GENOMIC MODIFICATIONS IN SABIN VACCINE STRAINS ISOLATED FROM VACCINATION-ASSOCIATED CASES, HEALTHY CONTACTS AND HEALTHY VACCINEES

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Received March 11, 1996

Summary. - The three attenuated strains developed by A.B. Sabin have been effectively used as an oral live poliovirus vaccine (OPV) to control poliomyelitis in many countries. Although rarely, vaccination-associated paralytic poliomyelitis (VAPP) cases occur with the type 2 and 3 strains, and less frequently with the type 1 strain. The greater number of attenuating mutations in the P1/Sabin strain is probably reflected in the higher safety of this strain in comparison to type 2 and 3 strains. For the P1/Sabin strain, many attenuating mutations were already identified in the 5'-non-coding region (5'NCR), in the capsid proteins coding region, in the 3Dpol coding region, and the 3'-non-coding region (3'NCR). For the P2/Sabin and P3/Sabin strains, one mutation in 5'NCR and another in the capsid proteins coding region have been demonstrated to be important determinants of attenuation, although it has been suggested that other mutations may also have some effect, though minor. Although reverting mutations in attenuating determinants, supressor mutations, mutations in antigenic sites and genomic recombination have been observed in strains isolated from VAPP cases, the observation of similar genomic modifications in strains isolated from healthy contacts and from healthy vaccinees has supported the view that host factors are also involved in the establishment of the disease. Reverting mutations at nucleotides (nt) 480 (G->A), 481 (A->G) and 472 (U->C) for the P1/Sabin, P2/Sabin and P3/Sabin strains, respectively, have been detected in almost all strains isolated from VAPP cases and also from healthy vaccinees. Although the Sabin vaccine strains have been implicated in rare VAPP cases, recent studies have suggested that the vaccine strains could also trigger the Guillain-Barré syndrome (GBS), transverse myelitis (TM) and facial paralysis.

Key words: poliovirus; Sabin vaccine strains; genome modifications; mutations; recombination; neuro-virulence; attenuation; vaccination-associated cases

Introduction

Polioviruses are members of the *enterovirus* genus (Melnick, 1993), belonging to the *Picornaviridae* family and consist of an icosahedrical particle composed of 60 copies of capsid proteins VP1, VP2, VP3 and VP4 (Hogle *et al.*, 1985),

Abbreviations: GBS = Guillain-Barré syndrome; NCR = noncoding region; OPV = oral poliovirus vaccine; ORF = open reading frame; VAPP = vaccination-associated paralytic poliomyelitis; VPg = viral genomic protein; TM = transverse myelitis surrounding a single-stranded positive-sense RNA genome of approximately 7500 nt (Kitamura *et al.*, 1981). The viral RNA contains a 5'NCR of about 740 nt with a terminally linked protein (viral genomic protein, VPg), preceding a single open reading frame (ORF) coding for the structural and nonstructural proteins, and terminates in a 3'NCR of about 70 nt followed by a poly(A)-sequence (Kitamura *et al.*, 1981; Wimmer and Nomoto, 1993). Polioviruses are grouped on the basis of the antigenicity of the capsid into three serotypes designated 1, 2, and 3. These viruses are the causative agents of poliomyelitis, a paralytic and sometimes fatal disease of humans (Almond, 1987; Racaniello, 1988).

The attenuated poliovirus strains (P1/Sabin, P2/Sabin, and P3/Sabin) developed by A.B. Sabin (Almond, 1987; Racaniello, 1988; Horaud, 1993) were obtained by passaging wild type isolates in monkey tissue in vitro and in vivo under a variety of conditions which differed for each of the three scrotypes. These attenuated strains have been effectively used as OPV to control poliomyelitis in many countries. Although rarely, VAPP cases occur with the type 2 and 3 strains, and even less frequently with the type 1 strain (Basilico and Bernat, 1978; Kew et al., 1981; WHO, 1982; Minor, 1982; Fiore et al., 1987; Nkowane et al., 1987; Strebel et al., 1992, 1994; Fillipis et al., 1994; Groom et al., 1994; Friedrich et al., 1996a). Molecular studies have demonstrated mutations in the genome of Sabin vaccine-derived strains isolated from VAPP cases (Cann et al., 1984; Evans et al., 1985; Pollard et al., 1989; Macadam et al., 1989, 1991a; Equestre et al., 1991; Muzychenko et al., 1991; Otelea et al., 1993; Georgescu et al., 1994; Friedrich et al., 1995b,c; Driesel et al., 1995).

A comparison of the nucleotide sequence of the attenuated vaccine strains, vaccine neurovirulent revertants and wild neurovirulent ancestors of the vaccine strains has led to identification of nucleotide differences in these strains and possible mutations involved in attenuation and reversion to neurovirulence. Poliovirus can be recovered from cloned cDNA copies of the genome (Racaniello and Baltimore, 1981a; Racaniello, 1993). This approach has permitted the construction of recombinants between neurovirulent and attenuated strains, and the use of site-directed mutagenesis in the identification of mutations involved in attenuation and reversion to neurovirulence. Knowledge of the molecular basis of attenuation and reversion towards neurovirulence of the Sabin strains (Almond, 1987; Racaniello, 1988; Ehrenfeld, 1992; Minor 1992, 1993; Minor et al., 1993; Racaniello et al., 1993; Macadam et al., 1994b) may allow rational improvement of vaccines (WHO, 1990; Ghendon, 1993; Agol, 1993) and vaccine production methods (Chumakov et al., 1994). The latters may provide alternative models for vaccine safety tests on transgenic mice (Ren et al., 1990; Koike et al., 1991, 1993; Abe et al., 1995a,b) and/ or molecular approaches (Chumakov et al., 1991, 1992, 1993; Fenyves, 1993; Svitkin et al., 1993; Rezapkin et al., 1994, 1995; Taffs et al., 1995), and may avoid costly safety testing of vaccine batches in primates.

Molecular basis of attenuation and reversion to neurovirulence of the P1/Sabin strain

The attenuated P1/Sabin strain (P1/LSc, 2ab) was derived from a wild neurovirulent strain, P1/Mahoney/41, isolated from stool of a healthy child (Almond, 1987; Racaniello, 1988). Comparison of the complete nucleotide sequence of the attenuated P1/Sabin strain (Nomoto *et al.*,

1982; Toyoda et al., 1984) with that of its neurovirulent ancestor, P1/Mahoney strain (Kitamura et al., 1981; Racaniello and Baltimore, 1981b) demonstrated that these two strains differ by more than 50 mutations. Neurovirulence tests in monkeys of recombinants between these two strains demonstrated that the mutations important for the attenuation of the PI/Sabin strain are scattered throughout the entire genome (Omata et al., 1986), with an important attenuating mutation A->G at nt 480 of 5'NCR (Kawamura et al., 1989). The analysis of P1/Sabin neurovirulent revertants selected at high temperatures suggested that an U->C mutation at nt 525 of 5'NCR, which has been suggested to supress the attenuating G at nt 480, a G->A mutation at nt 7441 of 3'NCR, and a C->U mutation at nt 6203 of the 3Dpol coding region, leading to a His->Tvr substitution at aa 73 of the viral RNA polymerase, are important for reversion of this strain to neurovirulence in monkeys (Christodoulou et al., 1990). This study also suggested that mutations at nt 2438 (VP3), 2741 (VP1) and 2795 (VP1), leading to amino acid substitutions in these capsid proteins, could also have some effect on the reversion to neurovirulence. The use of type 1/type 2 mouse-adapted chimeric polioviruses in the study of determinants of poliovirus type. I neurovirulence, strongly suggested that a C at nt 6203 of the 3Dpol coding region, in the codon for His at aa 73 in the viral RNA polymerase, was an attenuating determinant of the P1/Sabin strain, although its effect was weaker than that of a G at nt 480 of 5'NCR (Martin et al., 1991: Tardy-Panit et al., 1993).

Neurovirulence tests of recombinants between the virulent P1/Mahoney strain and the attenuated P1/Sabin strain in transgenic mice carring the human poliovirus receptor. suggested an important contribution of nt 480 to the expression of neurovirulence or attenuation (Horie et al., 1994). This study also suggested the participation of mutations at nt 189 (C->U) of 5'NCR, nt 21 (U->C) of 5'NCR, and/or nt 935 (G->U) of VP4 in the attenuation of the P1/Sabin strain. Other neurovirulence tests (Bouchard et al., 1995) in transgenic mice expressing the human poliovirus receptor of recombinants between the P1/Sabin and P1/Mahoney strains, and of site-directed mutants, identified additional attenuating mutations in the P1/Sabin strain at nt 935 (also identified in the previous study), 2438, 2795 and 2879. The attenuating G->U mutation at nt 935 led to an Ala->Ser substitution at aa 65 of VP4, the U->A mutation at nt 2438 to a Leu->Met substitution at aa 225 of VP3, the G->A mutation at nt 2795 to an Ala->Thr substitution at aa 106 of VP1, while the C->U mutation at nt 2879 to a Leu->Phe substitution at aa 134 of VP1.

Thus, these molecular studies have suggested that an A->G mutation at nt 480 of 5 NCR of the P1/Sabin strain has an important contribution to the attenuation, while an U->C mutation at nt 6203, resulting in an amino acid sub-

stitution in the viral RNA polymerase, contributes to attenuation to a lesser extent. To assess the contributions of these two mutations (McGoldrick *et al.*, 1995) for virus attenuation in monkeys, site-directed mutagenesis generating mutants of the P1/Sabin and P1/Mahoney strains at nt 480 and 6203 was performed, indicating that (in contrast to previous findings) G at nt 480 had only a slight effect on the attenuation, while C at nt 6203 had even a lesser one, confirming that attenuating mutations are located elsewhere in the genome of the P1/Sabin strain.

Other studies demonstrated that vaccine lots of the P1/Sabin strain with an increased portion of G->A (nt 480) and U->C (nt 525) revertants presented a higher neurovirulence (Rezapkin *et al.*, 1994). In still another study, cultured human neuroblastoma cells SK-N-MC were found to be highly resistant to the attenuated P1/Sabin strain, while they produced relatively good yields of the neurovirulent P1/Mahoney strain (Agol *et al.*, 1989). Experiments with intratypic poliovirus recombinants suggested that the major genomic determinants limiting the replication of the attenuated P1/Sabin strain in neuroblastoma cells are located in the 5'-half of the viral RNA, even though the 3'-half also appeared to contribute somewhat to this phenotype.

It is known that nt 480 pairs with nt 525 in a predicted secondary structure of 5'NCR (Pilipenko et al., 1989; Skinner et al., 1989; Agol, 1991; Muzychenko et al., 1991; Hellen et al., 1994). The attenuating G at nt 480 of 5'NCR of the P1/Sabin strain resulted in the alteration of the A-U base pair (nt 480-525) found in the neurovirulent wild P1/Mahoney strain (ancestor of the P1/Sabin strain) to the G-U base pair (nt 480-525) found in the P1/Sabin vaccine strain, suggesting that the attenuated phenotype is partially associated with a weakening of a base pairing in a highly conserved structure (Christodoulou et al., 1990; Muzychenko et al., 1991; Agol, 1991; Macadam et al., 1991a, 1994b; Minor, 1992, 1993; Minor et al., 1993; Tardy-Panit et al., 1993). The alteration of the secondary structure of 5'NCR, caused by the attenuating G at nt 480, could alter the interaction of the viral RNA with one or more host factors required for the initiation of translation of poliovirus RNA (Svitkin et al., 1988; Agol, 1991), leading to the observed deficiency in translation (Svitkin et al., 1985; Muzychenko et al., 1991) associated with an A->G attenuating mutation at nt 480 (Kawamura et al., 1989). The G->A reverting mutation at nt 480 or the U->C supressor mutation at nt 525 have been suggested to revert this process. The Tyr->His attenuating substituition at aa 73 of the viral RNA polymerase could act by decreasing the efficiency of the synthesis of viral RNA (Christodoulou et al., 1990; Tardy-Panit et al., 1993). The G at nt 7441 of 3'NCR could alter its secondary structure or the affinity of the host factor to viral RNA or both, inhibiting the initiation of replication (Christodoulou et al., 1990).

Genomic modifications in type 1 polioviruses isolated from VAPP cases and healthy vaccinees

The greater number of attenuating mutations in the P1/ Sabin strain has been proposed as an explanation for the higher degree of safety of this strain in comparison to the P2/Sabin and P3/Sabin strains. As the number of poliovirus type 1 VAPP cases was low, the genomic modifications occuring in these strains have therefore been studied less. A molecular study involving partial nucleotide sequencing of P1/Sabin-derived strains isolated from five VAPP cases (four from stool and one from CNS) demonstrated a G->A reverse mutation at nt 480 in all these strains (Otelea et al., 1993; see also Guillot et al., 1994). In one of these strains isolated from stool, many additional reverting mutations at nt 2749 (VP1), 6141 and 6203 (3Dpol), 7441 (3'NCR), and several new mutations were observed (Otelea et al., 1993). Thus, since all five P1/Sabin-derived strains isolated previously from VAPP cases mutated at nt 480 (Otelea et al., 1993), it is interesting to note that in a recent study, a P1/ Sabin-derived strain without mutations at nt 480 and 525, and also without mutations at nt 476, 2741, 2795, 6203 and 7441, was isolated from CNS of a VAPP case (Georgescu et al., 1994). In another recent study, a P1/Sabin-derived strain isolated from stool of a VAPP case was analysed and no mutations were observed at nt 480, 525 and 6203 (Friedrich et al., 1996a). Although this strain was isolated from stool and was not necessarily the etiological agent of the disease, the possibility that this strain also invaded CNS of the patient and caused the disease cannot be ruled out. These studies strenghten the hypothesis that some P1/Sabin-derived strains without mutations at nt 480, 525 and 6203 replicate efficiently in the human gut (Friedrich et al., 1995a, 1996a), reach CNS of the patient (Georgescu et al., 1994) and cause paralysis. The mutations at nt 480 (Minor and Dunn, 1988; Dunn et al., 1990; Muzychenko et al., 1991; Ogra et al., 1991; Abraham et al., 1993; Guillot et al., 1994) and 525 (Muzychenko et al., 1991) were also observed in P1/Sabin-derived strains after replication in the gut of healthy vaccinees (see also Minor 1992; Minor et al., 1993). In another study, although no G->A reverting mutation at nt 480 was observed in the P1/Sabin strain after passage in the intestinal tract of healthy infants, an U->A mutation at nt 476 was observed, and it was suggested that this mutation could also play a role in reversion to neurovirulence (Contreras et al., 1992). This mutation at nt 476 converts an U-U mismatch at nt 476-528 to an A-U pair in a secondary structure of 5'NCR in a P1/Sabin-derived strains (Macadam et al., 1994b).

Recent analysis of strains isolated from VAPP cases showed that His at position 73 (C at nt 6203) and Ile at position 362 (U at nt 7071) of the viral RNA polymerase, and G at nt 7441 of 3'NCR are selected against *in vivo*, although

Table 1. Characteristics of various P1/Sabin-derived poliovirus strains

	5'NCR		3Dpol		Source
Strain	nt 480	nt 525	codon	aa 73	
P1/Sabin	G	U	CAC	His	
P1/Mahoney	A	U	UAC	Tyr	
P1/PG	A	U	CAC	His	VAPP
P1/IG	A	U	CAC	His	VAPP
P1/NIR	A	U	CAC	His	VAPP
P1/BA	A	U	CAC	His	VAPP
P1/AF	A	U	UAC	Tyr	VAPP
P1/3-IVc	G	U	CAC	His	VAPP
P1/18876	G	U	CAC	His	VAPP
P1/2360	G	U	CAC	His	GBS
P1/2938	A	U	CAC	His	GBS
P1/8879	G/A	U/C	CAC	His	GBS
P1/7404	A	U	UAC	Tyr	GBS
P1/5838	A	U	CAC	His	FP
P1/2746	G	C	CAC	His	FP
P1/2933	G	U	CAC	His	ND

Data in bold indicate differences from the original P1/Sabin strain. FP = facial paralysis; ND = neuroviral disease.

Ile-362 appeared to be more stable than either His-73 or G-7441 (Georgescu *et al.*, 1995b). Although genomic recombination has been frequently observed in type 2 and type 3 Sabin-derived strains isolated from VAPP cases, none of the type 1 isolates from VAPP cases studied were found to be recombinants (Furione *et al.*, 1993; Otelea *et al.*, 1993; Georgescu *et al.*, 1994).

The characteristics of various P1/Sabin-derived strains are summarized in Table 1.

Molecular basis of attenuation and reversion to neurovirulence of the P2/Sabin strain

The attenuated P2/Sabin strain (P2/P712, Ch, 2ab) was derived from the wild P2/P712/56 strain, isolated from stool of a healthy child (Almond, 1987; Racaniello, 1988). Although the complete nucleotide sequence of the P2/Sabin strain is known (Toyoda et al., 1984; Pollard et al., 1989), the complete nucleotide sequence of its ancestor was not yet determined (Muzychenko et al., 1991). The construction of recombinants between the neurovirulent mouse-adapted P2/Lansing strain and an attenuated P2/P712 strain (a closely related strain to P2/Sabin), and the use of sitedirected mutagenesis have demonstrated that A at nt 481 of 5'NCR and Ile at nt 143 of the capsid protein VP1 are the major determinants of attenuation of this P2/P712 strain for normal mice and for transgenic mice expressing the human poliovirus receptor (Moss et al., 1989; Ren et al., 1991). The construction of recombinants between the attenuated P2/Sabin strain and the neurovirulent vaccine revertant P2/117, isolated from a VAPP case, and the use of site-directed

mutagenesis demonstrated that A at nt 481 and Ile at nt 143 of VP1 are also important determinants of attenuation of the P2/Sabin strain in primates (Macadam *et al.*, 1991a, 1993). Although mutations at these two positions are important for attenuation and reversion of the P2/Sabin strain towards neurovirulence, mutations at nt 398 and 437 of 5'NCR and at other nt positions could also have some effect, even though minor (Ren *et al.*, 1991; Macadam *et al.*, 1991a, 1993).

Molecular studies have suggested that A at nt 481 and U at nt 398 could act by destabilizing the secondary and/or tertiary structure of 5'NCR of the P2/Sabin strain (Muzychenko et al., 1991; Agol, 1991; Macadam et al., 1991a, 1992, 1993, 1994b; Minor, 1992, 1993; Minor et al., 1993), altering its interaction with host factors (Svitkin et al., 1988; Agol, 1991) necessary for translation initiation, leading to an unefficient translation of the viral RNA (Muzychenko et al., 1991), and partially decreasing its replication and neurovirulence. It is still unclear whether Ile-143 of VP1 of the P2/Sabin strain causes a conformational change of the viral surface such as to prevent its interaction with neural but not epithelial cells (Equestre et al., 1991; Macadam et al., 1993).

Genomic modifications in type 2 polioviruses isolated from VAPP cases, healthy contacts and healthy vaccinees

Reverting mutations in attenuating determinants of the P2/Sabin strain have been observed in strains isolated from VAPP cases. An A->G mutation at nt 481 of 5'NCR and mutations in the codon for aa 143 of VP1, leading to the substitution of the attenuating Ile by Val, Thr, Asn or Ser, were observed previously in all strains isolated from stool and/or CNS od VAPP cases (Pollard et al., 1989; Equestre et al., 1991; Muzychenko et al., 1991; Macadam et al., 1991a, 1993; Minor et al., 1993; Guillot et al., 1994; Georgescu et al., 1994, 1995a). The only exception in one of these studies (Georgecu et al., 1994) was a strain isolated from CNS of a VAPP case that mutated at nt 481 but maintained the attenuating 143-Ile of VP1. In our recent study (Friedrich et al., 1995b), although most of the strains isolated from stool of VAPP cases mutated at nt 481, and at aa 143 of VP1, some strains did not and maintained the original sequence, suggesting that reverting mutations in these attenuating determinants are not essential to the establishment of the disease. An U->C mutation at nt 398 of 5'NCR was also frequently observed in P2/Sabin-derived isolates from VAPP cases (Muzychenko et al., 1991; Macadam et al., 1991a; Friedrich et al., 1995b), while an U->C mutation at nt 500 of 5'NCR was also observed in strains isolated from two VAPP cases (Macadam et al., 1991a; Friedrich et al., 1995b). Mutations at nt 4201 of peptide 2C and at nt 7386 of 3'NCR were also observed in two strains isolated from VAPP cases (Equestre et al., 1991).

An A->G mutation at nt 481 observed in the P2/Sabinderived strains isolated from VAPP cases was also observed in the strains isolated from stool of healthy contacts of VAPP cases (Friedrich et al., 1995b) and in the strains isolated from stool of healthy vaccinees (Minor and Dunn, 1988; Dunn et al., 1990; Macadam et al., 1991a; Ogra et al., 1991; Abraham et al., 1993; Minor, 1992; Minor et al., 1993). As there is a strong selection against A at this nt position during replication of the virus in the human gut, it is interesting that some P2/Sabin-derived strains isolated from stool of VAPP cases maintained A at nt 481 (Friedrich et al., 1995b). One strain isolated from stool of a VAPP case, collected 138 days after the administration of a single dose of vaccine, maintained A at nt 481 and Ile at nt 143 of VP1. It is possible that one or more mutations in the viral genome could suppress the attenuating effect of 481- A. It also suggests that strains maintaining this attenuating determinant could replicate efficiently in the human gut, reaching CNS and causing paralysis in certain cases.

The substitution of Ile-143 of VP1 by other amino acids observed in P2/Sabin-derived strains isolated from VAPP cases, was also found in strains isolated from stool of healthy contacts of VAPP cases (Friedrich *et al.*, 1995b) and in strains isolated from stool of healthy vaccinees after replication in the gut (Minor, 1992; Minor *et al.*, 1993; Macadam *et al.*, 1993), also demonstrating a selection against Ile-143 of VP1. The latter was conserved in about half of the isolates from healthy vaccinees (Macadam *et al.*, 1993), but was substituted by other amino acids in most isolates from VAPP cases. As some isolates from VAPP cases and from healthy vaccinees maintained Ile-143 of VP1 (Georgescu *et al.*, 1994; Friedrich *et al.*, 1995b), the possibility cannot be excluded that supressor mutations occured in the capsid proteins of

Table 2. Comparison of aa 69 and 113 of the viral RNA polymerase of various poliovirus strains

	RNA polymerase					
Strain	codon	aa 69	codon	aa 113		
P2/Sabin	GAU	Asp	ACC	Thr		
P2/15517	GAG	Glu	AGU	Ser		
P2/15561	GAG	Glu	AGU	Ser		
P2/15562	GAG	Glu	AGU	Ser		
P2/15815	GAG	Glu	AGU	Ser		
P2/1400	GAA	Glu	AGU	Ser		
P2/1402	GAA	Glu	AGU	Ser		
P2/1397	GAA	Glu	UCC	Ser		
P2/Lansing	GAA	Glu	AGU	Ser		
P1/Sabin	GAA	Glu	UCC	Ser		
P1/Mahoney	GAA	Glu	UCC	Ser		
P3/Sabin	GAG	Glu	UCU	Ser		
P3/Leon/37	GAG	Glu	UCU	Ser		
P3/23127	GAA	Glu	AGC	Ser		

Data in bold indicate differences from the original P2/Sabin strain.

these isolates. These studies suggest that selection pressure against A-481 is stronger than that against Ile-143 of VP1 (Macadam *et al.*, 1993).

The frequent isolation of P2/Sabin-derived poliovirus recombinants from VAPP cases has suggested that genomic recombination could also increase the neurovirulence of

Table 3. Characteristics of various P2/Sabin-derived poliovirus

	5'NCR		V	VP1	
Strain	nt 3 98	nt 481	codon	aa 143	
P2/Sabin	U	A	AUU	Ile	
P2/712a	U	A	AUU	Ile	
P2/712 ^b	C	G	_	_	
P2/117	U	G	GUU	Val	VAPP
P2/144	C	G	AC U	Thr	VAPP
P2/154	C	G	GUU	Val	VAPP
P2/188	C	G	ACU	Thr	VAPP
P2/v1256	C	G	AAU	Asn	VAPP
P2/147	U	G	AAU	Asn	VAPP
P2/155	U	G	AGU	Ser	VAPP
P2/HW	Ü	G	AAU	Asn	VAPP
P2/VL	Ü	G	GUU	Val	VAPP
P2/GS	U	G	GUU	Val	VAPP
P2/2-Is	_	G	ACU	Thr	VAPP
P2/2-Ic	_	G	ACC	Thr	VAPP
P2/2-IIs	_	G	ACU		
P2/2-IIs P2/2-IIc	_	G	ACU	Thr	VAPP
P2/2-IIIs ¹				Thr	VAPP
P2/2-IIIs ¹¹		G	GUU	Val	VAPP
	_	G	ACU	Thr	VAPP
P2/2-IIIs ^{III}		G	ACU	Thr	VAPP
P2/2-IIIc ^{II}	_	G	AUU	Ile	VAPP
P2/2-IVs ¹	_	G	AAU	Asn	VAPP
P2/2-IVs ^{II}	-	G	ACU	Thr	VAPP
P2/2-IVc	-	G	AC U	Thr	VAPP
P2/15517	C	G	AAU	Asn	VAPP
P2/15561	C	G	AAU	Asn	hc
P2/15562	C	G	AAU	Asn	hc
P2/15815	C	G	AAU	Asn	hc
P2/1400	C	G	AAU	Asn	VAPP
P2/1401	C	G	AAU	Asn	hc
P2/1402	C	G	AAU	Asn	hc
P2/1397	C	G	ACU	Thr	VAPP
P2/1398	C	G	AC U	Thr	hc
P2/2645	C	G	AGU	Ser	VAPP
P2/1006	U/C	G	ACU	Thr	VAPP
P2/13121	U	G	AAU	Asn	VAPP
P2/10989	U	G	GUU	Val	VAPP
P2/1851	U	G	AUU	Ile	VAPP
P2/998	U	A>G	AUU	Ile	VAPP
P2/7790	Ü	A	AUU	Ile	VAPP
P2/2735	U	A	GUU	Val	sp
P2/2975	U	A	AUU	Ile	sp
P2/2864	U	\mathbf{G}	AUU	Ile	•
P2/1281	U	G	ACU	Thr	sp hc

⁽⁻⁾ = data not available; hc = healthy contact; sp = suspected poliomyelitis. For the rest of legend see Table 1.

^a The passage history of this strain closely, related to P2/Sabin strain, ist not known.

^b Predecessor of the P2/Sabin strain .

these strains or have some advantage in replication in the gut and in the CNS of the patients (Lipskaya et al., 1991; Furione et al., 1993; Georgescu et al., 1994, 1995a,b; Friedrich et al., 1996c). Both the vaccine/vaccine and vaccine/ non-vaccine recombinants were detected. P2/Sabin-derived recombinant strains have also been isolated from healthy contacts of VAPP cases (Friedrich et al., 1996c). A comparison of part of the amino acid sequence of the viral RNA polymerase of the P2/Sabin strain with the predicted one of P2/Sabin-derived recombinants isolated from VAPP cases and healthy contacts (Friedrich et al., 1996c) demonstrated that an Asp->Glu substitution at aa 69 was observed in most of these isolates, while a Thr->Ser substitution at aa 113 was observed in all these isolates (Table 2). Both the P1/Sabin and P3/Sabin strains (Friedrich et al., 1996c) and also other wild strains (La Morica et al., 1986; Hughes et al., 1986), have Glu at aa 69 and Ser at aa 113. Although the nucleotide sequence of the ancestor of the P2/Sabin strain is not known, it cannot be ruled out that Asp-69 and Thr-113 of the viral RNA polymerase play a role in attenuation, even though minor.

Mutations in antigenic sites of the capsid proteins of the P2/Sabin-derived strains isolated from VAPP cases (Fiore et al., 1987) were also observed, and could act as an escape mechanism from the immune response. Thus, these molecular studies have demonstrated that many genomic modifications, some of them alredy known as able to increase the neurovirulence, can occur in the P2/Sabin strain after replication in humans.

The characteristics of various P2/Sabin-derived strains are summarized in Table 3.

Molecular basis of attenuation and reversion to neurovirulence of the P3/Sabin strain

The P3/Sabin strain (P3/Leon 12a,b) was derived from the wild P3/Leon/37 strain, isolated from the brain and spinal cord of a victim of a fatal case of paralytic poliomyelitis (Almond, 1987; Racaniello, 1988). Comparison of the complete nucleotide sequence of the attenuated P3/Sabin strain (Stanway et al., 1983; Toyoda et al., 1984; Weeks-Levy et al., 1991) with that of its neurovirulent ancestor, P3/Leon/37 strain (Stanway et al., 1984) demonstrated that these two strains differ by several mutations. By constructing recombinant viruses between the attenuated P3/Sabin strain and the neurovirulent P3/Leon/37 strain, and by testing their neurovirulence in monkeys, two major mutations important for the attenuation of the P3/Sabin were found: a C->U mutation at nt 472 of 5 NCR, and a C->U mutation at nt 2034 leading to a Ser->Phe substitution at aa 91 of the capsid protein VP3 (Westrop et al., 1989). Recent evidence has suggested that an U->C mutation at nt 2493, leading to an Ile->Thr substitution at aa 6 of the capsid protein VP1, may also be involved in the attenuation (Weeks-Levy et al., 1991; Tatem et al., 1992; Mento et al., 1993). It was demonstrated (La Monica et al., 1987) that recombinant viruses having C at nt 472 are neurovirulent for mice, while those with an U at this nt position are attenuated. When viral recombinants were grown in human neuroblastoma cell line SH-SY5Y (La Monica and Racaniello, 1989), recombinants having U-472 replicated to approximately 10-foldlower titers than did neurovirulent viruses with a C at this position, although the viruses replicated equally well in Hela cells. It has also been shown (Chumakov et al., 1991) that OPV type 3 containing C at nt 472 is rapidly selected during serial passages in African green monkey kidney cells that are used to produce the vaccine, and vaccine lots that had failed in the intraspinal monkey neurovirulence test contained a higher proportion of C at nt 472 than all other lots that had passed this test.

The nt 472 and 537 of 5'NCR pair in a predicted secondary structure (Pilipenko et al., 1989; Skinner et al., 1989; Agol, 1991). The attenuating U at nt 472 of 5'NCR of the P3/Sabin strain resulted in the alteration of a C-G base pair (nt 472-537) found in the neurovirulent wild strain P3/Leon/37 (ancestor of the P3/Sabin strain) to a U-G base pair (nt 472-537) found in the P3/Sabin vaccine strain, suggesting that the attenuated phenotype is partially associated with a weakening of a base pairing in a highly conserved structure (Agol, 1991; Macadam et al., 1992, 1994b; Minor, 1992, 1993; Minor et al., 1993). The alteration of the secondary structure of 5'NCR caused by the attenuating U at nt 472 could alter the interaction of viral RNA with one or more host factors required for the initiation of translation of poliovirus RNA (Agol, 1991; Svitkin et al., 1988), leading to the observed deficiency in translation (Svitkin et al., 1985, 1990) and decrease in neurovirulence associated with this C->U (nt 472) mutation (Westrop et al., 1989). The attenuating Phe-91 of the capsid protein VP3 inhibits virion assembly, specifically at the promoter-to-pentamer step (Macadam et al., 1991b). The location of aa 91 of VP3 and of a number of candidate supressor mutations in the atomic structure of the virion suggested that it might act by destabilization of the particle and that supressor mutations may function by stabilizing specific interfaces (Minor et al., 1989).

Genomic modifications in type 3 polioviruses isolated from VAPP cases and healthy vaccinees

The attenuating U at nt 472 was observed to revert to C in all P3/Sabin-derived strains isolated from stool and/or CNS from VAPP cases, but Phe-91 of VP3 was maintained in most cases (Cann et al., 1984; Almond et al., 1985; Evans

et al., 1985; Macadam et al., 1989; Minor et al., 1989, 1993; Georgescu et. al., 1994; Friedrich et al., 1995c; Driesel et al., 1995). It was suggested that second site-mutations in the capsid proteins are able to suppress the attenuating effect of Phe 91 of VP3 (Macadam et al., 1989; Minor et al., 1989; Driesel et al., 1995). An additional mutation at aa 54 of VP1, leading to the substitution of Ala by Thr or Val, was also frequently found in isolates from VAPP cases (Minor et al., 1989; Macadam et al., 1989). A G->A mutation at nt 143 of 5'NCR occured in several strains isolated from VAPP cases (Driesel et al., 1995). An U->C mutation at nt 472 found in strains isolated from VAPP cases was also observed in strains isolated from stool of healthy vaccinees, demonstrating a strong selection against U at this position in virus replication (Evans et al., 1985; Minor and Dunn, 1988; Dunn et al., 1990; Macadam et al., 1989; Ogra et al., 1991; Tatem et al., 1991; Contreras et al., 1992; Minor, 1992; Abraham et al., 1993; Minor et al., 1993; Driesel et al., 1995). A Phe->Ser mutation at aa 91 of V P3 or supressor mutations in the capsid proteins were also observed in the strains isolated from healthy vaccinees (Macadam et al., 1989; see also Contreras et al., 1992). Although strains with C instead of U at nt 472 apparently grow more efficiently in the nervous system of primates, an isolate recovered from the brain of a monkey inoculated intraspinaly with the P3/Sabin strain (with U-472) was identified, which replicated efficiently in monkey nervous tissue and maintained the attenuating U-472 (Tatem et al., 1991). Since there is a strong selection against an U at nt 472 in the replication of P3/Sabin strain in the human gut (and also in CNS), it is very interesting that a strain isolated from stool of a transverse myelitis (TM) case, collected 136 days after the administration of a single dose of vaccine, maintained U-472 (Friedrich et al., 1995c). Although the strain was isolated from stool and might not be necessarily the etiological agent of the disease, we assume that viruses maintaining U-472 could also replicate efficiently in the human gut in certain cases.

Genomic recombination has also been observed in P3/Sabin-derived strains isolated from VAPP cases (Macadam et al., 1989; Furione et al., 1993; Georgescu et al., 1994, 1995b; Driesel et al., 1995) and healthy vaccinees (Minor et al., 1986; Cammack et al., 1988; Macadam et al., 1989; Tatem et al., 1991; Minor, 1992; Minor et al., 1993; Driesel et al., 1995). Also mutations in antigenic sites were observed in P3/Sabin-derived strains isolated from VAPP cases and healthy vaccinees (Minor et al., 1986, 1989; Macadam et al., 1989). These studies demonstrated that many genomic modifications, some of them known to increase the neurovirulence, also occur in the P3/Sabin strain after replication in humans.

The characteristics of various P3/Sabin-derived strains are summarized in Table 4.

Table 4. Characteristics of various P3/Sabin-derived poliovirus strains

Source	Isolate	Mutation at nt 472	Antigenic change protein/aa position/mutation	Possible supressor protein/aa position/mutation
VAPP	P3/106	U->C		VP, 178 Gln->Leu
VAPP	P3/115	U->C	VP, 166 Val->Ala	VP ₃ 178 Gln->Leu
VAPP	P3/116	U->C		VP ₃ 91 Phe->Ser
				VP, 54 Ala->Thr
VAPP	P3/119	U->C		VP ₂ 200 Arg->Lys
				VP ₂ 215 Leu->Met
VA DD	D2/100	11.0		VP ₁ 54 Ala->Val
VAPP	P3/122	U->C		VP ₂ 265 Val->Ala
VAPP	P3/131	U->C	VD 164 Ass > Ass	VP ₃ 108 Thr->Ala
VAPP	P3/131	0->0	VP ₂ 164 Asn->Asp VP ₃ 77 Asp->Asn	VP, 54 Ala->Val
VAPP	P3/132	U->C	3	VP ₁ 34 Ala->Val
				VP, 175 Thr->Ala
VAPP	P3/146	U->C		VP ₁ 54 Ala->Val
				VP, 215 Leu->Met
VAPP	P3/156	U->C	VP ₃ 77 Asp->Asn	VP ₁ 54 Ala->Thr
				VP ₃ 91 Phe->Ser
			VP ₁ 286 Arg->Lys	VP ₂ 146 Asn->Lys
VAPP	P3/158	U->C		VP ₁ 54 Ala->Val
				VP ₂ 215 Leu->Met
				VP ₁ 263 Lys->Thr
VAPP	P3/161	U->C	VP ₃ 77 Asp->Asn	VP ₃ 91 Phe->Ser
				VP ₁ 54 Ala->Thr
VAPP	P3/382	U->C		VP 54 Ala->Thr
	D2/5554		115 165 11 55	VP 263 Lys->Ile
VAPP	P3/7574	U->C	VP ₂ 165 Ala->Thr	VP ₃ 108 Thr->Ala
hv	P3/KT2-2	8 U->C	VP, 165 Ala->Thr	VP ₃ 91 Phe->Ser
			VP, 77 Asp->Asn	
hv	P3/DM66	U->C	VP ₂ 165 Ala->Thr	VP, 18 Leu->Ile
			VP ₃ 77 Asp->Asn	-
hv	P3/EM47	U->C	VP ₂ 165 Ala->Thr	VP ₄ 34 Lys->Arg
			-	VP ₃ 108 Thr->Ala
				VP ₁ 54 Ala->Val
				VP ₁ 105 Met->Thr
hv	P3/NH-15	U->C		VP ₃ 91 Phe->Ser

hv = healthy vaccinee. For the rest of legend see Tables 1,2.

Factors involved in the establishment of paralytic poliomyelitis

As reverting mutations in 5'NCR at nt 480 for the P1/Sabin strain, at nt 481 for the P2/Sabin strain and at nt 472 for the P3/Sabin strain have been observed in almost all isolates from stool and/or CNS of VAPP cases, it was suggested that reverting mutations at these positions are important for the establishment of the disease (Evans *et al.*, 1985; Pollard *et al.*, 1989; Equestre *et al.*, 1991; Macadam *et al.*, 1989, 1991a, 1993; Muzychenko *et al.*, 1991; Otelea

et al., 1993; Georgescu et al., 1994; Friedrich et al., 1995b,c). The recent analysis of Sabin vaccine-derived strains isolated from VAPP cases without mutations at these positions suggested that the abovementioned mutations are not essential for the establishment of poliomyelitis (Georgecu et al, 1994; Friedrich et al., 1995a,b,c, 1996a). One possibility is that other mutations are able to suppress the attenuatting effect of G-480, A-481 and U-472 for the P1/Sabin, P2/Sabin and P3/ Sabin strains respectively, and that they could include a mutation(s) occuring directly in 5'NCR or in the region coding for some viral factor interacting with 5'NCR. Another possibility is that mutations in the 2A protease coding region, suggested to be involved in cap-independent translation (Minor et al., 1993; Macadam et al., 1994a), are able to suppress the attenuating effect of G-480, A-481 and U-472, for the three Sabin strains, respectively. As host factor(s) is (are) involved in interactions with 5'NCR (Svitkin et al., 1988; Meerovitch et al., 1989; Agol, 1991), if not supressing mutations in the viral RNA exist for attenuating determinants in 5'NCR in certain isolates from VAPP cases, it cannot be excluded that certain biochemical characteristics of the host factor(s), interacting with 5 NCR of the viral RNA, could select isolates maintaining important attenuating determinants in 5'NCR, supressing the effect of attenuating mutations in 5'NCR.

Although mutations increasing the yield and neurovirulence of the Sabin strains are important for the establishment of the disease (Macadam et al., 1989, 1991a, 1993; Otelea et al., 1993), the frequent isolation of poliovirus recombinants from VAPP cases (Macadam et al., 1989; Lipskaya et al., 1991; Furione et al., 1993; Georgescu et al., 1994, 1995a,b; Driesel et al., 1995; Friedrich et al., 1996c) has suggested that recombination may also increase the neurovirulence of the Sabin strains, while mutations in antigenic sites (Fiore et al., 1987; Macadam et al., 1989; Minor et al., 1989) could act as an escape mechanism from the immune response. The isolation of the Sabin-derived neurovirulent isolates with similar genomic modifications from healthy contacts of VAPP cases (Friedrich et al., 1995b, 1996c) and from healthy vaccinees (Macadam et al., 1989, 1991a, 1993) has supported the view that host factors are also important in the establishment of poliomyelitis. They could be involved in the replication of the virus in human cells through interaction with 5'NCR (Agol, 1991). As host factors could be regarded also immuno-deficiencies (WHO, 1982; Nkowane et al., 1987; Groom et al., 1994; Zuckerman et al., 1994) such as heritable immunedeficiencies (Lederman and Winkelstein, 1985), immunedeficiencies caused by protein/calorie malnutrition (Arya, 1994), deficiency in vitamin A (Arya, 1994) or HIV infection (Arya, 1994; Wyatt, 1994, Ion-Nedelcu et al., 1994). Intramuscular injections within 30 days after exposure to OPV through vaccine or contact with a recent vaccinee might also be a risk

factor for VAPP cases (Strebel *et al.*, 1995). Other host factors and other pathological conditions could also be involved. The constant genomic characterization of Sabin-derived strains isolated from VAPP cases and healthy individuals might help to elucidate the complex interactions of host and virus factors that are important for the establishment of the disease.

Sabin-related poliovirus vaccine-related strains isolated from cases of GBS, transverse myelitis and facial paralysis

The cause of GBS and TM, demyelinating diseases of CNS, is unknown, although GBS (Leneman, 1966; Ropper, 1992; Stratton et al., 1994; Bolton, 1995) and TM (Holt et al., 1976; Whittle and Roberton, 1977; Barak and Schwartz, 1988; Vahidy et al., 1989; D'Costa et al., 1990; Dodson, 1990; Heller et al., 1990; Miles et al., 1993, Caldas et al.. 1994; Graber et al., 1994; Hill et al., 1994) are frequently preceded by viral infections and vaccinations. A significantly increased incidence of GBS cases were observed in Finland in 1985 during and soon after a mass vaccination campaign against poliomyelitis with OPV (Kinnunen et al., 1989; Uhari et al., 1989). In Finland, immunization against poliomyelitis is routinaly performed with inactivated poliovirus vaccine, and OPV was used in an one-time- campaign in 1985. Also A.B. Sabin himself developed GBS after working for many years with enteroviruses (Melnick and Horaud, 1993).

The isolation of Sabin-derived poliovirus vaccine strains in Brazil from eases of GBS, TM and facial paralysis has suggested that this paralysis could also be rarely caused or triggered by poliovirus infection (Friedrich et al., 1995a,c,d, 1996b). In these studies, the isolation of Sabin poliovirus vaccine-related strains in all the cases analysed, where the last vaccine dose was mostly given months or years before the establishment of the disease, has suggested a persistent infection or transmission of these strains to the patients. The isolation of Sabin poliovirus vaccine-related strains from cases of GBS, TM and facial paralysis several days or weeks after the onset of motor deficiency demonstrated a temporal association between the disease and the isolated viruses. The analysis of four isolates from stool of GBS cases at nt 480, 525 and 6203, demonstrated a G->A mutation at nt 480 and a C->U mutation at nt 6203 in the first strain, a G->A mutation at nt 480 in the second strain, a G->A mutation at nt 480 and an U->C mutation at nt 525 in the third strain (demonstrating the presence of at least two subpopulations), while the fourth strain did not mutate either at nt 480, 525 or 6203 (Friedrich et al., 1995a). Interestingly, in three out of four of these GBS cases, where mutations in the isolates were observed, the last vaccine dose was given several months or years before the onset of the disease. The mutation at nt 480 or 525 were also observed in strains isolated from facial paralysis cases (Friedrich et al., 1995a). In another study (Friedrich et al., 1995c), a P3/Sabin-derived

strain isolated from stool, collected 17 days after a single OPV administration, from a patient presenting GBS also presented a mutation at nt 472. Still another P3/Sabin-derived strain isolated from stool, collected more than four months after a single OPV dose from a patient presenting TM, maintained the attenuating U-472 of 5'NCR (Friedrich *et al.*, 1995c).

The capacity of Sabin-derived poliovirus strains to cause a persistent infection in human neuroblastoma cells has been demonstrated (Colbere-Garapin et al., 1989). The nucleotide sequence analysis of the P1/Sabin-derived strains revealed mutations at nt 525 and elsewhere (Pelletier et al., 1991; Borzakian et al., 1993). Other studies have demonstrated the capacity of Theiler's virus, also a member of the *Picor*naviridae family, to cause a persistent infection leading to demyelination of CNS in mice (Jarousse et al., 1994; Yauch and Kim, 1994; Johnston et al., 1995; Michiels et al., 1995). Although the Sabin poliovirus vaccine-derived strains isolated from cases of GBS and TM in Brazil may not be the etiological agents of the disease, these studies support the idea that infections caused by these strains could also trigger demyelination of CNS of humans in certain cases (Friedrich et al., 1995a,c,d, 1996b).

Conclusions

Many studies have demonstrated that most of the rare VAPP cases are related to poliovirus type 2 and 3 strains, and more rarely to type 1 strain. As more mutations are involved in the attenuation of the P1/Sabin strain in comparison with the other two vaccine strains, this property has been suggested to be an important factor for the greater safety of this strain. Although many genomic modifications have been detected in Sabin vaccine strains isolated from VAPP cases, similar genomic modifications have been found in strains isolated from healthy contacts and healthy vaccinees, supporting the view that host factors are also involved in the establishment of poliomyelitis. The observation of isolates from VAPP cases without reverting mutations in important attenuating determinants has led us to assume that reverting mutations may not be essential for the establishment of the disease. It is likely that other mutations could increase the neurovirulence or participate in some way in the establishment of the disease. The isolation of Sabin poliovirus vaccine-derived strains from GBS, TM and facial paralysis cases has suggested that in general the vaccine strains could also trigger these diseases in rare cases and not just poliomyelitis.

Acknowledgements. I thank Dr. H.G. Schatzmayr, the head of the Department of Virology, and Dr. E.E. Da Silva, the head of the Enterovirus Laboratory of the Department of Virology, both from Instituto Oswaldo Cruz, for supporting my studies on polioviruses.

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