Report no:	04/09	2dmVNT						LPBE			
Field Isolate:	SAU Isolate ref:	2dmVNT test ref:	O Manisa UV pool	O Bfs VP pool	O Ind R2/75 9418	O Kauf VQ pool		ELISA test ref:	O Manisa VT62 + 63	O 4174	O Tunisia 89
O Sud 3/2008	B58/09	mn11/09	no cpe	no cpe							
		mn13/09	no cpe	no cpe	no cpe						
	B60.09							SD 9/09		0.08	
		mean						mean		0.08	
O Sud 4/2008	B57/09	mn08/09	0.36	0.35				SD 9/09	Fail	0.13	0.50
		mn11/09	1.00	0.62				SD 15/09		Fail	>1
		mn13/09			1.00			SD 16/09	No trap		
		mn15/09			0.62*	0.40		SD 18/09	0.17		
		mn20/09				0.32		SD 19/09	0.25		
		mn21/09			0.72			SD 25/09	Fail		
		mn22/09			0.79			SD 27/09	1		
								SD 44/09		0.25	
								SD 45/09		0.13	
		mean	0.68	0.49	0.78	0.36		mean	0.47	0.17	≥0.75
O Sud 8/2008	B59/09	mn11/09	0.50	0.38							
		mn13/09	fail	0.32	1.00						
		mn15/09			0.68*	0.36					
		mn20/09	0.60*			0.38					
		mn21/09	0.36		0.93						
		mn22/09	0.50		1.00						
	B61/09							SD 9/09	Fail	0.33	0.50
								SD 15/09		Fail	1.00
								SD 16/09	No Trap		
								SD 18/09	No Trap		
								SD 25/09	Fail		
								SD 27/09	Fail		
								SD 44/09		0.25	
		mean	0.49	0.35	0.90	0.37		mean	Fail	0.29	0.75

Interpretation of r_1 values

In the case of ELISA:

r_1 = 0.4-1.0. Suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.
r_1 = 0.2-0.39, Suggests that the field isolate is antigenically related to the vaccine strain. The vaccine strain might be suitable for use if no closer match can be found provided that a potent vaccine is used and animals are preferably immunised more than once.
r_1 = <0.2. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect.

In the case of neutralisation:

r_1 = ≥ 0.3. Suggests that there is a close relationship between field isolate and vaccine strain. A potent vaccine containing the vaccine strain is likely to confer protection.
r_1 = < 0.3. Suggests that the field isolate is so different from the vaccine strain that the vaccine is unlikely to protect.

N.B.

All of our phylogenetic trees can be accessed via the internet at:

http://www.iah.bbsrc.ac.uk/primary_index/current_research/virus/Picornaviridae/Aphthovirus/index.html