

## "Patch" for DNA.

**Abstract.** The article reviewed a technique of diagnosing and treating gene viral diseases by way of identification and subsequent recovery (repair) of abnormal chromosomes.

### Introduction.

One of the technologies used by the author in recent years to study any disease is to consider the state of the chromosome set in specific systems and/or organs. The author started to use this method most frequently, but has never described its characteristics. As a result, this respected medical scientist gently noticed when had read my articles published on the Internet that the medicine states that there are 23 pairs of chromosomes in the chromosome set of the human body. 22 pairs are autosomes, i.e. paired chromosomes, which are identical in male and female organisms, and the 23th pair characterizes the female (XX) or male (XY) sex. All of my articles deal with a chromosome set consisting of 46 chromosomes, which does not meet the claims of classical medicine as the reader sees. The legitimacy of such approach from the standpoint of information wave medicine (IWM) as well as the issue of DNA repair by this method is the subject of this article.

### Chromosome set

The chromosome set is a set consisting of 23 pairs from the IWM standpoint, and looks as follows:

Table 1:

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46

First of all, it should be noted that the 23<sup>th</sup> pair as a sex indicator is only legitimate in the generally genome. If we consider a chromosome set of e.g. male and female eyes, then the 23<sup>th</sup> pair will have nothing to do with the sexual characters. Nevertheless, we think that most of the paired chromosomes are not autosomes. This is because virtually the majority of organs and systems carry sex characters. It should also be noted that chromosome count starts from the top row in the male and female body. Epy concept of 'autosomes' loses its meaning in the presence of abnormal chromosomes in the chromosome set.

Let us remind the reader what such abnormal chromosomes are from the IWM standpoint. The IWM considers the human genome to be a genetic structure consisting of two parts. The genes contained in the first part secure the normal development of the human body from birth to death (ontogenesis). The second part is a group of pathogenic genes that are unique for each person (pathogenesis). They are accumulated in the genome for many years under the influence of external or internal adverse conditions. We think that the mechanism of formation of these genes is mutations of appropriate chromosomes from the first part of the genome and their translation to an abnormal state. The genes corresponding to abnormal chromosomes are become pathogenic genes. We have established that an information wave structure which we call '**gene virus**' exists in the program present in any gene.

***It is important to understand that gene viruses are not 'biological entities', but merely a set of information wave structures from the IWM standpoint. In other words, gene viruses are***

***pathogenic information wave structure causing the same pathological lesions in the body as live virus groups that are adequate to them in radiation.***

The detection of abnormal chromosomes begins with checking the chromosome set of the central nervous system (CNS) with a known diagnosis of the disease. If this structure is found to contain an appropriate abnormal chromosome, then it is sure to be also present in smaller structures subordinate to the CNS such as midbrain, hippocampus or cerebral cortex. The autonomic nervous system, and then the peripheral one are subject to check after the CNS check. Thus, all the systems and organs containing abnormal chromosomes in the chromosome set can be identified.

The practice of investigating various diseases and sick conditions from the IWM standpoint has shown that abnormal chromosomes occupy mainly positions 24 to 46. Table 2 shows some of the results obtained by the author during many years of studying a series of diseases and their sources and determining the corresponding abnormal chromosomes:

Table 2:

No. Ser. No.	Disease / sick condition	Source	No. of chromosome	Note
1	Oncology	Gene;	9	29 - two adenoviruses, oncovirus, cytomegalovirus, crown virus; 34 - all DNA and RNA viruses
		pathogenic refrigerator radiations;	9, 29	
		iPhone radiations	9, 34	
2	Type 1 diabetes	Gene; Viral attack	16	Two adenoviruses
3	Tremor	Gene; Parkinson's disease	20	Two adenoviruses, crown virus, retro virus, coxsackie virus, herpes family virus
4	Hypertensive	Gene; Renal insufficiency; Heart failure	26, 42	26 - systolic pressure, 42 - diastolic pressure
5	Geopathogenic disease (GP disease)	Geopathogenic zones and their radiations	27, 31, 33	Impact in the prenatal condition
6	ALS	Geopathogenic zones and their radiations	27, 31, 33, 35	The last stage of the GP disease
7	Disorder of motor function of individual organs	Dysfunction of local motor neurons	32	Adenovirus, cytomegalovirus, RS virus
8	Alzheimer disease	Gene	37	DNA viruses
9	Epilepsy	Gene	38	Herpes family virus, crown virus, retro virus, coxsackie virus
10	Parkinson's disease	Gene	39	Herpes family virus, crown virus, retro virus, coxsackie virus
11	Polyps, benign tumors	Viruses	40	Adenovirus, paragrappal virus, corona virus

**Notes.** The term 'virus' is used for convenience in the table, and it should be understood as 'gene virus' essentially explained above.

One can see from table 2 that the majority of abnormal chromosomes are located in the second row of Table 1. The technology described enables curing any gene virus disease by normalizing the relevant abnormal chromosomes. This normalization can be performed by two ways. The first one is

changing the abnormal chromosome polarization sign from negative to positive using the biolocation technique. The second one is normalizing the abnormal chromosomes by creating a special matrix containing the relevant healthy chromosome on the final information medium. Drinking water structured using such matrix is a healing factor normalizing this abnormal chromosome. It should be noted that the first method gives the result in a shorter time. Both methods transfer pathogenic genes from the pathogenesis group to the ontogenesis group, i.e. into genes implementing a normal development of respective organs and systems. Thus, we get an opportunity to get rid of many diseases caused by pathogenic genes. If one takes into account that the mutation of a chromosome by an external or internal factor is nothing but a DNA damage, then the mechanism of abnormal chromosome normalization can be rightly considered to be a DNA repair, i.e. its recovery. True, the abnormal chromosome may be not the only pathological site violating the DNA integrity. In that case, its normalization will not result in full repair. However, in our view, the abnormal chromosome causes the greatest destruction to DNA compared with other pathogenic sites.

I would like to point out another important feature of the technology described. The fact of the matter is that the knowledge of the values of abnormal chromosomes of virtually incurable diseases such as Alzheimer's disease, Parkinson's disease, epilepsy or others, enables their early diagnostics. Its idea is that inactive genes, that is abnormal chromosomes of said diseases, can be found in children already at a very young age. This enables registration of such children for periodic health examination.

We remind the reader without a second thought what the Nobel Prize was awarded for in chemistry in 2015. It was awarded exactly for the development of DNA repair technologies. The Nobel Committee had noted the contribution of the three scientists 'in the study of the DNA recovery (repair) mechanisms, an important intracellular system aimed at finding and correcting the numerous damages occurring during normal DNA replication in cells or as a result of exposure to physical or chemical agents. A violation of functioning of this system is associated with a variety of severe hereditary diseases, and complex forms of life could hardly exist without it. If we compare the technology developed by Nobel laureates with the one proposed by the author, then we can see that the latter is much simpler. However, unfortunately, this technology cannot yet be implemented by classical medicine specialists while the technologies proposed by the Nobel laureates can be implemented everywhere.

## **Conclusion.**

The article shows the legitimacy of considering the chromosome set of systems, organs, cells and DNA molecules in the form of 46 chromosomes, not 23 pairs. This approach is explained by the fact that the paradigm of classical medicine does not match the paradigm of information wave medicine. This distinction is justified in [1]. It should also be noted that removal of pathogenic genes from the human genome increases life expectancy, which is an important factor in the development of mankind as a whole.

## **References**

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