ANALYSIS OF METAGENOMICS VACCINE VACV-IOC USED IN AGAINST SMALLPOX VACCINATION IN BRAZIL

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INTRODUCTION: Vaccines used in campaigns were composed of Vaccinia (VACV) live virus. Many Vaccinia virus strains were used in these vaccines, including Dryvax (DVX) produced by Wyeth in lyophilized form. After intensive vaccination campaigns smallpox was considered eradicated. In these campaigns, different types of vaccine were distributed in lyophilized form, but little information on the virus strain used was recorded. OBJECTIVE: To characterize the metagenome of the vaccine strain VACV-IOC, produced in the Oswaldo Cruz Foundation and used in anti-smallpox vaccination campaign in Brazil. MATERIALS AND METHODS: A sample of the lyophilized vaccine VACV-IOC contained in tube sealed was processed to extract the DNA with the DNA Isolation Kit PowerSoil® (MO Bio). DNA was quantified using the Qubit™ dsDNA HS Assay (Invitrogen). The library was prepared for next-generation sequencing of random type in Ion PGM platform according to manufacturer’s specifications. The generated sequences were processed and analyzed using CLC Genomics Workbench v.7.5 software. The BLASTn tool was used to search sequences in nucleotide database nt/nr GenBank. Sequences were trimmed with a minimum size of 50 contigs. MULTBLAST was made of 5,661 sequences. RESULTS: We obtained 2.13 g / ml of DNA from 12 mg of lyophilized vaccine. 6739 sequences were generated and processed by quality and size, resulting in 5,661 sequences with 62 bp average size. BLASTn results identified sequences of the vaccine strain Dryvax clone DPP21, bovine, human and bacterial in the sample. CONCLUSION: Our preliminary results showed that the 5661 sequences generated in sequencing were insufficient to metagenome analysis, identification of the virus variants and other organisms present in the sample. A new sequence being programmed to obtain more sequences to evaluate the variant vaccine strain and the process of getting the vaccine. Nevertheless, our findings contribute to the understanding of genomic diversity of the viruses used and origin of these first-generation vaccines.

Key Words: metagenomic, next generation sequencing, smallpox.

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