

Case of poliomyelitis caused by significantly diverged derivative of the poliovirus type 3 vaccine Sabin strain circulating in the orphanage

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Supplementary material

Table S1. Mutations in the genomes of the Syzran isolates

| Genome region | Nucleotide (amino acid) mutation | Genome(s) of Syzran isolates harboring mutation | Genome region | Nucleotide (amino acid) mutation | Genome(s) of Syzran isolates harboring mutation | |
|--|--|---|--|--|---|-------------|
| 5'-UTR | G ₁₁₃ →A | all | VP1 | C ₂₄₉₃ →U (T ₆ →I)* | all | |
| | C ₁₂₃ →U | C-2 | | U ₂₅₆₉ →C | P-2 | |
| | G ₁₆₂ →A | all but C-3 | | A ₂₅₉₉ →G | all | |
| | G ₁₈₉ →C | P-2 | | C ₂₆₁₁ →U | all | |
| | C ₃₄₆ →U | C-2 | | C ₂₆₃₇ →U (A ₅₄ →V) | all | |
| | G ₃₉₅ →A | all | | A ₂₆₃₈ →G | C-2 | |
| | U ₄₇₂ →C* | all | | U ₂₆₉₃ →A (S ₇₃ →T) | all | |
| | U ₄₈₀ →C | all | | A ₂₇₆₂ →G (T ₉₆ →A) | all | |
| | U ₆₀₂ →C | all | | U ₂₇₉₀ →C (M ₁₀₅ →T) | all | |
| | G ₆₇₃ →G/A | C-3 | | G ₂₉₅₉ →A | all | |
| | U ₇₀₈ →C | C-3 | | G ₂₉₇₄ →A | all | |
| | U ₇₃₈ →C | C-3 | | A ₃₃₃₈ →G (N ₂₈₈ →D)** | all | |
| VP4 | A ₇₇₂ →G | all | | G ₃₃₄₄ →A (D ₂₉₀ →N)** | all | |
| VP2 | A ₉₆₄ →G | C-3 | 2A | C ₃₅₂₂ →U (T ₄₉ →I) | all | |
| | C ₁₀₃₅ →U (A ₂₉ →V) | P-1 and P-2 | | G ₃₅₇₉ →A (R ₆₈ →K) | C-2 | |
| | C ₁₀₈₄ →U | C-2 | | G ₃₆₇₆ →U | all | |
| | U ₁₁₂₆ →C | C-3 | | U ₃₇₁₅ →C | C-2 | |
| | C ₁₁₄₁ →U | C-3 | 2B | U ₃₇₇₈ →C | all but C-3 | |
| | A ₁₂₅₂ →G | all | | U ₃₈₃₈ →C | all | |
| | G ₁₃₉₀ →A | all | | G ₄₀₆₆ →A | all | |
| | A ₁₄₄₀ →U (N ₁₆₄ →I)** | C-1 | | 2C | G ₄₃₄₂ →A | all |
| | G ₁₄₄₂ →A (A ₁₆₅ →T)** | all | | | A ₄₄₁₇ →C | all |
| | U ₁₄₄₆ →C (V ₁₆₆ →A)** | all | | | A ₄₄₃₃ →G (T ₁₀₇ →A) | all |
| | G ₁₄₇₇ →A | all | | | A ₄₆₁₂ →U | C-3 |
| | U ₁₅₄₀ →C | all | | | G ₄₆₃₀ →A | all |
| | U ₁₅₄₃ →C | all | | | U ₄₆₆₃ →C | all |
| | U ₁₅₉₁ →C | P-1 and P-2 | | | A ₄₇₇₁ →G | P-1 and P-2 |
| U ₁₅₉₂ →C (L ₂₁₅ →M) | all | C ₄₇₇₄ →U | C-2 | | | |
| C ₁₅₉₆ →U (A ₂₁₆ →V) | C-3 | C ₄₇₈₆ →U | P-2 | | | |
| VP3 | C ₁₇₉₅ →U | all but C-3 | U ₄₈₄₉ →C | | all | |
| | G ₁₈₀₇ →A | C-2 | A ₄₈₆₁ →G | all | | |
| | U ₁₈₅₅ →C | C-2 | G ₄₈₆₈ →A (G ₂₅₂ →S) | all | | |
| | C ₁₉₉₈ →U (S ₇₉ →L)** | C-2 | A ₄₈₇₂ →G (E ₂₅₃ →G) | all | | |
| | U ₂₀₃₄ →C (F ₉₁ →S)* | all but C-3 | C ₄₉₁₇ →U (T ₂₆₈ →M) | all | | |
| | U ₂₂₉₉ →C | all but C-3 | U ₅₀₃₅ →C | P-1 and P-2 | | |
| | U ₂₃₄₀ →A (F ₁₉₃ →Y) | C-3 | | | | |
| | U ₂₄₁₃ →C | all | | | | |

*Adaptive mutations

**Mutations in the antigenic sites

| Genome region | Nucleotide (amino acid) mutation | Genome(s) of Syzran isolates harboring mutation |
|---------------|--|---|
| 3A | C ₅₁₁₆ →U | C-3 |
| | A ₅₁₁₉ →G | P-1 and P-2 |
| | G ₅₁₄₆ →U (R ₁₅ →S) | all |
| | A ₅₁₅₈ →G | P-1 and P-2 |
| | C ₅₃₅₇ →U (H ₈₆ →Y) | C-3 |
| 3B | A ₅₃₆₅ →G | C-2 |
| | C ₅₃₈₆ →U | all |
| | U ₅₃₉₈ →C | all |
| | G ₅₄₂₅ →A | all |
| 3C | C ₅₅₂₄ →U | all |
| | A ₅₅₆₇ →G (I ₄₇ →V) | all |
| | C ₅₅₉₇ →U | C-2 |
| | C ₅₆₀₂ →A (D ₅₈ →E) | all but C-3 |
| | C ₅₆₇₇ →U | all |
| | U ₅₈₃₂ →C (I ₁₃₅ →T) | all |
| | C ₅₈₅₄ →U | all |

| Genome region | Nucleotide (amino acid) mutation | Genome(s) of Syzran isolates harboring mutation |
|---------------|--|---|
| 3D | G ₆₀₈₆ →A (V ₃₇ →I) | all |
| | A ₆₁₀₉ →G | all |
| | U ₆₁₅₇ →C | all but C-3 |
| | U ₆₂₄₄ →C | all |
| | C ₆₂₆₆ →C/U | C-3 |
| | G ₆₃₀₄ →C | all |
| | C ₆₃₃₇ →U | C-2 |
| | U ₆₃₆₄ →U/C | C-3 |
| | A ₆₄₉₀ →G | all |
| | U ₆₅₅₀ →C | all |
| | U ₆₅₆₂ →C | all |
| | C ₆₅₈₉ →U | all |
| | C ₆₅₉₂ →U | C-2 |
| | A ₆₆₅₈ →G | C-2 |
| | A ₆₆₆₄ →A/G | C-3 |
| | C ₆₇₆₉ →U | all |
| | U ₆₈₇₇ →C | all |
| | A ₆₉₁₈ →A/G (K ₃₁₄ →K/R) | C-3 |
| | U ₆₉₃₈ →C | all |
| | U ₇₂₉₁ →C | all |
| | A ₇₃₀₃ →A/G | C-3 |
| | A ₇₃₂₁ →A/U | C-1 |
| | U ₇₃₆₀ →C | C-2 |

*Adaptive mutations

**Mutations in the antigenic sites

Table S2. Mutations* in the genomes of Syzran isolates found in other vaccine-related polioviruses type 3.

| Genome region | Nucleotide (amino acid) mutation | Genome(s) of Syzran isolates harboring mutation | Known or assumed biological relevance of mutation | Previous report (s) of same mutation in Sabin-3-derived viruses |
|--|--|---|---|---|
| 5'-UTR | G ₁₆₂ →A | all but C-3 | Stabilization of domain II structure | 1, 2 |
| | G ₃₉₅ →A | all | Stabilization of domain IV structure | 1-4 |
| | U ₄₈₀ →C | all | Stabilization of domain V structure | 1, 2 |
| | U ₆₀₂ →C | all | – | 1, 5 |
| | U ₇₃₈ →C | C-3 | – | 1 |
| VP4 | A ₇₇₂ →G | all | – | 4 |
| VP2 | A ₉₆₄ →G | C-3 | – | 2 |
| | C ₁₀₃₅ →U (A ₂₉ →V) | P-1, P-2 | – | 6 |
| | G ₁₃₉₀ →A | all | – | 2 |
| | G ₁₄₄₂ →A (A ₁₆₅ →T) | all | Region of antigenic site 2 | 1, 7**, 8 |
| | U ₁₄₄₆ →C (V ₁₆₆ →A) | all | Antigenic site 2 | 1, 7 |
| U ₁₅₉₂ →C (L ₂₁₅ →M) | all | – | 1 | |
| VP3 | C ₁₇₉₅ →U | all but C-3 | – | 1 |
| | C ₁₉₉₈ →U (S ₇₉ →L) | C-2 | Antigenic site 4 | 9 |
| | U ₂₂₉₉ →C | all but C-3 | – | 1, 2 |
| | U ₂₄₁₃ →C | all | – | 5 |
| VP1 | C ₂₆₃₇ →U (A ₅₄ →V) | all | – | 1, 2, 4, 5, 9, 10 |
| | U ₂₇₉₀ →C (M ₁₀₅ →T) | all | Interaction with poliovirus receptor | 1, 2, 3, 5, 7, 9, 10 |
| | A ₃₃₃₈ →G (N ₂₈₈ →D) | all | Antigenic site 3 | 1, 2, 9 |
| | G ₃₃₄₄ →A (D ₂₉₀ →N) | all | Antigenic site 3 | 1 |
| 2A | G ₃₆₇₆ →U | all | – | 1 |
| | U ₃₇₇₈ →C | all but C-3 | – | 2 |
| 2C | A ₄₄₃₃ →G (T ₁₀₇ →A) | all | – | 1 |
| | C ₄₉₁₇ →U (T ₂₆₈ →M) | all | – | 4, 9 |
| 3C | U ₅₈₃₂ →C (I ₁₃₅ →T) | all | Stabilization of ciRNA structure | 1, 11 |

*Without three known adaptive mutations observed in most variants of Sabin-3.

**In this article only amino acid substitutions were listed.

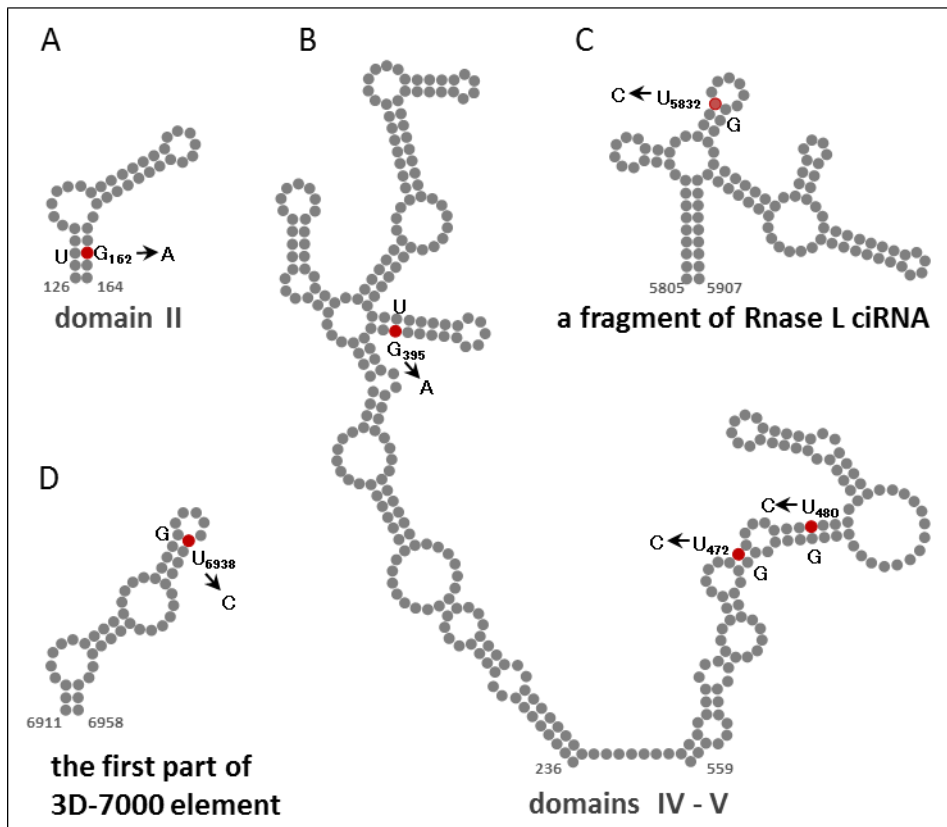


Figure S1. Nucleotide substitutions in the phylogenetically conserved RNA structural elements of the genomes of the poliovirus isolates, in comparison with the Sabin-3 strain. The positions of changed nucleotides are marked in red, and corresponding mutations are indicated; the nucleotides involved in the resulting base-pairing are also shown. A. Domain II of 5'UTR. B. Domains IV-V of 5'UTR [12]. C. A fragment of Rnase L competitive inhibitor element of viral RNA (ciRNA) [13]. D. The first conservative structural element of 3D-7000 [14].

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