EVENT, network for harmonizing HAV typing and for alerting on hepatitis A outbreaks

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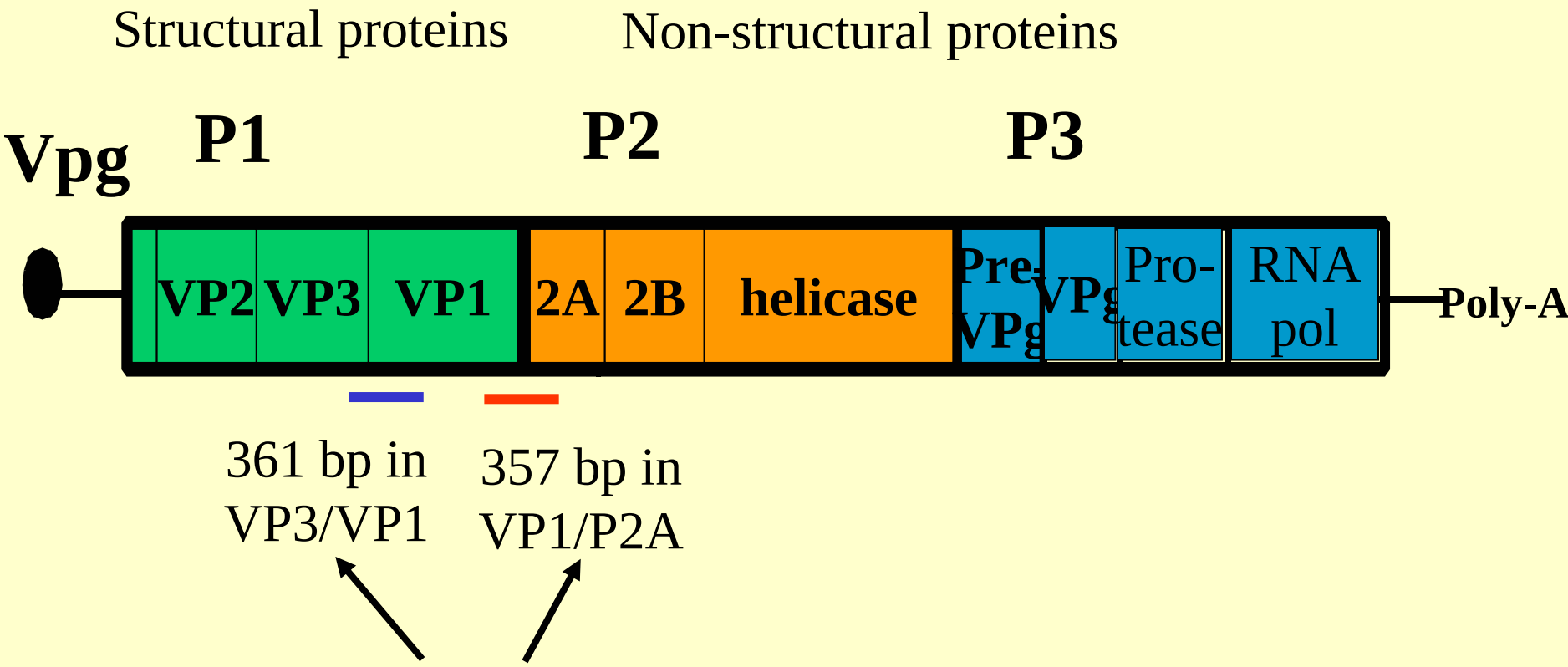
HAV genotype distribution

Genotype	Origin
IA	Most common type, cosmopolitic
IB	Cosmopotitic, dominating in Middle East
IIA	France now in spread
IIB	Sierra Leone, Israel
IIIA	Europe, USA, India, Nepal, Malaysia, Japan, Georgia
IIIB	Japan, Denmark, Panamian owl monkey
IV	Macaque
V	African green monkey
VI	Macaque

Genomic organization of HAV



Regions amplified and sequenced for comparison

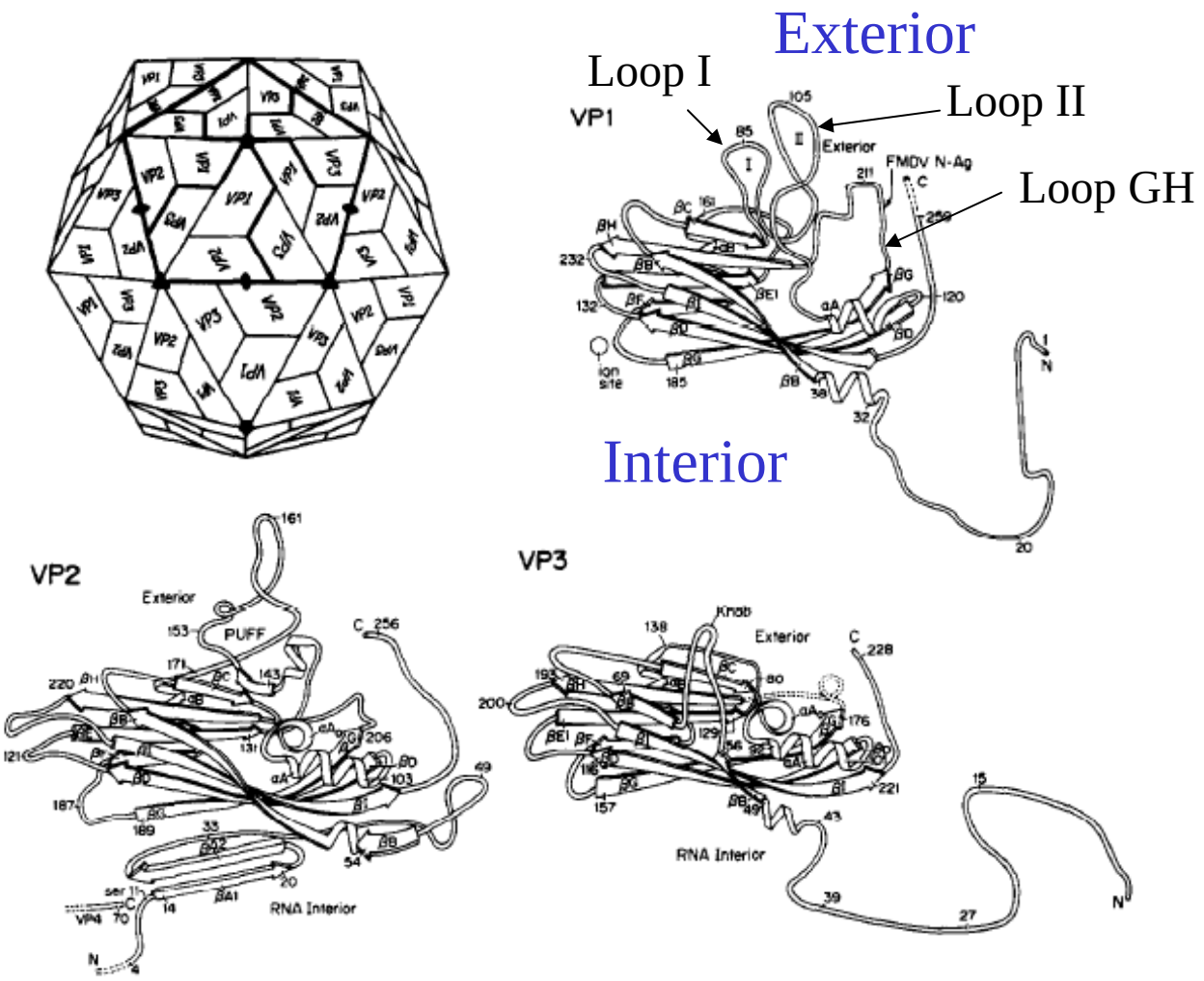
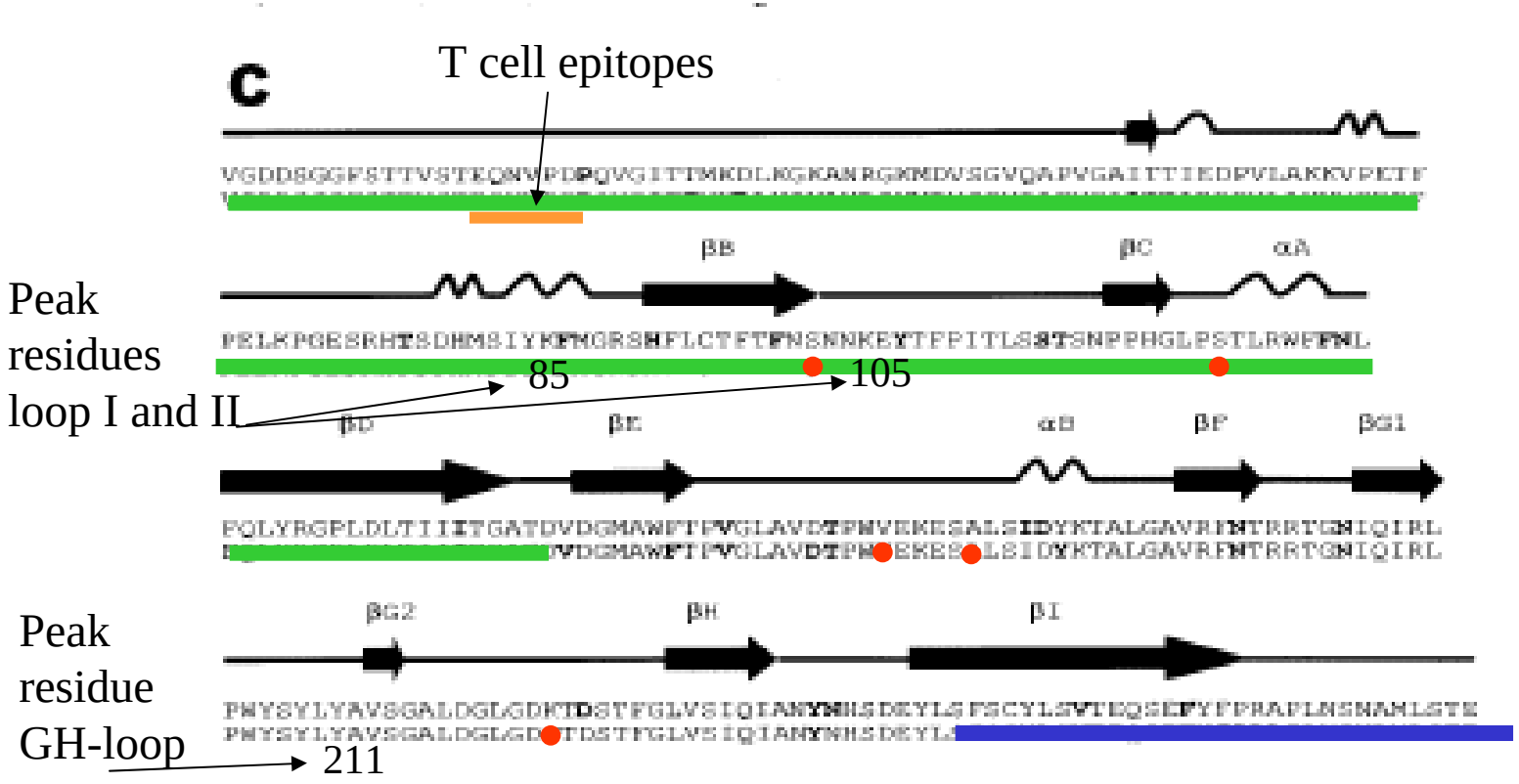


FIG. 1. (Top left) Diagrammatic representation of an icosahedral capsid in picornaviruses. The thickly outlined VP1, VP3, and VP2 units correspond to the 6 S (VP1, VP3, VP0) protomer and the pentadecamer cap to the 14 S pentamer observed in assembly experiments (Boege, 1986). Ribbon drawings of the three larger viral proteins VP1 (top right), VP2 (bottom left), and VP3 (bottom right) for Mengo virus. Each protein has the same wedge shaped, eight stranded, anti-parallel β-barrel, but differs because of insertions and deletions mostly at the ends of β-strands. The approximate amino acid numbering and secondary structural nomenclature is also shown.

Rossman and Palmenberg 1988

VP1 structural plot model deduced from data on poliovirus

Green shows the N-terminal VP3-VP1 fragment
Blue shows the C-terminal VP1 (-2A) fragment
Red residues are important for neutralization



Adapted from Sánchez et al., 2003

Origin of isolates used for comparing the VP3/VP1 and VP1/P2A region as target for analyses

Origin of isolates within EVENT	**Number of isolates**
Hungary	24
Spain	4
The Netherlands	8
Sweden	48
GenBank	18
TOTAL	**102**

Number of isolates and strains with unique or identical sequences in the VP3/VP1 and VP1/P2A region

	Number of isolates	Number of strains N-terminal/C-terminal
Strains identical in both N - and C-terminal region	36 (35 %)	12
Strains identical in N- but unique in C-terminal region	2 (2 %)	(2/2)
Strains identical in C-but unique in N-terminal region	10 (10 %)	(10/5)
Strains unique in both regions	54 (54 %)	54
TOTAL	**102**	**78/70**

Origin of strains sequenced in the VP1/P2A region

Country	IA	IB	IIA	IIIA	Total
Hungary	33	17	0	0	50
Netherlands	22	30	0	14	66
France	6	4	0	0	10
Germany	8	1	0	0	9
Spain	15	5	0	0	20
Denmark	2	3	0	0	5
Sweden	10	9	0	3	22
GenBank	54	24	4	14	96
TOTAL	**150**	**93**	**4**	**31**	**278**

EVENT Network continuation

Marion Koopmanns has kindly offered to build and keep a data base for HAV sequences from this network at RIVM.

The data base will be easy to access for the network members and sequences obtained can be blasted to easily identify identical sequences.

Since most groups have sequenced the C-terminal region, this region will be used and compared.

EVENT Network continuation

If an identical sequence is found in another country, the laboratory will be alerted and the N-terminal region will be sequenced for these strains.

If identical strains are encountered, epidemiologists from these countries will be informed to search for a possible common source of infection.

When the database is established, more countries will be invited to participate in the network

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