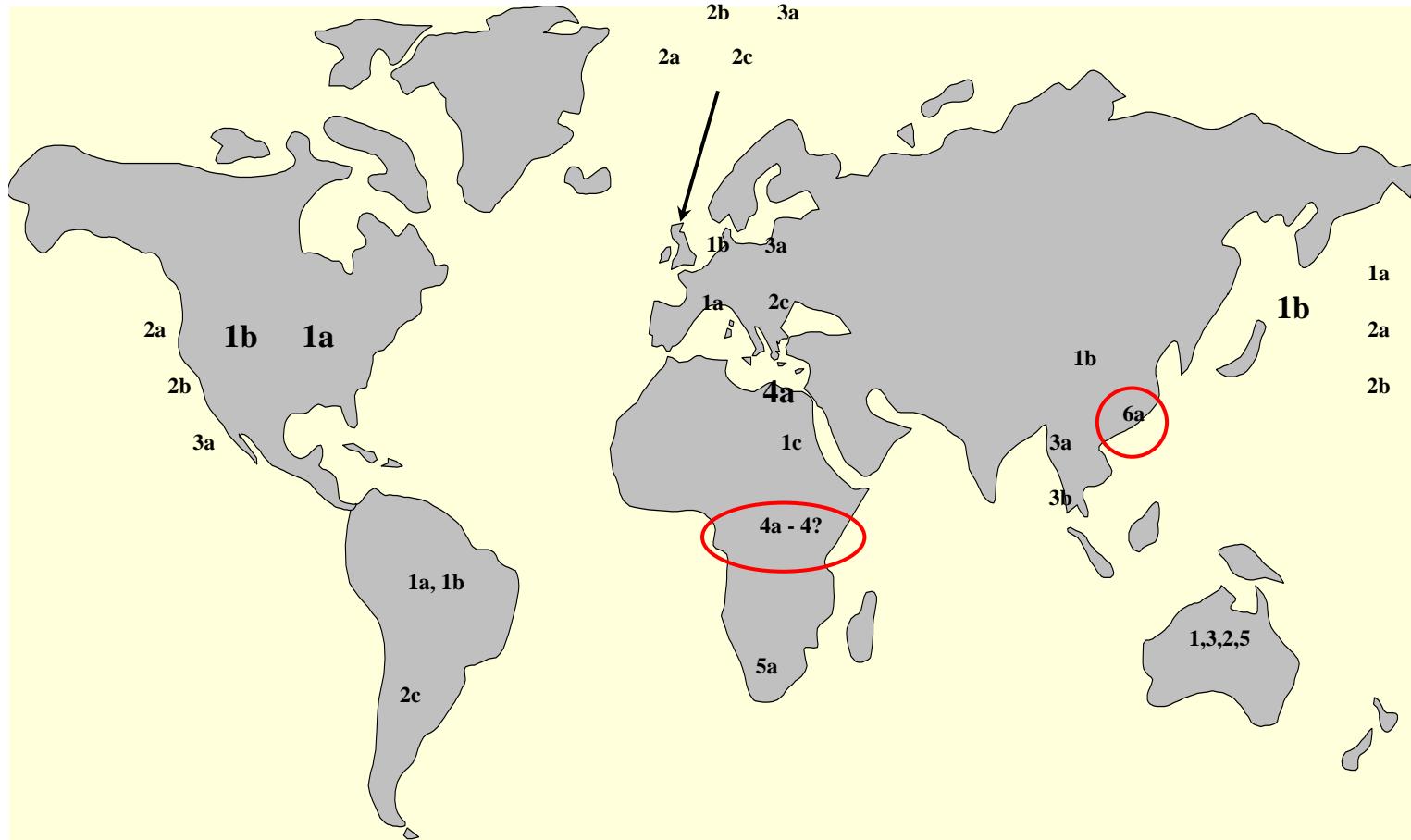
Evolutionary tree of known HCV  
genotypes/subtypes

- HCV can be classified into six genetically distinct genotypes/clades (Seq.divergence ~30%)
- HCV genotypes can be further subdivided into at least (90 subtypes Seq. divergence ~20%)
- Different HCV genotypes may exhibit differing phenotypic properties
  - ▶ Severity of liver disease
  - ▶ Response to antiviral therapy
  - ▶ Antigenic heterogeneity/Impact in diagnostic assays and vaccine development
- Functional properties of viral proteins.

# WORLDWIDE DISTRIBUTION OF HCV GENOTYPES

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## GOALS

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To assess the impact of the HCV genotypes (particularly HCV-4 and HCV-6) on the detection of anti-HCV antibodies in human sera

## **EXPERIMENTAL OBJECTIVES**

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- ➲ To produce home-made HCV antigens for core, NS3 and NS4B from HCV isolates of selected HCV genotypes
  - Peptides
  - Recombinant proteins
- ➲ To generate a sera panel
- ➲ To develop home-made ELISA assays and assess the antibody reactivity in HCV patient sera using type-homologous and type-heterologous antigens

# CAMBODIAN PANEL: 90 plasma from Cambodian blood donors

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## 58-Positive [RNA HCV (+) and Ab HCV (+)]

28 HCV-6

9 HCV-1a

20 HCV-1b

1 HCV-2

3 False Negative [RNA HCV (+) but Ab HCV (-)]

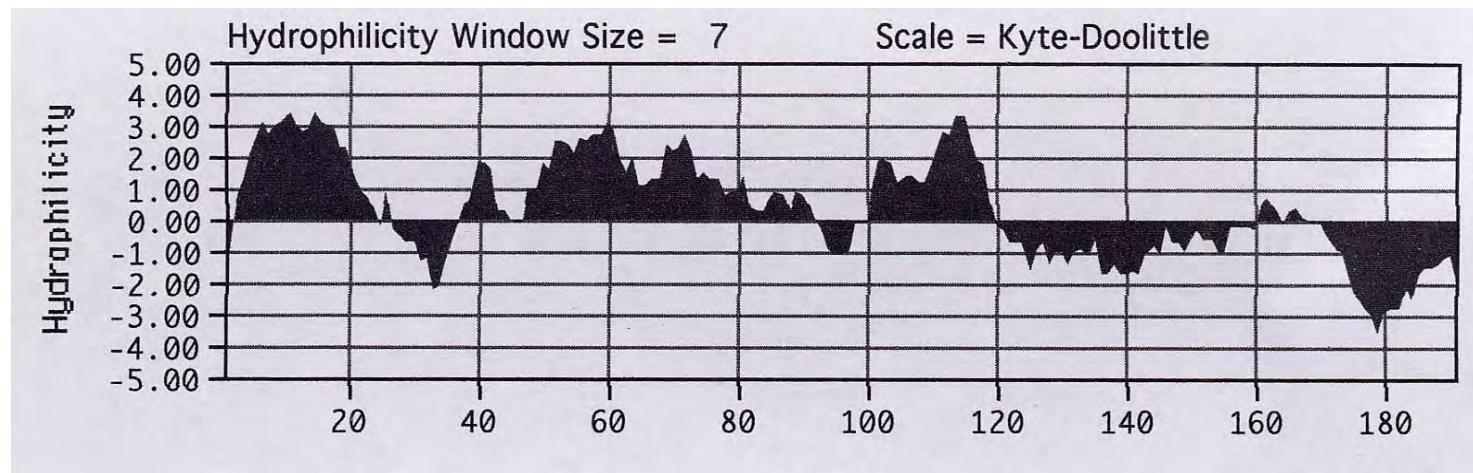
29 HCV-Negatives [RNA HCV (-) and Ab HCV (-)]

2 Controls (-)

1 HBsAg (+) HCV (-)

# CORE PEPTIDE ANTIGENS

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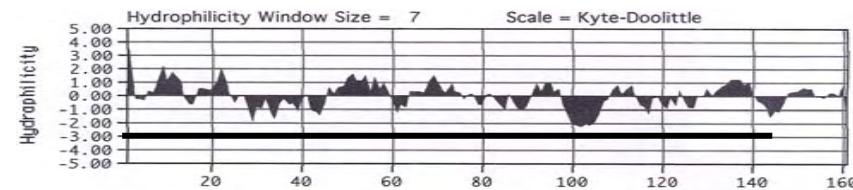
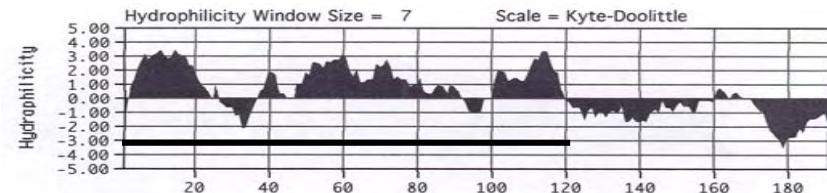


## Peptides

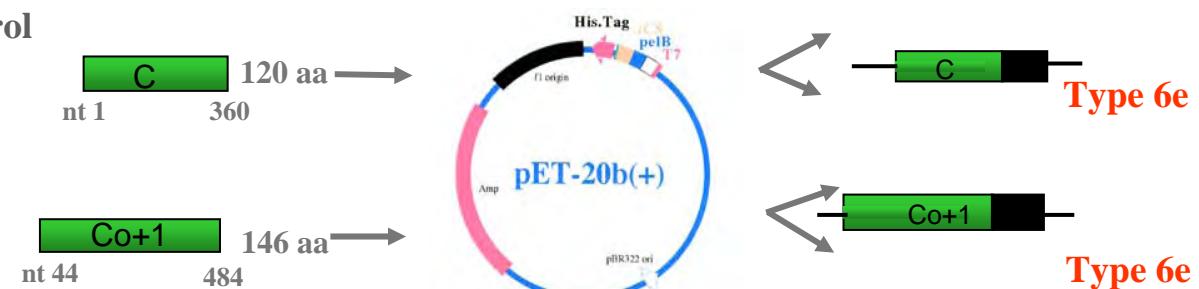
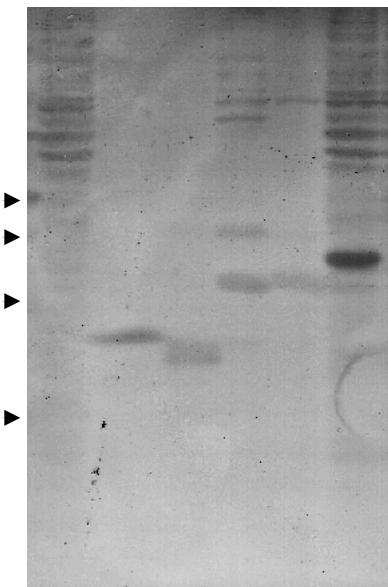
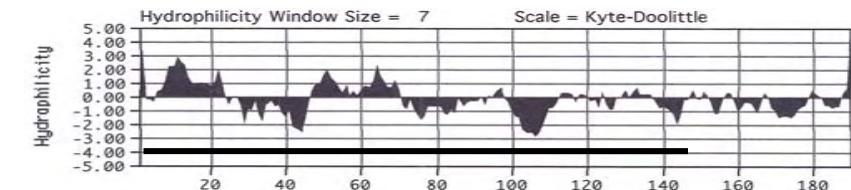
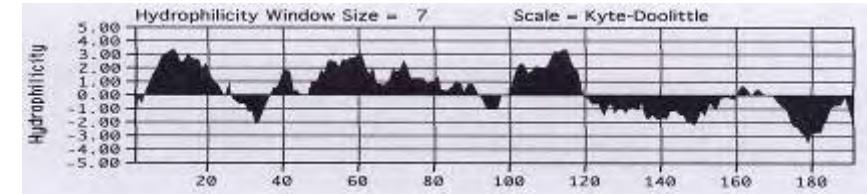
|        |          |         |
|--------|----------|---------|
| HCV-21 | core: 1b | 3-75aa  |
| HCV-26 | core: 2α | 11-45aa |
| HCV-34 | core: 1b | 11-45aa |

# PROKARYOTIC EXPRESSION OF THE HCV $\Delta$ CORE AND $\Delta$ CORE+1 PROTEINS TYPE 1a OR 6e

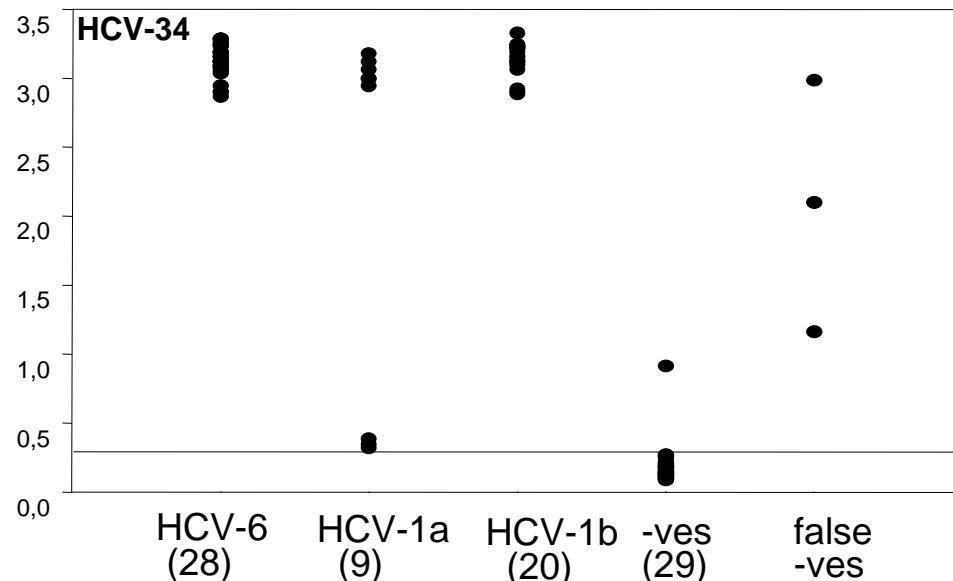
**Genotype 1a**



**Genotype 6e**



# ELISA DATA WITH CORE PEPTIDES



## HCV-34 (11-45aa/1b)

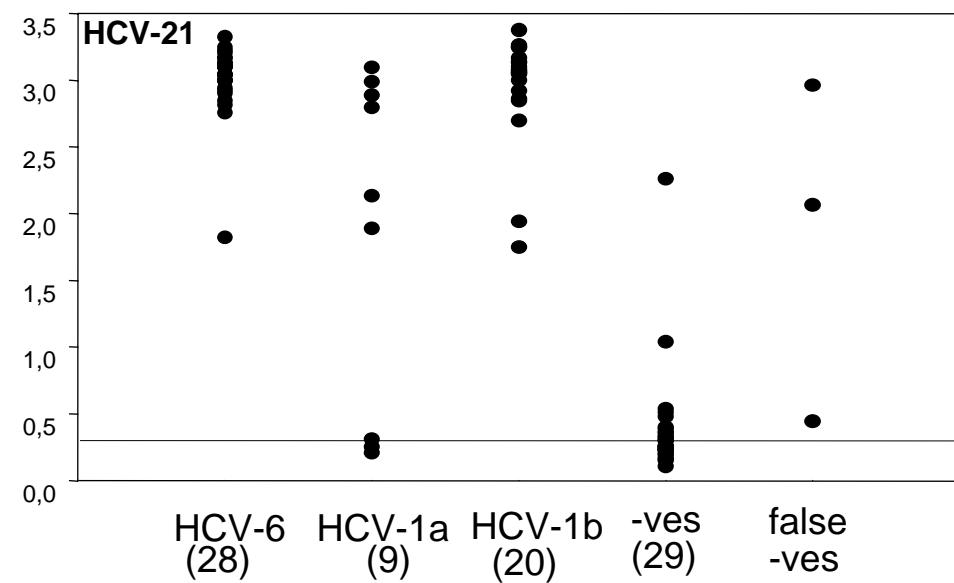
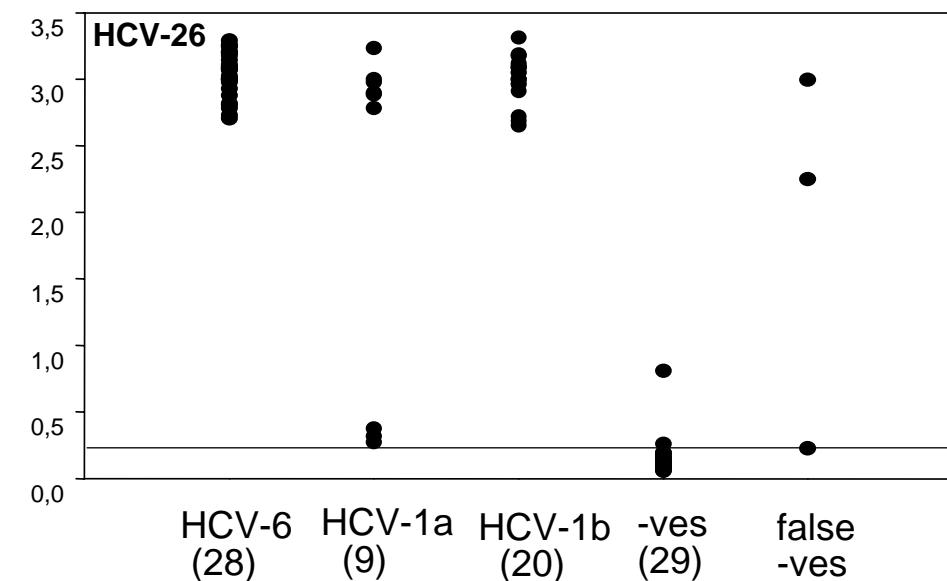
57/57 +ves (100%)  
28/29 -ves (97%)  
3/3 false -ves

## HCV-26 (11-45aa/2a)

57/57 +ves (100%)  
28/29 -ves (97%)  
3/3 false -ves

## HCV-21 (3-75aa/1b)

55/57 +ves (96%)  
16/29 -ves (55%)  
3/3 false -ves

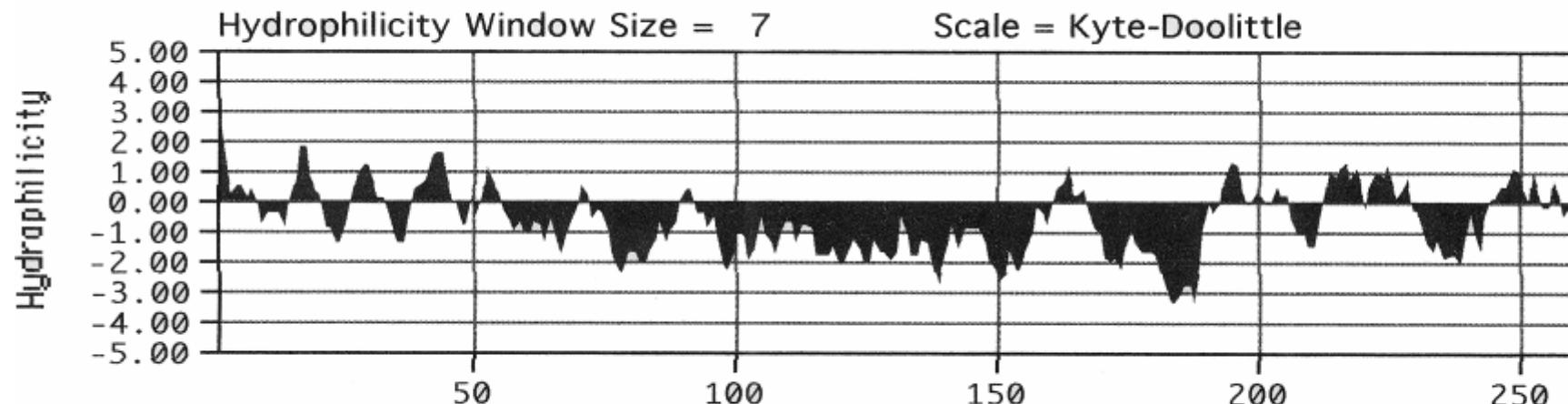


## CONCLUSIONS

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- All three core peptides are immunoreactive with all HCV positive sera
- All three core peptides are immunoreactive with the 3 false-negative sera
- The shorter core peptides (aa 11-45) exhibit better specificity

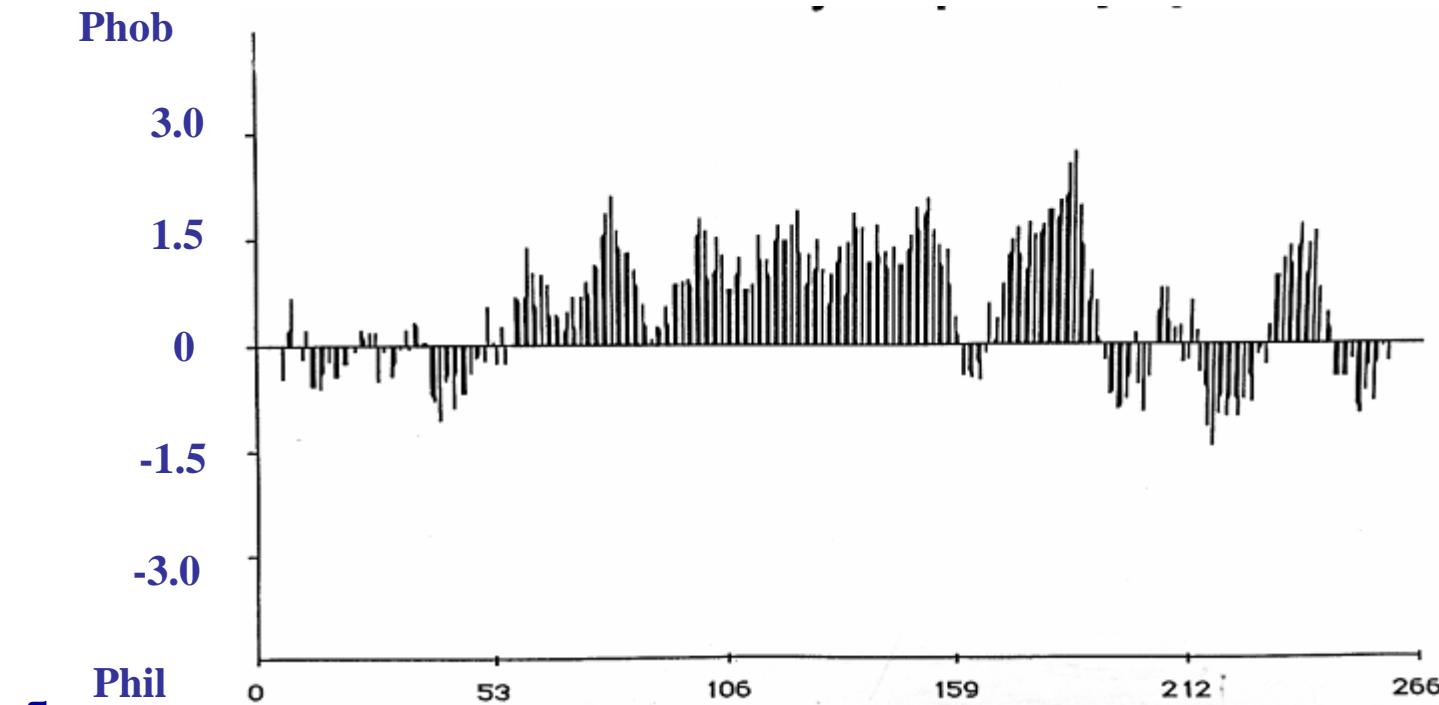
## NS4 PEPTIDE ANTIGENS



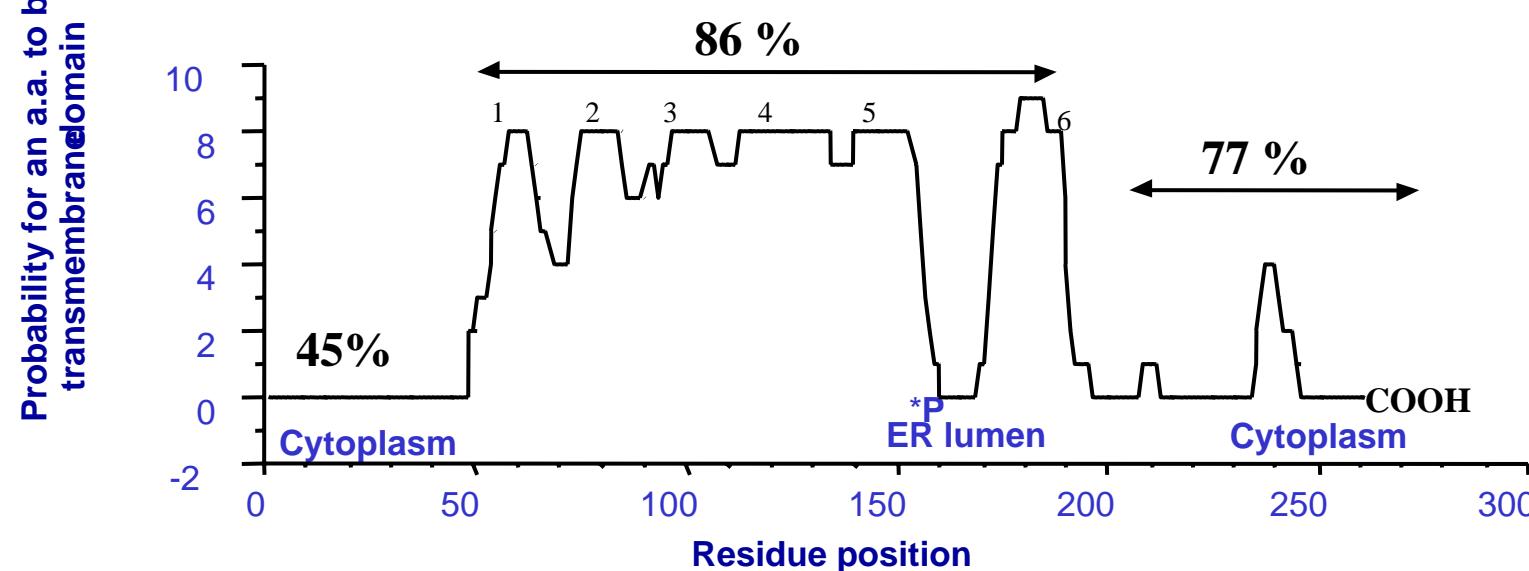
### Peptides tested:

|         |        |                               |
|---------|--------|-------------------------------|
| HCV-6   | NS4:1b | 1921-1940 aa                  |
| HCV-45  | NS4:1b | 1689-1738 aa                  |
| HCV-452 | NS4:2a | 1688-1740 aa                  |
| HCV-645 | NS4:1b | 1689-1738 aa +<br>1921-1940aa |

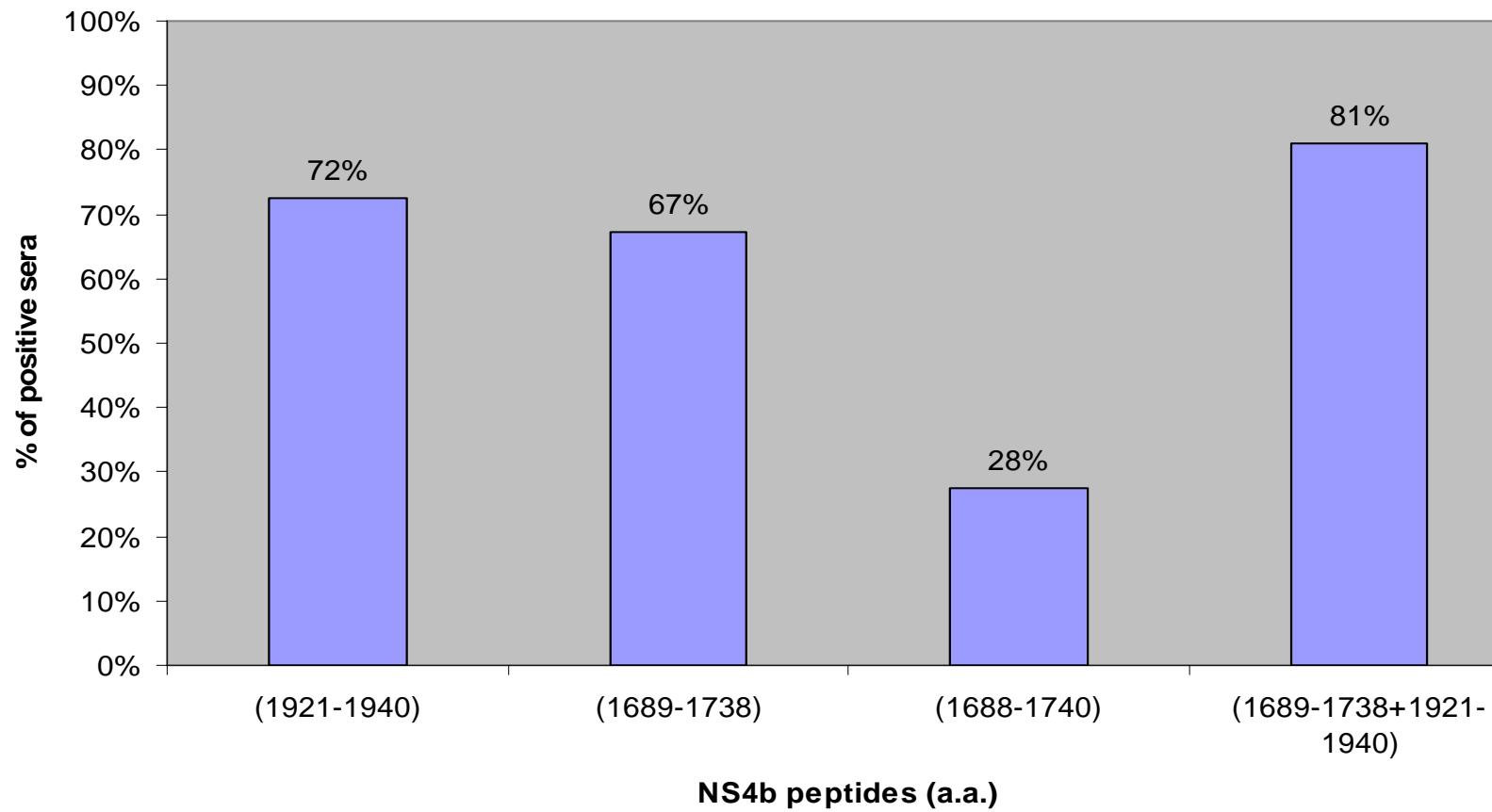
## Hydrophobicity profile of NS4B

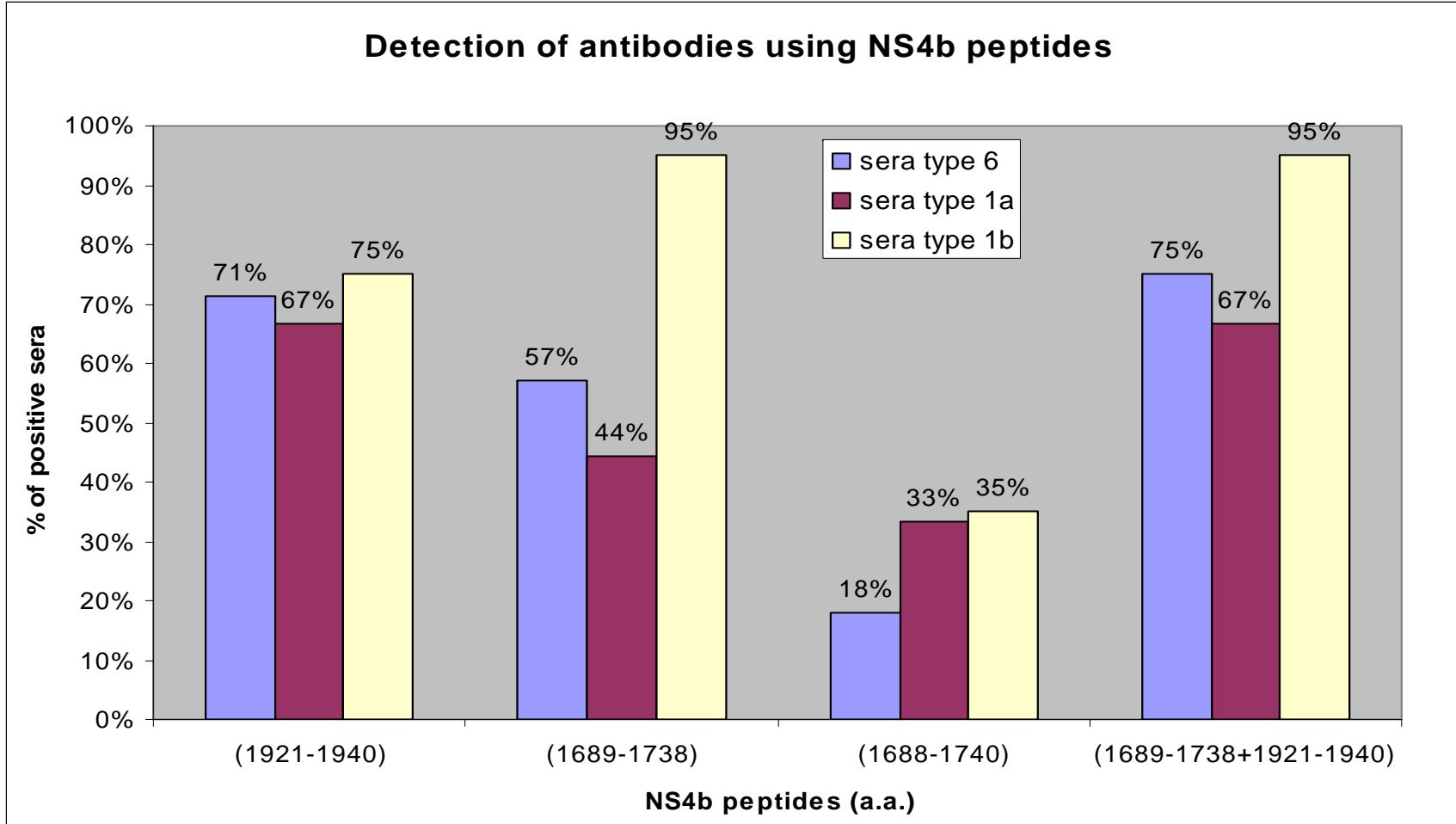


## Prediction of transmembrane domains

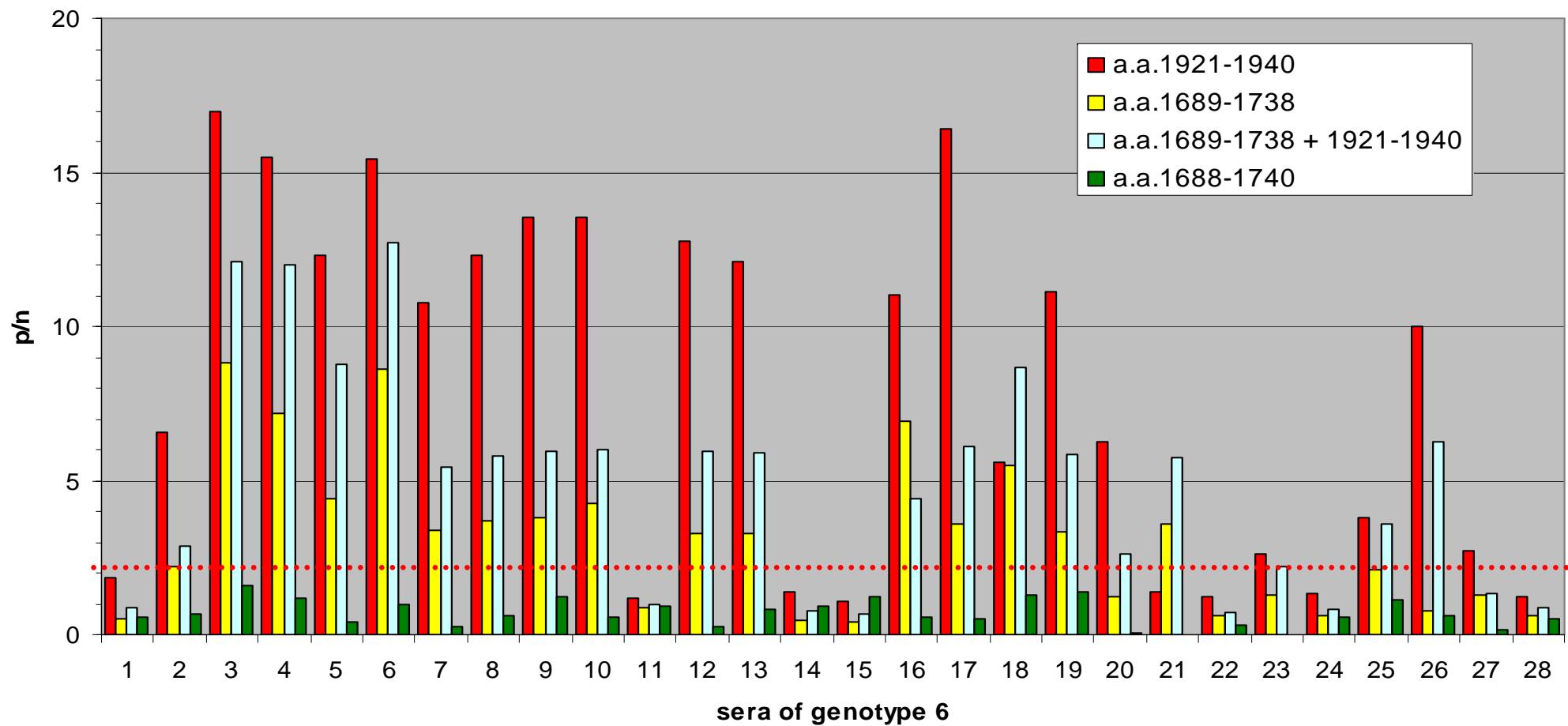


### **Detection of antibodies using NS4b peptides**

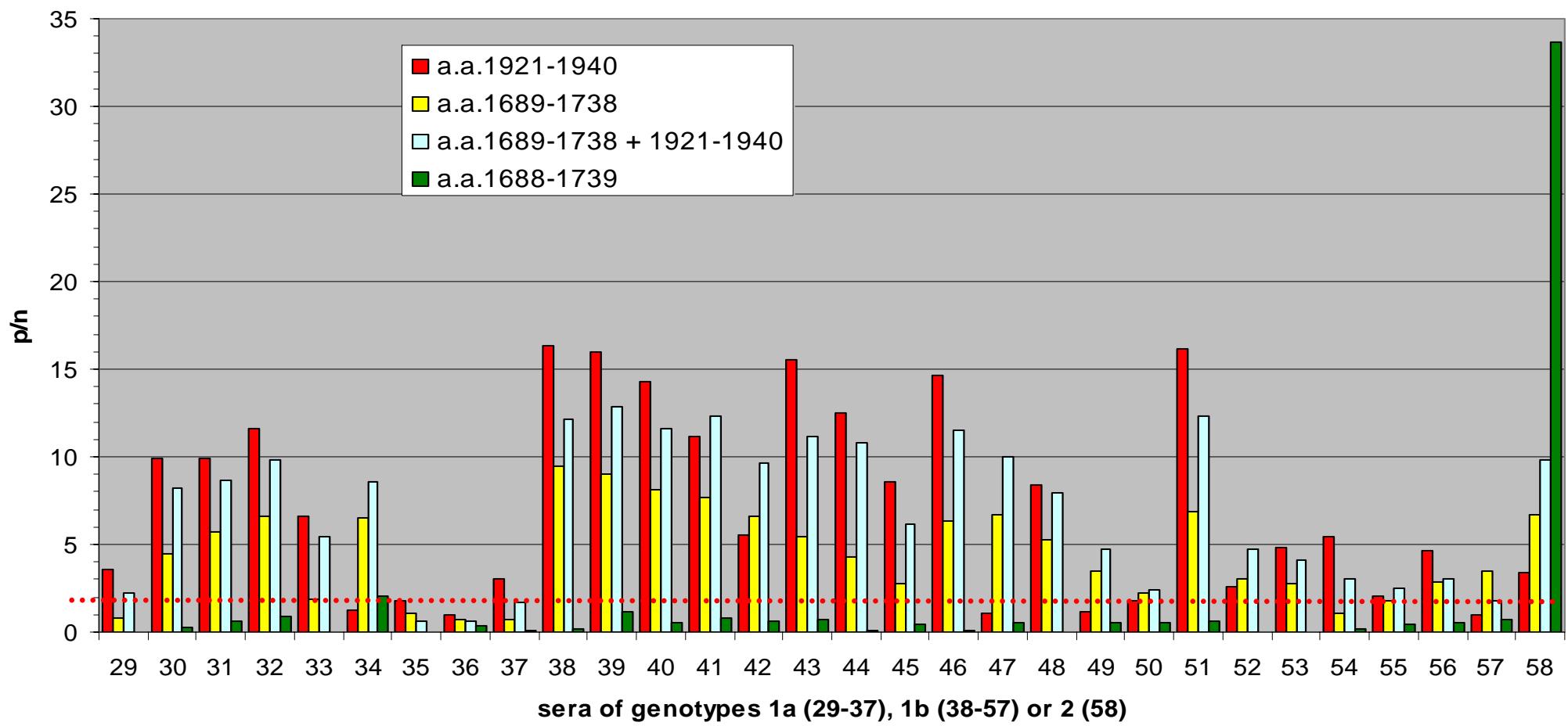




### Detection of antibodies using NS4b peptides



### Detection of antibodies using NS4b peptides



## CONCLUSIONS

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- NS4 peptides recognize both HCV-1 and HCV-6 genotypes
- NS4 peptide HCV-645 (aa 1689-1738+1921+1940/1b) has the highest positivity rate (80%)

# Implications of HCV diversity in the diagnosis and pathogenesis of virus infection in SE Asia, Eastern Europe and Central Africa (PTR126)

