ORIGINAL ARTICLE

VIROLOGY

Retrospective molecular and phenotypic analysis of poliovirus vaccine strains isolated in Greece

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Abstract

The live oral poliovirus vaccine (OPV) strains are genetically unstable, causing, in rare cases, vaccine-associated paralytic poliomyelitis. Reversions of the known attenuating mutations in OPV strains and intertypic recombination have been identified as the underlying causes of the increased neurovirulence of poliovirus isolates. In this study, three OPV isolates (one non-recombinant and two recombinants) were tested in order to correlate phenotypic traits such as temperature sensitivity (Rct test) and growth kinetics (one-step growth curve test) with mutations and recombination events of the viral genome. Moreover, the immunity level of the western Greek population aged 1–40 years was evaluated against OPV isolates and Sabin vaccine strains, with a microneutralization assay. Members of the 1–40-year age group (both pooled and individual sera) showed no significant differences in neutralization test (NT) titres against OPV isolates in comparison with the Sabin vaccine strains. However, all three OPV isolates showed reverted phenotypic traits in Rct or one-step growth curve assays. The results of our study revealed a significant decrease in immunity level from the 1–10-year age group to the 21–30-year age group (pooled sera) for both poliovirus types 1 and 3. For both poliovirus types, the highest NT titres were observed in the 1–10-year age group, and the lowest NT titre was observed in the 21–30-year age group, towards poliovirus type 3. Our study underlines the need for immunological studies in all age groups, in order to allow reconsideration of the current vaccination policies and to avoid epidemics caused by the circulation of highly evolved OPV derivatives.

Keywords: Greece, immunity, mutations, neurovirulence, oral poliovirus vaccine isolates, polioviruses, recombination Original Submission: 15 September 2010; Accepted: 10 January 2011

Editor: T. A. Zupanc **Article published online:** 24 January 2011 *Clin Microbiol Infect* 2011; **17:** 1554–1562 10.1111/j.1469-0691.2011.03470.x

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Introduction

Polioviruses are the aetiological agents of acute paralytic poliomyelitis, belong to the genus *Enterovirus* of the family *Picornaviridae*, and exist as three immunologically defined serotypes (P1, P2 and P3). The genome of polioviruses is a 7.5-kb positive-sense single-stranded polyadenylated RNA. The viral RNA contains a long open reading frame flanked by a 5'-noncoding region (5'-NCR) and a 3'-noncoding region, which are involved in viral replication and translation. The structural (VP4, VP2, VP3 and VP1) and non-structural (2A, 2B, 2C, 3A, 3B, 3C and 3D) viral proteins are produced by

translation of the coding region and proteolytic cleavage of the polyprotein [1]. The poliovirus capsid consists of 60 copies of each of the four structural virion proteins. Surfaceexposed loops of structural proteins VP1, VP2 and VP3 contain the four antigenic sites designated AgS1–AgS4 [2].

Since 1960, poliomyelitis has been effectively controlled by the use of inactivated poliovirus vaccine (IPV) or live oral poliovirus vaccine (OPV). OPV consists of attenuated and thermosensitive strains of each of the three serotypes (Sabin 1, 2 and 3). The molecular determinants of attenuation and temperature sensitivity have been intensively studied, to elucidate the mechanisms involved and to improve the safety of Sabin vaccine strains [3–5].

OPV was the vaccine adopted throughout most of the world by 1964, because it multiplies actively in the gut of vaccinees, eliciting a strong, long-lasting immune response, and local immunity induced by OPV prevents or limits re-infection of humans. However, the selection of variants with increased neurovirulence, caused by genetic instability, constituted a real problem with respect to OPV safety [6-8]. In rare cases (one case per 750 000 primary vaccinees), OPV strains have been implicated in vaccine-associated paralytic poliomyelitis (VAPP). Genetic recombination and mutations at attenuating sites of the genome have been associated with the emergence of VAPP cases [9,10]. Moreover, changes are frequently observed in the antigenic properties of OPV strains, representing a selection of viral variants that are less prone to be neutralized by human antibodies [11].

OPV was introduced into Greece in 1964, and was administrated to 2 million persons aged <18 years. A standard vaccination schedule of four doses at the ages of 2, 4, 6 and 18 months, with a booster dose at 4-6 years, led to the elimination of indigenous cases of poliomyelitis after 1982 [12]. However, Greece has switched to the exclusive use of IPV since 2005, as is also the case in most polio-free countries.

In this study, three OPV isolates (one non-recombinant and two recombinants) were tested in order to correlate the reverted phenotypic traits, such as temperature sensitivity and growth kinetics, with mutations and recombination events in the viral genome. Moreover, the immunity level of the western Greek population aged 1-40 years was evaluated against OPV isolates and Sabin vaccine strains.

Materials and Methods

Virus isolation

Two viral strains were isolated from faecal samples of a VAPP patient or a healthy vaccinee and one from the environment during the time period 1978-1985. They were recultured for the purpose of the present study in Hep-2 cells (Table I), as previously described [13]. The vaccine strains (Sabin I, 2 and 3) that were used in this study were provided by the WHO.

Genotyping and identification of recombinant OPV isolates

Primer pair UG52/UC53 was used for identification of vaccine origin and for genotyping of the isolates in the 5'-NCR [14]. Also, the genotype of isolates according to VPI capsid protein was determined by sequencing. The primer pairs used for complete VPI gene sequencing were UG1/222 [15,16] for the first half of the VPI gene and serotype-specific primer pairs S137/S1688 and S326/S3651 for Sabin I and Sabin 3 isolates, respectively, for the second half of the VPI gene [17].

Identification of recombination sites of OPV isolates was initially performed by restriction fragment length polymorphism screening analysis followed by sequencing, as previously described [18,19].

Extraction of viral RNA

Two hundred microlitres of frozen and thawed viral stocks were subjected to viral RNA extraction as previously described [20].

Sequencing of OPV isolates

Reverse transcription and PCR reactions for OPV isolates were performed with an MJ Research Minicycler, as previously described [19].

Complete genomic sequencing of isolate MBI and sequencing of VPI-VP4 capsid genes of isolates 522 and 742 were performed. Also, the partial 5'-NCR sequences of isolates 522 and 742 were determined with primer pair UG52/ UC53. The primer pairs used in this study are shown in Table 2. For all primer pairs, PCR conditions were as described in the original publications (Table 2). Analysis of PCR products was performed by agarose gel electrophoresis (2% agarose; I mg/L ethidium bromide in Tris-boric acid-EDTA buffer), with the 100-bp DNA ladder as molecular mass marker (Invitrogen Life Technologies, Paisley, UK). PCR products were cleaned up with a PCR gel extraction kit (Qiagen, Hilden, Germany). All PCR products were sequenced at Macrogen Inc.

Computational analysis/computer graphics

ClustalW was used for alignment of nucleotide and amino acid sequences of OPV isolates with those of the reference strains cited in GenBank (Sabin I, AY184219; Sabin 2,

TABLE I. Available data for oral poliovirus vaccine isolates

| Isolate | and VPI genotype | Source | Recombination site/type/junction | Accession numbers ^a 5′-NCR/Capsid/2A–3D | Reference |
|---------|---------------------|------------------|--|---|------------|
| 522 | SI | Healthy vaccinee | Non-recombinant | FJ609754/HM537000/- | [21] |
| 742 | SI | Environment | 2A SI/S3 3461–3465 2C S3/S2 4511–4527 | EU598472/HM537002/EU598488 | [19] |
| MBI | S3 | VAPP | 2C S3/S1 4880-4887 | GU180608 | This study |

^aThe accession number of isolate MBI refers to the complete genome. The 2A–3D genomic region of isolate 522 was not sequenced.

| P rimer ^a | Polarity | Sequence $(5' \rightarrow 3')^{b}$ | Reference |
|-----------------------------|-----------|------------------------------------|-----------|
| 72437 | Sense | 001-TTAAAACAGCTCTGGGGTTG-020 | [31] |
| 216616 | Antisense | 545-GGAACACGGACACCCAAAGTA-565 | [32] |
| UG52* | Sense | 162-CAAGCACTTCTGTTTCCCCGG-182 | [14] |
| UC53* | Antisense | 577-ACCGACCAATACCACTGTT-595 | [14] |
| S₃309 | Sense | 309-GTAGCTTGGGCCGATGAGT-327 | [33] |
| S ₃ 044 | Antisense | 1025-ACTGAATTTGCTGCCTCCTG-1044 | [33] |
| S₃936 | Sense | 936-CTCCAGCACTCAATTCACCA-955 | [33] |
| S ₃ 510 | Antisense | 1491-TCCCAGTAACACCCCACATC-1510 | [33] |
| S₃78 | Sense | 1378-TTATGCAAATGCGAATCCAG-1397 | [33] |
| S₃864 | Antisense | 1844-AATAGGCGGAGTGACATCAAA-1864 | [33] |
| S ₃ 709 | Sense | 1709-CCCAATGTGTAGCGAGTTCA-1728 | [33] |
| S ₃ 218 | Antisense | 2200-GTGCCCAACATAGCCTCCT-2218 | [33] |
| S ₃ 40 | Sense | 2140-TACGGGGAAAATCCTAGTGG-2159 | [33] |
| S ₃ 659 | Antisense | 2640-CGTTTGAACTGTGTCGGATG-2659 | [33] |
| ŬĜI | Sense | 2402-TTTGTGTCAGCGTGTTAATG-2421 | r151 |
| 222 | Antisense | 2982-CICCIGGIGGIAYRWACA-2999 | ř۱61 |
| S-26 | Sense | 2826-GCCGTAAGTTGGAGTTTTTCAC-2847 | เ |
| S-651 | Antisense | 3451-CTCCTTAGTGGCGAGATGGTAG-3430 | r171 |
| S,23* | Sense | 323-GAGTCTGGACATCCCTCACC-342 | [34] |
| S.976* | Antisense | 957-TACCCGCAAGCCTCTATGTT-976 | [34] |
| S ₁ 82* | Sense | 882-CTCAAGACCCTTCCAAGTTCA-902 | [34] |
| S. 542* | Antisense | | [34] |
| S-350* | Sense | | [34] |
| S,693* | Antisense | | [34] |
| S ₁ 476* | Sense | | [34] |
| S.154* | Antisense | | [34] |
| 5.013* | Sense | | [34] |
| S.669* | Antisense | | [34] |
| \$.37* | Sense | | [] 7] |
| 5.688* | Antisense | 3488-ACATGACGTTCACTGCGTTTT -3468 | [17] |
| 71935 | Sonco | 3206 GTCAATGATCACAACCC 3222 | [25] |
| FUC2 | Anticonco | | [35] |
| | Same | | [30] |
| | Anticonco | | [37] |
| | Anusense | | [37] |
| 53141 | Sense | | [10] |
| S3368 | Antisense | 5239-AIGIIGACGAICCAICCIIICI-5217 | [18] |
| S248 | Sense | | [18] |
| 52911 | Antisense | 5812-GTTTGTCGTCCACCGAGATT-5832 | [18] |
| UG16 | Sense | 5921-GTTGGTGGGAACGGTTCACA-5940 | [37] |
| 6.70 | Antisense | | [37] |
| S ₁ /0 | Sense | | [18] |
| S ₁ 450 | Antisense | 6851-ATTGAAGTGCCTGAGCAACC-68/1 | [18] |
| S ₁ 198 | Sense | 6728-GCACTAAAGATGGTGCTTGAGAAA-6752 | [18] |
| S ₁ 885 | Antisense | /415-CTACAACAGTATGACCCAATCCAA-7391 | [18] |
| S ₂ 107 | Sense | 6647-1 CCCAGTGCTAATGGAAGAGA-6668 | [18] |
| S ₂ 872 | Antisense | /393-ACAACAGCATGACCCAATCC-7413 | [18] |

TABLE 2. Primer pairs used foramplification of the complete gen-ome of isolate MB1 and of the par-tial 5'-noncoding region (5'-NCR)and capsid region of isolates 522and 742

^aPrimer pairs marked with an asterisk were used for amplification of the partial 5'-NCR and capsid region of isolates 522 and 742. Primer pair UG1/222 was used for amplification of all three isolates. ^bPositions refer to Sabin 1 strain, AY184219; S2, Sabin 2 strain, AY184220; S3, Sabin 3 strain, AY184221). For all other primers, positions refer to Sabin 1 strain.

AY184220; and Sabin 3, AY184221). Amino acid sequences of OPV isolates were obtained with Gene-Runner V. 3.05.

Rasmol V. 2.7.1.1 (http://www.umass.edu/microbio/rasmol) was used for depiction of the amino acid substitutions, which were identified in the capsid proteins of OPV isolates. For visualization of the observed amino acid substitutions, the capsid protomer structure of the poliovirus type I Mahoney strain (IASJ.pdb) was used for Sabin I isolates, and the structure of the poliovirus type 3 Sabin strain (IVBE.pdb) was used for Sabin 3 isolates.

Rct marker test

Reproductive capacities at different temperatures (Rct marker) were evaluated with the Rct test. The Rct value is defined as the difference between the log_{10} virus titre of a viral stock measured at the optimal temperature (37° C) and that measured at the supraoptimal temperature (40° C). Rct values of OPV isolates and Sabin vaccine strains were determined as previously described [13]. Viruses were considered to be thermosensitive if the Rct value (between 37 and 40° C) was greater or equal to 2.00, and thermoresistant if the Rct value was lower than 2.00.

One-step growth curve experiment

One-step growth curve experiments were performed in Hep-2 cells at 37° C and 40° C for 0–16 h, with a multiplicity of infection of 10 (determined by titration of virus stocks on Hep-2 cells), as previously described [13].

Neutralization assay with human sera

The level of immunity of the human population against poliovirus was determined with a microneutralization assay, as previously described [21]. Pooled sera (ten mixed serum samples) were used from each age group (1-10, 11-20, 21–30 and 31–40 years) for the neutralization test (NT). The serum samples were provided by volunteers from regions of western Greece during the time period 2009–2010.

Moreover, the immunity level against poliovirus of two individuals randomly selected from each age group (1-10, 11-20, 21-30 and 31-40 years) was determined with the same microneutralization assay.

Statistical analysis

Student's t-test (paired samples test) was used to compare the mean values of log_{10} reciprocal NT titres of four age groups (1–10, 11–20, 21–30 and 31–40 years; pooled sera of ten individuals for each) against each Sabin vaccine strain (Sabin I or Sabin 3) with those against each OPV isolate of the same serotype. It was also used to compare the mean values of log_{10} reciprocal NT titres of four age groups (1–10, 11–20, 21–30 and 31–40 years; two individual sera for each) against each Sabin vaccine strain (Sabin I or Sabin 3) with those against each OPV isolate of the same serotype.

A one-way ANOVA (Duncan's multiple range test) was used to compare the mean values of \log_{10} reciprocal NT titres against all polioviruses of the same serotype between the 1–10-year, 11–20-year, 21–30-year and 31–40-year age groups (pooled sera of ten individuals each). It was also used to compare the mean values of \log_{10} reciprocal NT titres against all polioviruses of the same serotype between the 1–10-year, 11–20-year, 21–30-year and 31–40-year age groups (sera of two individuals for each).

Student's t-test was used to compare the mean values of log_{10} reciprocal NT titres of four age groups (1–10, 11–20, 21–30 and 31–40 years) against each poliovirus strain shown in the neutralization assay of pooled sera with those of individual sera.

Results

Genotypes and recombination types of OPV isolates

The 5'-NCR and VPI genotypes of isolates were identified. Two strains were genotyped as Sabin I and one strain as Sabin 3 (Table I). Among the three isolates, one (522) was identified as non-recombinant, and two, MBI and 742, as recombinant in one or two sites, respectively. The recombination type was S3/S1 for isolate MBI, and the recombination site was located in the 2C genomic region, from nucleotides 4880 to 4887. Isolate 742 was identified previously as S1/S3/S2 recombinant, with the first recombination site located in the 2A region from nucleotides 3461 to 3465 and the second in the 2C region from nucleotides 4511 to 4527 (Table I).

Temperature sensitivity of OPV isolates

The non-recombinant Sabin I isolate 522 and the recombinant Sabin 3 isolate MBI showed a thermosensitive phenotype, with Rct values of 3.5 and 4.5 units, respectively. The bi-recombinant Sabin I isolate 742 showed partial reversion to a thermoresistant phenotype, with an Rct value of 2.00 units. The Sabin vaccine strains (Sabin I and Sabin 3) exhibited, as expected, Rct values greater than 2.00 units (Table 3).

One-step growth curve experiment

The growth rates and virus yields of each isolate were compared with those of the corresponding genotype of the Sabin vaccine strain (Sabin 1 or Sabin 3) in one-step growth experiments in Hep-2 cells at 37° C and 40° C.

The non-recombinant Sabin I isolate 522 showed different growth kinetics from that of its progenitor Sabin I vaccine strain (Fig. I). More specifically, isolate 522 showed $1.5-2.5 \log_{10}$ units higher viral yield than the Sabin I vaccine strain at both 37° C and 40° C during the infectious life cycle.

TABLE 3. Location of mutations in the 5'-noncoding region and capsid region sequences of oral poliovirus vaccine (OPV) isolates, and comparison with the corresponding nucleotide and amino acid positions in Sabin vaccine strains

| Origin | Region | Isolate | Mutations ^a | $\Delta \log \text{Rct-40}$ |
|--------|--------|---------|----------------------------------|-----------------------------|
| SI | 5'-NCR | 522 | U344C | 3.5 |
| | | | G480A | |
| | | | C583G | |
| SI | 5'-NCR | 742 | G480A | 2.0 |
| | | | C583G | |
| S3 | 5'-NCR | MBI | U472C | 4.5 |
| SI | VP2 | 522 | CIII9A, Asp56 \rightarrow Glu | |
| | | | G1207A | |
| | | | G1479A | |
| | | | C1695U | |
| SI | VP2 | 742 | CI44IU | |
| S3 | VP2 | MBI | - | |
| SI | VP3 | 522 | G1775U, Val4 \rightarrow lle | |
| | | | C1941A, Ala59 \rightarrow Glu | |
| | | | G2003A, Asp80 \rightarrow Asn | |
| SI | VP3 | 742 | | |
| S3 | VP3 | MBI | A2207U | |
| | | | U2208G, Met149 \rightarrow Trp | |
| SI | VPI | 522 | A2623G | |
| | | | A2749G, Ile90 \rightarrow Met | |
| | | | A3248G, Ile257 \rightarrow Val | |
| SI | VPI | 742 | G2502A, Ser8 \rightarrow Asn | |
| | | | G2776U, Lys99 \rightarrow Asn | |
| | | | A2833G | |
| | | | U2904G, Phe142 \rightarrow Cys | |
| S3 | VPI | MBI | C2493U, Thr6 \rightarrow lle | |
| | | | C2855A | |
| | | | U2857A | |
| | | | C2863A, Asp129 \rightarrow Glu | |
| | | | U2865G, Met130 \rightarrow Arg | |
| | | | G2882U, Val136 \rightarrow Leu | |
| | | | A3248G, lle258 \rightarrow Val | |
| NI I I | 11 | | | |

Numbering according to vaccine strains Sabin I (AY184219) and Sabin 3 (AY184221). Reproductive capacity values of OPV isolates and Sabin vaccine strains at different temperatures (Rct marker) are also indicated.

^aThe first nucleotide or amino acid refers to the Sabin vaccine strain. Amino acid substitutions situated near or in antigenic sites are underlined. No mutations were identified in VP4 capsid protein of all three isolates.



FIG. 1. One-step growth curve analysis of oral poliovirus vaccine isolates 522, 742 and MB1 in comparison with Sabin vaccine strains in Hep2 cells. Cells were infected at a multiplicity of infection of 10, and incubated at 37° C or 40° C. Total virus production at different times (0–16 h) post-infection was determined by TCID₅₀ assay on Hep2 cells. Each point represents the mean (± standard deviation) of virus titres from five different experiments.

However, the growth of isolate 522 showed a flat curve at 40°C, like that of the Sabin I vaccine strain. The bi-recombinant Sabin I isolate 742 replicated with kinetics similar to those of its progenitor Sabin I vaccine strain, showing that the virus yield rose 2 h post-infection at $37^{\circ}C$ (Fig. I), whereas at 40°C its growth was blocked, as it was also for the Sabin I vaccine strain.

The recombinant Sabin 3 isolate MB1 showed different growth kinetics from that of its progenitor Sabin 3 vaccine strain (Fig. 1). More specifically, the viral yield of isolate MB1 rose 2 h post-infection at 37°C, whereas that of the Sabin 3 vaccine strain rose 4 h post-infection. This initial difference resulted in a 1.5 \log_{10} units higher viral yield of isolate MBI than of the Sabin 3 vaccine strain 4 h post-infection. However, isolate MBI showed a similar viral yield to that of the Sabin 3 vaccine strain at the final stages of the infectious life cycle (8 and 16 h post-infection). At 40°C, the growth of isolate MBI was blocked, as was that of the Sabin 3 vaccine strain.

Nucleotide and amino acid sequence analysis

Table 3 shows the 5'-NCR and capsid sequence differences of OPV isolates with respect to Sabin vaccine strains. Both Sabin I isolates (522 and 742) displayed the mutation G480A in the 5'-NCR, which has been correlated with reversion to neurovirulence and thermoresistance [7]. They also displayed the mutation C583G, which has been observed in isolates of previous studies [13,22], and may confer a selective advantage. In VPI of isolate 522, the amino acid substitution lle90 \rightarrow Met is situated in the exterior of the capsid, near AgSI [2]. The amino acid substitution lle257 \rightarrow Val is partially exposed at the outer surface of the virion, situated on the last strand of VPI, which is located next to strand B, where residue 90 is located (data not shown). The amino acid substitution Lys99 \rightarrow Asn in VP1 of isolate 742, which is highly exposed in the exterior of the capsid, is located in AgSI as well as in the VPI BC loop, which participates in the formation of the north rim of the canyon and is involved in the binding of receptor CD155 to the virus [2,23]. The amino acid substitution PheI42 \rightarrow Cys is exposed on the external surface of the virion in the DE loop (data not shown), and may contribute to restoring neurovirulence, like residue 143, a well-known determinant of neurovirulence in Sabin 2 isolates [6]. The amino acid substitutions Ala59 \rightarrow Glu and Asp80 \rightarrow Asn in VP3 of isolate 522 are located in AgS3 and near AgS4, respectively [2]. The amino acid substitutions Asp56 \rightarrow Glu in VP2 and Val4 \rightarrow IIe in VP3 of isolate 522, as well as Ser8 \rightarrow Asn in VPI of isolate 742, are situated in the N-terminus of capsid proteins, which participates in hydrophobic interactions contributing to the stability of the virion [24].

The Sabin 3 isolate MBI displayed the mutation U472C in the 5'-NCR, which has been correlated with reversion to neurovirulence and thermoresistance [8,10]. In the VPI coding region, it displayed the reversion at nucleotide 2493 ($C \rightarrow U$ (Thr6 \rightarrow IIe)), which is a determinant of attenuation [25]. The amino acid substitutions Asp129 \rightarrow Glu and Met130 \rightarrow Arg are situated in the bottom of the canyon (data not shown), and may be involved in the interaction of receptor CD155 with the virus. The amino acid substitutions Val136 \rightarrow Leu and IIe258 \rightarrow Val are partially exposed at the outer surface of the virion, and are situated in the hydrocarbon-binding pocket of VP1, interacting with a sphingosine molecule (data not shown). The amino acid substitution Met149 \rightarrow Trp in VP3 is located in the inner surface of the capsid (data not shown), where the N-termini of capsid proteins interact, contributing to the integrity of the virion [24].

Nucleotide and amino acid substitutions were also identified in the 2A–3D non-structural genomic region of isolates 742 and MBI (data not shown). The reversion at nucleotide 6203 (C \rightarrow U (His73 \rightarrow Tyr)) of the 3D polymerase coding region, which has been correlated with the attenuated and thermosensitive phenotype of the Sabin I vaccine strain [4], was not identified in the 3D region of isolate MBI. Other mutations in 2A–3D coding regions appeared rarely and with no obvious preferences, and will not be considered further.

Neutralizing capacity with human antisera

The levels of immunity towards all three OPV isolates and Sabin vaccine strains of the western Greek population of the 1-10-year, 11-20-year, 21-30-year and 31-40-year age groups were measured. Pooled (Table 4) or individual (data not shown) sera were tested against each poliovirus strain. Table 4 shows the statistical analysis of the log_{10} reciprocal NT titres against OPV isolates and Sabin vaccine strains.

Members of the 1–40-year age group (both pooled and individual sera) showed no significant differences in NT titres against OPV isolates in comparison with the Sabin vaccine strains.

A significant decrease in NT titre was observed from the I-I0-year age group to the 2I-30-year age group for both poliovirus types (PI and P3). An increase in NT titre was observed from the 2I-30-year age group to the 3I-40-year age group for poliovirus types I and 3. However, this increase was significant only for poliovirus type I (Table 4).

In the neutralization assay with individual sera, no significant differences in NT titres were observed for poliovirus type I between the I-I0-year, II-20-year, 2I-30-year and 3I-40-year age groups. For poliovirus type 3, the results are consistent with those of pooled sera. Sequential decreases in NT titre were observed from the 1-10-year age group to the 11-20-year and 21-30-year age groups, with the first being significant.

The mean values of NT titres of the four age groups against each poliovirus strain with pooled sera showed no significant differences in comparison with those of individual sera (data not shown).

Discussion

The OPV strains are genetically unstable. Thermosensitivity of reproduction (the Rct-40 marker), antigenic modifications and one-step growth curve experiment have been used as indirect markers of reversion to neurovirulence [4,26,27].

Reversions of the known attenuating mutations in OPV strains and intertypic recombination have been identified as the underlying causes of the phenotypic changes and increased neurovirulence of poliovirus isolates [6–8]. Natural recombinants of Sabin vaccine origin have been isolated from VAPP patients [9,18]. Administration of trivalent OPV provides optimal conditions for multiple infections of human intestinal target cells, thus favouring the possibility of intermolecular recombination between heterotypic viral genomes [28].

In this study, we determined phenotypic traits such as thermosensitivity, growth kinetics and neutralizing capacity with human antisera of three OPV isolates, and attempted to correlate them with genomic modifications.

Two Sabin I isolates, one non-recombinant (522) and one bi-recombinant (742), were tested. The presence of mutations at known determinants of attenuation and thermosensitivity and of the rare recombination event (S1/S3/S2) did not affect the growth phenotype of isolate 742 at either 37° C or 40° C, as it replicated similarly to the Sabin I vaccine strain. However, it showed partial reversion to a

TABLE 4. Statistical analysis of the log₁₀ reciprocal neutralization test (NT) titres (pooled sera) against Sabin vaccine strains and oral poliovirus vaccine (OPV) isolates

| | Virus strain | Mean values of log₁₀ reciprocal NT titres of four age groups, I-10, 11-20, 21-30 and 31-40 years (each consisting of the pooled sera from ten individuals) against each poliovirus strain ^a | Mean values of log_{10} reciprocal NT titres against all polioviruses of the same serotype in each age group: I-10, I1-20, 21-30 or 31-40 years (each consisting of the pooled sera from ten individuals) ^b | | | |
|----------|-----------------------|---|--|----------------|----------------|----------------|
| Serotype | | | 1-10 | 11–20 | 21-30 | 31-40 |
| 1 | Sabin I 522 742 | 2.50 2.50 2.42 (= 0.391) | 2.50 (p 1.0) | 2.50 (p 1.0) | 2.20 (p 1.0) | 2.70 (p 1.0) |
| 3 | Sabin 3 MBI | 2.42 2.42 2.20 (p 0.215) | 2.80 (p 0.275) | 2.05 (p 0.068) | 1.90 (p 0.068) | 2.50 (p 0.068) |

^aMean values of all three OPV isolates have no significant differences from the respective values of Sabin vaccine strains according to Student's t-test. ^bMean values in italic for each poliovirus serotype have no significant differences according to ANOVA. thermoresistant phenotype (Rct value = 2.00). The discrepancy in the results between the two assays may correlate with the fact that they show viral multiplication for different time periods. Isolate 522 showed a thermosensitive phenotype in both the Rct test (Rct value = 3.5) and the one-step growth curve test (flat curve at 40°C). However, it showed a higher viral yield than the Sabin I vaccine strain at both 37°C and 40°C throughout the infectious life cycle (0-16 h post-infection). In general, the presence of many determinants of thermosensitivity scattered along the whole genome of the Sabin I vaccine strain makes the reversion of Sabin I isolates to a thermoresistant phenotype difficult [4]. It is noteworthy that isolate 522 showed a higher virus titre (2.5 log₁₀ unit) than the Sabin I vaccine strain at the initial stages of the infectious life cycle (0, 1 and 2 h post-infection). This initial difference leads to a higher virus titre of isolate 522 than of the Sabin I vaccine strain throughout the infectious life cycle, and may originate from the different adsorption and/or penetration properties of isolate 522 from those of the Sabin I vaccine strain. The presence of mutations in antigenic sites of isolate 522 (Ala59 \rightarrow Glu and Asp80 \rightarrow Asn in VP3, and IIe90 \rightarrow Met in VP1) may be responsible for the difference in properties between isolate 522 and the Sabin I vaccine strain. Because of the structural proximity and even overlapping of antigenic sites and the capsid regions that interact with poliovirus receptors, it seems reasonable to hypothesize that the amino acids likely to be replaced in antigenic sites may interfere with optimal virus-cell recognition. Moreover, the mutation $IIe257 \rightarrow Val$, which is situated in the hydrocarbon-binding pocket of VPI that interacts with a sphingosine molecule, may contribute to the different adsorption and/or penetration properties of isolate 522.

The recombinant Sabin 3 isolate MB1 showed a thermosensitive phenotype in both the Rct test (Rct value = 4.5) and the one-step growth curve test (blocking of its growth at 40°C). Moreover, isolate MBI showed a similar viral yield to that of the Sabin 3 vaccine strain at the final stages of the infectious life cycle (8 and 16 h post-infection). Consequently, the presence of mutations at known determinants of attenuation and thermosensitivity (U472C in the 5'-NCR, Thr6 \rightarrow lle in VPI) does not affect its phenotype. However, the amino acid substitutions Asp129 \rightarrow Glu, Met130 \rightarrow Arg, Val136 \rightarrow Leu and Ile258–Val in VP1 may be responsible for the earlier increase in titre of isolate MBI (2 h post-infection) than of the Sabin 3 vaccine strain (4 h post-infection), resulting in a difference in titre of 1.5 log10 units at 4 h post-infection. These residues, which are situated in the canyon and in the hydrocarbonbinding pocket of VPI, may lead to different adsorption and/or penetration properties of isolate MBI from those of the Sabin 3 vaccine strain.

The capacity of human antisera to neutralize OPV isolates was also evaluated. More specifically, the levels of immunity towards all three OPV isolates and Sabin vaccine strains of the western Greek population of the 1–10-year, 11–20-year, 21–30-year and 31–40-year age groups was investigated. No significant differences from the homotypic Sabin strains were observed in the capacity of OPV isolates to be neutralized in both assays with pooled or individual sera. The presence of mutations in antigenic sites of isolates 522 and 742 did not affect their antigenic properties. The above reinforces the notion that the driving force behind antigenic alterations of OPV is not immune evasion, but negative selection of unfavourable mutations interfering with optimal virus–cell recognition [11].

The results of our study showed a significant decrease in immunity level from the 1-10-year age group to the 21-30-year age group (pooled sera) for both poliovirus types I and 3. These findings are consistent with those reported in previous studies [21,29]. An increase in NT titre was observed from the 21-30-year age group to the 31-40-year age group for both poliovirus types I and 3, which is consistent with the results of our previous study [21].

For both poliovirus types, the highest NT titres were observed in the 1-10-year age group, indicating a good response to vaccination. The lowest NT titre was observed in the 21-30-year age group towards poliovirus type 3, indicating an unsatisfactory level of immunity against poliovirus type 3 in young adults. These results are consistent with those of previous studies [21,29,30]. The presence of the lowest NT titre in the 21-30-year age group towards poliovirus type 3 suggests the need for a booster dose of monovalent Sabin 3 vaccine to ensure personal and herd immunity.

In the post-eradication era of wild polioviruses, the only remaining sources of poliovirus infection worldwide will be vaccine-derived polioviruses. As the majority of countries certified as being polio-free have switched from OPV to IPV, and taking into consideration the fact that IPV does not induce the same immunity levels as OPV, importation of recombinant evolved derivatives of vaccine strains would have serious implications for public health. Our study underlines the need for poliovirus surveillance. The repeated occurrence of highly divergent pathogenic poliovirus strains that have retained Sabin-like antigenic properties presents a serious challenge to the current poliovirus surveillance strategy. Phenotypic markers such as one-step growth curve analysis and the Rct assay, along with genomic analysis, are effective markers for the estimation of neurovirulence of OPV isolates. Additionally, there is a vital need for immunological studies in all age groups, in order to allow reconsideration of the current vaccination policies and to avoid epidemics caused by the circulation of highly evolved OPV derivatives.

Transparency Declaration

This work was supported by research grants of the Postgraduate Programme 'Applications of Molecular Biology-Genetics. Diagnostic Biomarkers', code 3817, of the University of Thessaly, School of Health Sciences, Department of Biochemistry & Biotechnology. All authors declare that they have no conflicting or dual interests.

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