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Vaccinegate:

MRC-5 contained in Priorix Tetra - Complete genome sequencing

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Complete genome sequencing

Introduction

New generation sequencing have become the preferred tool for in-depth analysis in the field of biology and medical science, especially high precision ones. Thanks to these tools, we can approach in a more modern and comprehensive way a number of applications such as de novo sequencing, metagenomic and epigenomic studies, transcriptome sequencing and genome re-sequencing.
This last one (re-sequencing) is largely used in human field, both for research and diagnostic purposes and consists of **NGS - Next Generation Sequencing of an entire single genome, to map the Single Nucleotide mutations (SNP)**, *insertions and deletions of more or less long sequences that have occurred in certain locations of the genome, and variations in the number of copies of genomic portions/genes (CNV, Copy Number Variants).*
This procedure helps to understand the development mechanism of some pathologies, in order to identify the directions for a future clinical treatment as in the case of cancer for example. Indeed, by this method the genetic heritage of a cancer patient can be fully decoded in both normal and cancerous tissue, thus allowing us to comprehend what exactly has changed within the genome, and, if possible, how to intervene with targeted measures.

The re-sequencing procedure requires that the DNA of an individual is mechanically broken into small dimension fragments (400-500 base pairs) and artificial DNA parts named adapters are tied to these fragments; adapters make it possible to tie the human DNA fragments to a glass surface on which the bases reading (A, C, G, T) is performed. The DNA base pairs reading takes place by means of chemical reactions, namely the incorporation of nucleotides that have been marked by fluorescent molecules. The million sequences (reads) thus obtained are then mapped on the human reference genome by specific software and all the variants are identified comparing the analyzed genome with the reference genome.

This same procedure has been performed on the human genome in Priorix® Tetra lot n. A71CB256A, genome which belongs to cell line MRC-5 (of fetal origin); the work has been carried out by a company in the USA, that routinely deals with human genome re-sequencing analysis. *

** the name of the laboratory that has performed the analysis will be included in the next formal complaint we will file at the Public Prosecutor of Rome and as well at the Italian and European regulatory bodies. The associations who are filing the analysis funded by Corvelva will be promptly kept up to date with these shocking results too. We are no denying that we feel, especially as parents, distressed by these results we are reporting - as if what we have found out so far was not enough to worry about.*

Results

The human reference genome was found to be matched by 99.76% reads from vaccine DNA, that means nearly in all its entirety. **The human fetal DNA presented in this vaccine is a single entire genome**, that means the vaccine contains genomic DNA with all the chromosomes of a male individual (in fact MRC-5 originates from a male fetus).
Given below are the analysis results of different types of variants compared to the reference human genome.

Single nucleotide variant (SNP – single nucleotide polymorphism) and short insertions/deletions (InDels)

DNA single bases variants (SNP) are polymorphisms, which means genetic material mutations of a single nucleotide.
The 'InDels' are instead small insertions and deletions of less than 50 bp length and constitute a different class of genomic variants in the human genome.
In the vaccine human genome, 3.6 million SNP have been identified (98.31% of which are already reported in the public database dbSNP and 61.805 new, that means original in this DNA) and about 804.000 InDels (89.42% of which already reported in dbSNP and 85.106 new).
The amount of SNP is in line with what has been reported in literature on/in "typical human genome", whereas the InDels results in a higher quantity compared to what has been reported by "The 1000 Genomes Project Consortium" [1] **namely 800.000 compared to 600.000.**

[1] A global reference for human genetic variation - Nature, vol. 526, 10 Ott. 2015 - https://www.nature.com/articles/nature15393

CNV (Copy Number Variants) and SV (Structural Variants)

The copy number variants (CNVs) are genomic variants due to variations in the number of copies of relatively large fragments (longer than 50 bp) between individual genomes. There are two types of CNVs: type "gain" (gain of copies) and type "loss" (loss of copies). 218 CNVs were detected in the human vaccination genome, of which 82 were "gain" (covering a portion of the genome of about 6.9 million base pairs) and 136 CNVs of the "loss" type (covering a portion of the genome of about 70 million bases).

As described by *The 1000 Genomes Project Consortium* in "A global reference for human genetic variation (Nature, vol. 526, 10 Oct. 2015)" a typical human genome contains from 2,100 to 2,500 large variants including:

- 1,000 large deletions
- 160 variants in number of copies (CNVs)
- 10 inversions

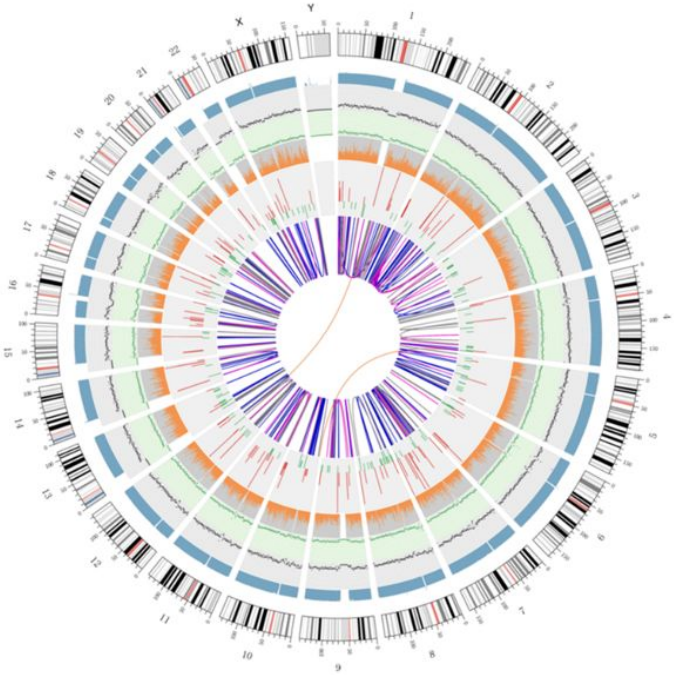
Which together affect the 20 million bases of the sequence, considering the insertions as well.

As seen for the short INDELs, even in the case of large insertions and deletions, the vaccine genome is therefore **not in line with a "normal" human genome**, being much more "rearranged" than a genome of a common person.

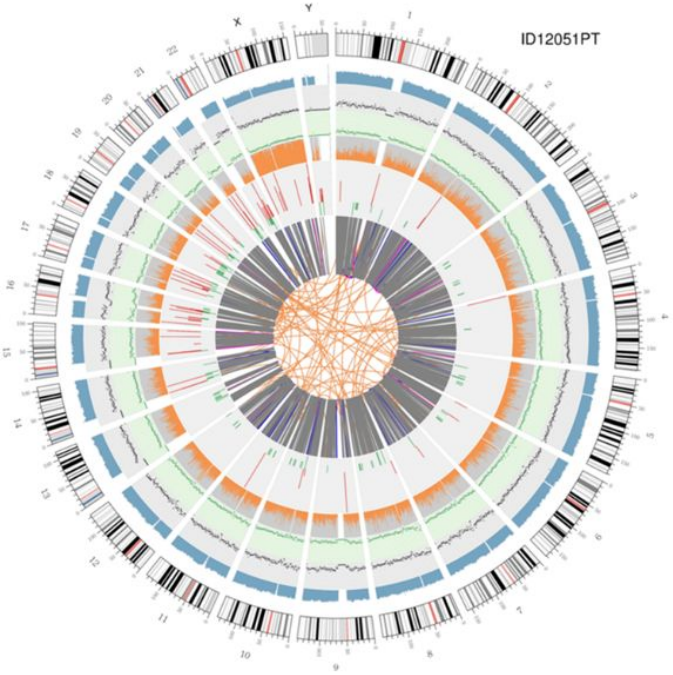
Circular vision of genome (circos plot)

A graphical representation of the vaccine genome called "circos plot" (commonly used to represent a re-sequenced genome), is shown below, alongside another representing a genome re-sequenced from DNA extracted from blood of a healthy individual - "normal" genome:

MODEL OF A NORMAL HUMAN GENOME



Priorix Tetra lot. A71CB256A, MRC-5V



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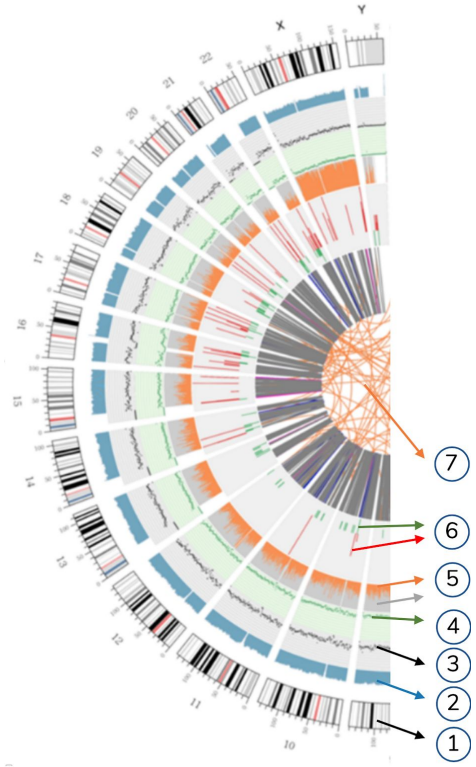
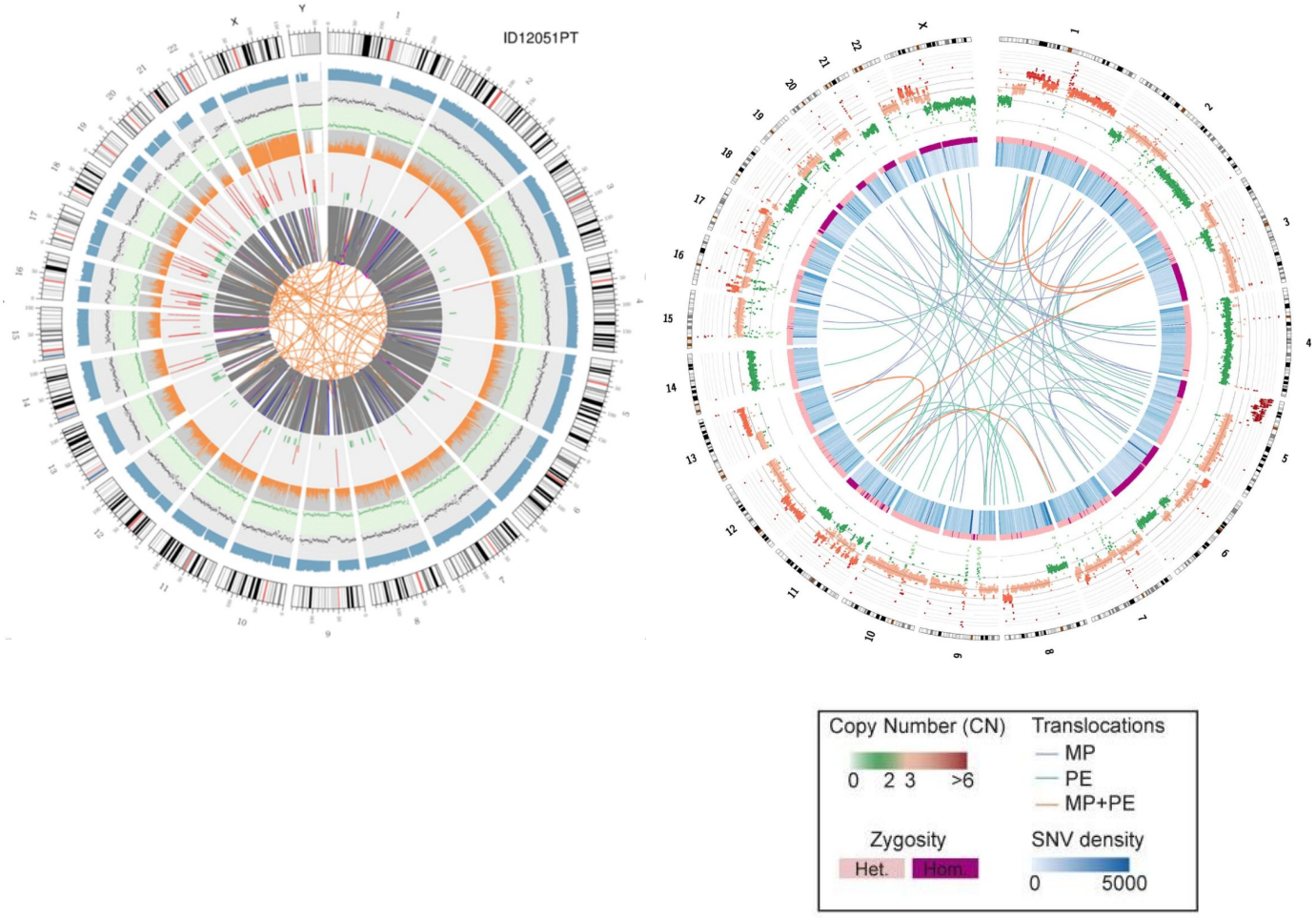
Meaning of the concentric circles



7) The most central ring represents the SV (Structural Variants) inference in the exon and splicing regions. TRA (**orange**, translocations), INS (**green**, insertions), DEL (deletions, **gray**), DUP (duplications, **pink**) and INV (inversions, **blue**).
6) the sixth circle represents the CNV inference (copy number variants). **Red** means DNA sequences gain and **green** means loss.
5) The fifth ring represents the SNP proportion in homozygosity (**orange**) and heterozygosity (**grey**) in histogram layout.
4) The fourth ring (**green**) represents the SNP density in scatter chart layout.
3) The third ring (**black**) represents the INDELs density in scatter chart layout.
2) The second ring (**light blue**) represents the reads covering in histogram layout.
1) The external circle (the first circle) is the chromosome number.

An approximate comparison can also be made between fetal DNA and the HeLa cells [2] DNA, the immortalized cell line used as well to produce the polio vaccine.

Priorix Tetra lot. A71CB256A, MRC-5V human genome



Please note that the HeLa cells translocations represented in the circos plot by the lines of the nucleus, are referred to the entire genome (hence the coding and non-coding part), while in the case of fetal vaccination cells they refer only to coding genes.

There is no need to be a scientist to understand from the circos, simply at a glance, that the vaccine genome is not a genome that can be defined as "normal". The orange lines intertwined at the center of the circos, not so numerous in the corresponding ring of the "normal" genome, already make sense to the anomaly of this genome.

Variant analysis in cancer genes

[2] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3737162/pdf/1213.pdf
G3 (Bethesda). 2013 Aug 7;3(8):1213-24. doi: 10.1534/g3.113.005777.
The genomic and transcriptomic landscape of a HeLa cell line.
Landry JJ1, Pyl PT, Rausch T, Zichner T, Tekkedil MM, Stütz AM, Jauch A, Aiyar RS, Pau G, Delhomme N, Gagneur J, Korbel JO, Huber W, Steinmetz LM.

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4458465/pdf/nihms695162.pdf
J Health Care Poor Underserved. 2012 Nov; 23(4 0): 5–10.
Development of the Polio Vaccine: A Historical Perspective of Tuskegee University's Role in Mass Production and Distribution of HeLa Cells
Timothy Turner

The analysis on SNP, InDels, CNV, SV variants on 560 genes chosen because they involved in different forms of human cancer shows the presence of numerous "original" variants, that's to say that they are, not even present in public databases, therefore are not known in the literature. In other words, important modifications of genes known to be associated with various tumor forms have been identified, for all the 560 verified genes; furthermore, there are variants whose consequences are not known, but which, however, affects genes involved in the induction of human cancer.

Conclusion

The human genomic DNA contained in the Priorix lot vaccine. n. A71CB256A is evidently anomalous, presenting important inconsistencies if compared to a typical human genome, i.e. the one of a healthy human being. **There are several unknown variants** (not noted in public databases) **and some of them are located in genes involved in cancer**. What is also apparently anomalous, is the excess of genome that shows changes in the number of copies (CNV) and structural variants (SV), such as translocations, insertions, deletions, duplications and inversions, many of which involve genes.

The potential contribution of the numerous variants (not present in the scientific literature and in public databases) to the phenotype of the cells used for the growth of vaccine viruses is not known.

Discussion and health implications

For completeness, we report what has already been disclosed regarding the first in-depth study of the human DNA contained in Priorix Tetra ®

The direct evidence is that inside this product there is a **complete human genome (i.e. with non-coding genes and sequences), with high molecular weight (see PFGE) and / or fragmented**, and is given by the result of the alignment of the human derivation reads (70-80% of the dataset in the three lots tested, of which the first batch was sequenced in 2017, but no data were presented in this report) on the human reference UCSC hg19, performed with a standard software (BWA) used by the scientific community to align NGS sequences on reference genomes (*Bioinformatics, Volume 25, Issue 14, 15 July 2009. Fast and accurate short read alignment with Burrows – Wheeler transform*).
The following table, highlighted in orange, shows the result expressed in "Av_cov = average coverage" of the alignment of the human sequences of the 3 Priorix® tetra lots tested (1st-2nd and 3rd lot) on human chromosomes. In column 1, chM is the mitochondrial DNA, while Ch1 to ChY are human chromosomes, including sex chromosomes X and Y. Column 2 shows the length of assembled human chromosomes expressed in base pairs.

		1st lot	2nd lot	3rd lot	BS (10M)	CE (10M)	G10A (10M	PM (10M)	RM313 (10M)	
Chromosome	Seq_length	Avg_Cov	Avg_Cov	Avg_Cov	Avg_Cov	Avg_Cov	Avg_Cov	Avg_Cov	Avg_Cov	
chrM	16571	40,1184	23,58222	32,13506	20,9446	59,89711	39,25919	61,1423	87,49194	
chr1	249250621	0,81201	0,24186	0,41086	0,46169	0,45822	0,4554	0,4678	0,45614	
chr2	243199373	0,83347	0,22501	0,4223	0,49022	0,48612	0,48535	0,49661	0,48405	
chr3	198022430	0,80242	0,20776	0,40803	0,4844	0,48386	0,47962	0,49129	0,48178	
chr4	191154276	0,7654	0,17642	0,38695	0,5033	0,49459	0,49555	0,50295	0,49525	
chr5	180915260	0,79244	0,20331	0,40246	0,48103	0,47858	0,47473	0,4874	0,47499	
chr6	171115067	0,83064	0,20288	0,41623	0,49379	0,4895	0,48903	0,49976	0,49119	
chr7	159138663	0,83164	0,23375	0,42305	0,48337	0,4854	0,47833	0,49012	0,48432	
chr8	146364022	0,81973	0,21866	0,41321	0,49326	0,48588	0,4897	0,49762	0,48886	
chr9	141213431	0,70806	0,2057	0,35761	0,39299	0,39643	0,39269	0,40348	0,39228	
chr10	135534747	0,89197	0,26017	0,44729	0,51634	0,52864	0,52964	0,54055	0,52381	
chr11	135006516	0,83492	0,24654	0,42453	0,47968	0,47948	0,47167	0,49087	0,47533	
chr12	133851895	0,84722	0,2398	0,42918	0,47405	0,47687	0,47172	0,48268	0,47762	
chr13	115169878	0,6818	0,16314	0,34137	0,41366	0,40891	0,40357	0,41406	0,4055	
chr14	107349540	0,73104	0,20494	0,36788	0,39801	0,40228	0,39989	0,4103	0,40084	
chr15	102531392	0,75714	0,22622	0,37697	0,37623	0,38238	0,37569	0,39433	0,37908	
chr16	90354753	0,83691	0,29683	0,43056	0,46182	0,47042	0,4559	0,46135	0,47302	
chr17	81195210	0,99561	0,36168	0,50436	0,45489	0,4692	0,46487	0,47822	0,47487	
chr18	78077248	0,82858	0,21594	0,41601	0,49041	0,49321	0,48505	0,5018	0,48076	
chr19	59128983	0,96649	0,40967	0,50464	0,44628	0,47007	0,4585	0,47399	0,48635	
chr20	63025520	0,92351	0,31226	0,47041	0,45225	0,46378	0,45925	0,47233	0,46192	
chr21	48129895	0,6867	0,19264	0,3426	0,38309	0,387	0,38069	0,39009	0,38467	
chr22	51304566	0,71927	0,29316	0,37037	0,30212	0,32245	0,30939	0,32671	0,32092	
chrX	155270560	0,36431	0,08803	0,18499	0,46744	0,46305	0,46235	0,23612	0,45686	
chrY	59373566	0,11235	0,03024	0,0606	0,02776	0,03256	0,03447	0,10811	0,02722	
		3,242635	2,911045	3,05264	16,83862	14,22144	13,41311	2,184072	16,78398237	X/Y ratio

The coverage is low (average Avg_cov along each chromosome <of 1x) but the homogeneity of distribution of the reads that align univocally along all human chromosomes and the presence of reads that align with higher coverage on the mitochondrial genome, allows to recognize unquestionably a situation similar to a low-pass genome sequencing of an individual human genome. For an easier understanding of what has been stated, the green part reports the low-pass whole genome sequencing (5 samples, 4 females and 1 male) human with about 10 million reads, that is a depth similar to that produced for the 3 vaccine lots of Priorix®Tetra.
From the ratio between the average coverage for the X and Y chromosome (indicated in red in the last row of the table) the indication of the sex of the individual (male) also emerges.
The human DNA contained in the Priorix® batches sequenced so far, has also been qualified as belonging to the MRC-5 fetal line (i.e. the cell line derived from pulmonary tissue of male aborted fetuses of the 1960s, in which chicken pox and rubella viruses are cultivated).
The analysis of mitochondrial DNA variants included in the vaccine against the mitochondrial DNA of the MRC-5 line (cell line DNA was purchased from ATCC) showed that it is the same 'individual', since there is no genetic variant.

Below is an **extract of the answer given by the EMA** to our question regarding the safety of MRC-5 residues in the Priorix® tetra vaccine (EMA request reference ASK-43967 3 August 2018)

According to chapter 5.2.3, an acceptable limit must be established for the residual DNA of the host cell (which is specific to the product and depends on various factors, including the nature of the cell substrate / the characteristics of the production process / the type of product , etc.) only when the production process uses certain cell lines with the ability to multiply indefinitely in vitro (i.e. continuous cell lines). As indicated in the same chapter, "For vaccines produced in continuous cell lines, both carcinogenic and non-carcinogenic, risk assessment and risk mitigation must be performed to assess the suitability of the cell substrate, to define acceptable DNA criteria residue of host cells in the final product and to evaluate the consistency of host cell proteins. "

Based on the published information, Priorix®-Tetra contains viral strains produced separately in chicken embryo cells (mumps and measles) or in MRC-5 human diploid cells (rubella and chicken pox).

The cell lines used for Priorix® Tetra include lines of human diploid cells that cannot divide continuously. Note that, according to the European Pharmacopoeia, MRC-5 diploid cell lines are not carcinogenic, as demonstrated by decades of use and control, and therefore no maximum limit is applied for the DNA of MRC-5 cells.

We also advise you to consult the WHO document "Recommendations for the evaluation of cultures of animal cells as substrates for the production of biological drugs and for the characterization of cellular banks (2013)" which provides extensive clarification on the risks associated with the various types of cells used in vaccine production and confirms once again that "Diploid cell lines have been used successfully for many years for the production of viral vaccines and the residual cellular DNA resulting from these cells has not been (and is not) considered to pose any significant risk. " For more information on this, we advise you to consult the following link:

http://www.who.int/biologicals/vaccines/TRS_978_Annex_3.pdf?ua=1

The **international guidelines** are of particular interest about what follows:

https://www.fda.gov/media/78428/download
Guidance for Industry
Characterization and Qualification of Cell Substrates and Other Biological Materials Used in the Production of Viral Vaccines for Infectious Disease Indications
U.S. Department of Health and Human Services Food and Drug Administration Center for Biologics Evaluation and Research [February 2010]

1. Testing for Genetic Stability
You should demonstrate the genetic stability of your cell substrate from the establishment of the MCB through and perhaps beyond the end of production. For an engineered cell line, the inserted gene of interest should remain intact and at the same copy number, and be expressed at comparable levels throughout production. Also, **a diploid cell strain should remain diploid throughout. If such characteristics are not stable, then you should demonstrate that the instability does not adversely impact manufacturing or product consistency**. For methods to assess a cell substrate's genetic stability, reference is made to the ICH Q5B and Q5D documents (Refs. 30 and 3, respectively).

C. OTHER TESTS
1. *Testing for the Presence of Residual Cells*
You should assure that your final vaccine product does not contain residual cells. Processes, such as filtration, should be implemented and validated to ensure that intact cells are not present in the final product. Validation that residual cell removal processes are robust is important for immortalized cells. Determining the extent to which intact cells (or other materials known to be smaller than intact cells) are cleared by these processes is an important part of this validation. 36 Contains Nonbinding Recommendations

2. *Testing for Residual Cellular DNA*
Residual DNA might be a risk to your final product because of oncogenic and/or infectivity potential. There are several potential mechanisms by which residual DNA could be oncogenic, including the integration and expression of encoded oncogenes or insertional mutagenesis following DNA integration. Residual DNA also might be capable of transmitting viral infections if retroviral proviruses, integrated copies of DNA viruses, or extrachromosomal genomes are present. The risks of oncogenicity and infectivity of your cell-substrate DNA can be lessened by decreasing its biological activity. This can be accomplished by decreasing the amount of residual DNA and reducing the size of the DNA (e.g., by DNAse treatment or other methods) to below the size of a functional gene (based on current evidence, approximately 200 base pairs). Chemical inactivation can decrease both the size and biological activity of DNA. If DNA removal, digestion, or inactivation is undertaken, you should validate your methods. You should measure the amount and size distribution of residual DNA in your final product. **For widely used human diploid cell strains, such as MRC-5 and WI-38 cells, measurement of residual DNA might be unnecessary because we do not consider residual DNA from these human diploid cells to be a safety issue**. We might require limitation of the amount of residual DNA, depending on the potential risks associated with that DNA, for human diploid or primary cell types for which there is less experience. You should limit residual DNA for continuous non-tumorigenic cells, such as low-passage Vero cells, to **less than 10 ng/dose for parenteral inoculation** as recommended by WHO (Ref. 31). Because orally administered DNA is taken up approximately 10,000-fold less efficiently than parenterally administered DNA, we recommend limiting DNA to less than 100 µg/dose for oral vaccines (Ref. 32). If you are using cells with tumorigenic phenotypes or other characteristics that give rise to special concerns, more stringent limitation of residual DNA quantities might be needed to assure product safety

https://www.who.int/biologicals/vaccines/TRS_978_Annex_3.pdf?ua=1
Annex 3 Recommendations for the evaluation of animal cell cultures as substrates for the manufacture of biological medicinal products and for the characterization of cell banks. Replacement of Annex 1 of WHO Technical Report Series, No. 878

5.1.2 Diploid cell lines (DCLs)
The practicality of using human DCLs for the production of viral vaccines was demonstrated in the 1960s. Experience gained with oral poliomyelitis and other viral vaccines in successfully immunizing billions of children in many countries **has shown clearly that such substrates can be used in the production of safe and effective vaccines** (3). The essential features of DCLs of human (e.g. WI-38, MRC-5) and monkey (i.e. FRhL-2) origin are:

- they are cells passaged from primary cultures that have become established as cell lines with apparently stable characteristics over numerous PDLs (population doubling level);
- they have a finite capacity for serial propagation which ends in senescence, a state in which the culture ceases to replicate; the cells remain alive and metabolically active but may show morphological and biochemical changes, some of which begin to appear before replication ceases;
- they are non-tumorigenic;

- **they display diploid cytogenetic characteristics with a low frequency of chromosomal abnormalities of number and structure until they enter senescence.**

Substantial experience has been accumulated on the cytogenetics of WI-38 and MRC-5 since the 1960s, and ranges of expected frequencies of chromosomal abnormalities have been published (19, 20). Similar data are available for FRhL-2 (21). More sophisticated cytogenetic techniques (e.g. high-resolution banding, comparative genome hybridization) (22, 23) have demonstrated the presence of subtle chromosomal abnormalities that were previously undetectable. Recent studies have shown that subpopulations of human DCLs with such abnormalities may appear and disappear over time, that they are non-tumorigenic and that they undergo senescence in the same manner as the dominant population. Thus, possessing a stable karyotype might not be such an important characteristic as was previously thought.

19. Jacobs JP. Updated results on the karyology of the WI-38, MRC-5 and MRC-9 cell strains. Developments in Biological Standardization, **1976**, 37:155–156.
20. Jacobs JP et al. Guidelines for the acceptability, management and testing of serially propagated human diploid cells for the production of live virus vaccines for use in man. Journal of Biological Standardization, **1981**, 9:331–342.
21. Petricciani JC et al. Karyology standards for rhesus diploid cell line DBS-FRhL-2. Journal of Biological Standardization, **1976**, 4:43–49.
22. Schollmayer E et al. High resolution analysis and differential condensation in RBA-banded human chromosomes. Human Genetics, 1981, 59:187–193.
23. Rønne M. Chromosome preparation and high resolution banding techniques: a review. Journal of Dairy Science, **1989**, 72:1363–1377.

As foreseen by the above-mentioned guidelines, there are no upper limits for the presence of fetal DNA from the MRC-5 and WI-38 cell line, as they are diploids. The motivation lies in the fact that these lines are not considered cancerous because they have a finished replicative cycle.

It should be noted as well that the reference literature, which claims that diploid cells used for vaccine production are safe from the genetic stability point of view, is obsolete. The first genetic anomalies had been found already 40 years ago, and had been considered negligible for the safety of vaccines; from what reported in the WHO guideline, since then no updates have been made with the new sequencing technologies, in particular in NGS (which is moreover economic and quick), with the consequence that in the vaccines administered for decades, the presence of DNA more and more genetically modified and in an uncontrolled quantity has been increasingly allowed.

Dr. Theresa Deisher, a global expert on the use of fetal and stem cells and health risks related to the presence of residual fetal DNA in vaccines, responded with a letter to the politicians, also published on the Corvelva [3] website.

Below is an extract of the document kindly provided by Dr. Theresa Deisher: [4]

- Recently, duplications and de novo deletions have been recognized in up to 10% of simplex autism spectrum disorders, corroborating environmental triggers on the genetics of autism spectrum disorders.
- The rubella portion of the MMR vaccine contains human derived fetal DNA contaminants of about 175 ngs, more than 10x over the recommended WHO threshold of 10 ng per vaccine dose.
- No other drug on the market would receive FDA approval without thorough toxicity profiling (FDA follows international ICH guidelines) -> this was never conducted by the pharmaceutical industry for the DNA contamination in the MMR vaccine.
- Vaccines produced with human fetal cell lines contain cell debris and contaminating residual human DNA, which cannot be fully eliminated during the downstream purification process of the virus. Moreover, DNA is not only characterized by its sequence (ATCG), but also by its epigenetic modification (e.g. DNA methylation pattern etc.). This decoration is highly species specific, which is why non-human DNA will be eliminated, while this is not necessarily the case with fetal human DNA.

Injecting our children with human fetal DNA contaminants bears the risk of causing two well-established pathologies:

1. **Insertional mutagenesis:** fetal human DNA incorporates into the child's DNA causing mutations. Gene therapy using small fragment homologous recombination has demonstrated that as low as 1.9 ng/ml of DNA fragments results in insertion into the genome of stem cells in 100% of mice injected.
   The levels of human fetal DNA fragments in our children after vaccination with MMR, Varivax (chickenpox) or Hepatitis A containing vaccines reach levels beyond 1.9 ng/ml.
2. **Autoimmune disease:** fetal human DNA triggers a child's immune system to attack his/her own body.

[3] https://www.corvelva.it/it/approfondimenti/notizie/mondo/lettera-aperta-ai-legislatori-sul-dna-fetale-nei-vaccini-theresa-deisher.html
[4] https://www.soundchoice.org/about-us/

The results that we obtained in this first part of sequencing of the complete MRC-5 genome present in the vaccine (the second part is the sequencing of the entire genome of the MRC-5 cell line used to cultivate the vaccine virus and the comparative analysis with the Fetal DNA vaccine) considerably strengthen the experimental observations of Dr. Deisher and above all the fact that the contaminating fetal DNA present in all the samples analyzed in variable quantities (therefore not controlled) is up to 300 times higher than the limit imposed by the EMA for the carcinogenic DNA (10 ng / dose, corresponding to the DNA contained in about 1000 tumor cells, obtained on the basis of a statistical calculation, while the precautionary limit is 100 pg / dose) limit that must necessarily be applied also to the fetal DNA that inevitably contaminates the Priorix® tetra.

As a consequence, this vaccine should be considered defective and potentially dangerous for human health, in particular of the pediatric population, who is much more vulnerable to genetic and autoimmune damage due to immaturity in their repair systems.