

Structural abnormalities of chromosomes caused by the electric charges and their implications on cancer and other human diseases and health conditions

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Abstract

Background: For many years, we have studied the electric charge properties of chromosomes that have been doubted and ignored in genetics and molecular biology. We have identified and described the positive and negative effects of charge concerning the construction and function of chromosomes and their consequences in human syndromes. In this study, charge was studied to explain structural abnormalities of chromosomes and their implications in the cancer and other human disease.

Materials and methods: Chromosome material, technologies, and methods used in this study were provided by the Human Genetics Laboratory, Munroe-Meyer Institute for Genetics and Rehabilitation, University of Nebraska Medical Center, USA.

Results and discussions: This study revealed that: charge of chromosomes is a possible factor for causing structural abnormalities in areas where chromosomes are free of important genes, proteins and enzymes seen in disease; charge provided a reasonable explanation for the mechanism responsible for the development of breaks, translocations, fusions and other structural abnormalities of oncogenes and tumor suppressing genes; and charge provides information for better understanding and more effective methods of predicting, treating and preventing cancer.

Conclusion: After many years of research and billions in spending, diseases with a chromosomal etiology including cancer, Alzheimer, and Parkinson are still not fully understood and are difficult to predict, cure, and prevent. Using chromosome charge, which has been ignored and doubted in genetics and molecular biology, we present and propose a solution for issues concerning the development of structural abnormalities of DNA and genes causing these diseases.

Keywords: Cancer; charge based mechanism; numerical and structural abnormality of chromosomes

Introduction

During the last 100 years, cancer has been one of the most extensively studied human diseases. The mechanism responsible for the development of structural abnormalities of chromosomes causing cancer is presented with several theories.

Chromosomal theory was proposed by Hansemann [1]. He observed asymmetric cell divisions in cancer cells and suggested that these abnormal cell divisions were responsible for the decreased or increased number of chromosomes found in tumors. Boveri [2] took Hansemann's suggestion a step further by suggesting that cancerous tumors begin with a single cell in which the makeup of its chromosomes becomes scrambled. This

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scrambling then causes the cells to divide uncontrollably. This uncontrolled cell division then causes alterations in the number of chromosomes which leads the cells to a transformed malignant state. The original ideas suggested by Boveri were described in a book entitled, "The Origin of Malignant Tumors". The proof was found 70 years later by Nowell and Hungerford [3]. They discovered the first structural abnormality of chromosomes which is known to cause cancer. This abnormality was reported at a conference held in Philadelphia and after that it became well known as the "Philadelphia chromosome" which is a typical abnormality for the patient suffering from a type of blood cancer known as chronic myelogenous leukemia (CML). Today, over 400 types of blood cell cancers and solid tissue tumors are recognized and classified. The structural abnormalities of chromosomes found in cancer cells are the most abundant and the most extensively studied structures in the human body. During the last 40 years, Felix Mitelman and his colleagues [Mitelman 4 - 6] worked on a "catalog of chromosome aberrations in cancer". The first edition, published by Mitelman in 1983, contained 3,144 neoplasms in abnormal karyotypes. Today, his catalogs list over 50,000 chromosomal abnormalities in cancer. The problem is what kind of forces or factors are able to change 50,000 normal chromosomes and to scramble them in a way that affects their construction, function and number? The exact answer of this question is still unknown.

Gene theory was suggested by Beadle and Tatum [7]. According to their theory, every gene produces a single protein that affects a single step in a metabolic pathway. This theory has been characterized as inaccurate due to oversimplification as this one protein and enzyme has been described to then have influence over only one of the genetically based make up of traits. Meanwhile, the results obtained in cell and molecular biology studies has indicated that this theory is too simple to describe the complex relationship between genes and proteins [Bussard 8].

The fragile sites and chromosomal instability theory was formulated after the studies performed by Giraud et al. [9]. They found the first constitutional fragile site in human chromosomes. Dekaban [10] then described the first case of a persistent clone of cancer cells containing fragile sites in an abnormal chromosome of a woman who had been exposed to radiation. Sutherland and Hecht [11] described a fragile site as a point on the chromosome at which the given chromosome is liable to break and was able to publish a list of fragile sites found in human chromosomes. They are found in both the long and short arms of human chromosomes. Known as fragile sites and chromosomal instability, these places are considered to be an important factor in the mechanism responsible for the development of cancer. However, the exact mechanism responsible for the development of abnormalities caused by fragile sites and chromosomal instability is not fully understood.

Oncogene theory was developed by Huebner et al. [12-13]. They discovered unique genes associated with cancer known as "oncogenes" and "tumor suppressor genes". Today, over 100 genes in the human genome are considered to be associated with

the stimulation or suppression of the development of cancer cells. Among them, the most studied gene are: ABL, located on chromosome 9q34; AML1, on 21q22; APC, on 5q21; BCL2, on 18q21; BCL6, on 3q27; BCR, on 22q11; BRCA1, on 17q21; BRCA2, on 13q12; CCND1, on 11q13; ETO, on 8q22; IGH, on 14q32; MYC, on 8q24; NF1, on 17q11.2; TP53, on 17p13.1; and RB1, on 13q14.1-q14.2. These genes are considered a trigger responsible for the development of cancer. Abnormalities in the construction and function of oncogenes and tumor suppressing genes results in abnormalities of the encoded gene product which plays an important role in the malignancy transformation. However, these genes and their end products are not in a position to provide an adequate explanation how exactly two or more chromosomes are broken, translocated, placed in specific positions, aligned or fused permanently. All these processes require a lot of energy which is not available to genes, proteins and enzymes. Also, it is unknown why the same patterns of abnormal chromosomes and genes are found in the same type of cancers and can also be found in very different types of cancer. Another problem arises from the fact that the number of oncogenes and tumor suppressor genes that are found in the same type of cancer are rising and/or constantly changing. For example, twenty years ago, Lynch et al. [14] described only one gene abnormality that was found in the hereditary non-polyposis colorectal cancer. Several years later, Lynch and de la Chapelle [15] and Lynch and Lynch [16] reported several more chromosomal abnormalities for the same cancer, and the name was change to Lynch syndrome. Today, over 30 different genes are found to be abnormal in the tumorous tissue samples of colorectal cancer. The same situation exists with the origin of many other types of cancer. One of them is a hereditary form of pancreatic cancer. The affected genes found in this type of cancer cell increased from one to over 20 different genes. The difficulty lies in how to understand the origin of one type of cancer where 20 or more different genes are found to be abnormal? Another problem is how to understand cases where the same abnormal gene is found in different types of tumors. For example, we found an amplification of CCND1 in tumors removed surgically from the colon of a grandmother, breast of her daughter, and ovary of her granddaughter [17]. The problem is also how to define and classify over 400 types of cancers with variable gene abnormalities like those described above? The difficulty to define and classify the present day knowledge for oncogenes raises more questions than answers.

The random "bad luck" theory was formulated by two mathematicians, Tomasetti and Vogelstein [18]. They suggested that random "bad luck" is the major factor responsible for the origin of about 2/3 (66%) of all cancers. According to their theory, only 1/3 (33%) of cancer is caused by genetic or environmental factors and agents. Using statistical methods, they calculated that the majority of cancer occurrences are due to "bad luck" or random mutations that arise during DNA replication in normal, noncancerous stem cells. They suggest that this "random bad luck" is important not only to understand the disease but also for designing strategies to limit the mortality it causes. The

problem with this theory is in the cases where cancer developed not randomly but in family lines like those described by Lynch and Lynch (16). Particularly, this problem is visible in cases where cancer occurred in epidemic proportions after humans were exposed to charge in the form of ionizing and nonionizing radiation.

The facts presented above showed that after many years of study and four theories developed, the structural abnormalities of chromosomes and their implication in the origin of cancer are not fully understood.

In this study, we use charges of chromosomes to reveal issues and to propose solutions concerning both – the mechanism responsible for the development of structural abnormalities of chromosomes and their implication on the origin, understanding, predicting, treatment and preventing cancer and other human diseases and health conditions with a chromosomal etiology.

Materials and methods

The chromosome materials, classical and modern methods used in this study were provided by the Human Genetics Laboratory (HGL) at the University of Nebraska Medical Center (UNMC). They are identical with those described in detail in a previous publication [19]. All microphotographs of chromosomes were taken with the microscope “Opton” in magnifications $\times 1000$.

Our studies included structural abnormalities of all human chromosomes. In addition, several chromosomes were selected and studied deliberately with high attention. Among them are the abnormalities found at the qh areas of human chromosomes 9 and translocations involving the long arms of human chromosomes 9 and 22.

Results and discussions

1. We use charge of chromosomes to study the mechanism responsible for the development of breaks, translocations, fusions and other structural abnormalities associated with cancer that occurred at the areas where chromosomes are free of important genes, proteins and enzymes

In human chromosomes four areas are known to be free of important genes for encoding important proteins and enzymes. They are satellites of acrocentric human chromosomes numbers 13, 14, 15, 21 and 22, centromeres and telomeres of all chromosomes and qh areas of chromosomes 1, 9, 16 and Y. We have studied structural abnormalities of all four areas and the results obtained are similar for all four areas. Therefore, in hopes to eliminate redundancy, the results for this work primarily highlights results concerning the structural abnormalities of human chromosome number 9. The structural abnormalities of this chromosome were selected for presentation deliberately for several reasons:

First, because from all human chromosomes number 9 possesses the largest qh area that is built of tightly coiled highly repetitive

heterochromatin known as the heterochromatic variant. Selected images of our studies with multiple chromosomes 9 possessing different qh sizes are shown in Figure 1. The inversion of chromosome 9 [inv(9)(p12q13)] shown in the last chromosome of Figure 1e is considered to be the most frequently found aberration in human chromosomes [22].

Figure 1

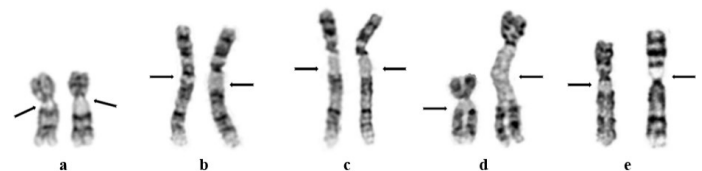


Figure 1a-e. Microphotographs of five pairs of the human homologous chromosome number 9 with qh areas of different sizes and shapes in each pair (arrows). In Figure 1e, the right chromosome's qh area is abnormal in the form of an inversion.

Second, because the heterochromatic qh variants of chromosome 9 are the place where the most severe breaks, translocations and fusions are found. We know this fact from our long time clinical diagnostic studies of breakage studies of chromosomes from peripheral blood samples from patients that were diagnosed or suspected to have a type of blood cancer known as Fanconi anemia. Selected images of these studies are presented in Figures 2-4.

Figure 2

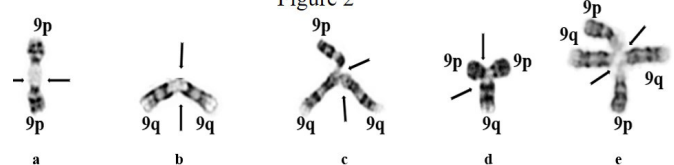


Figure 2a-e. Microphotographs of the qh areas of two short (p) arms of chromosome 9 fused (arrows) together (Figure 2a); two long (q) arms (Figure 2b); one short arm and two long arms (Figure 2c); two short arms and one long arm (Figure 2d); and two short and two long arms (Figure 2e).

Third, because the heterochromatic qh variants of chromosome 9 are free of important genes, proteins and enzymes. Therefore, the structural abnormalities found in these heterochromatic qh variant areas are not caused by genes, proteins or enzymes because they are not available there.

Figure 3

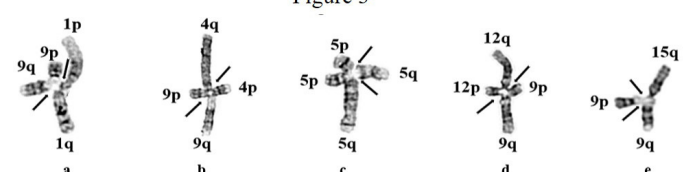


Figure 3a-e. Microphotographs of the qh areas of one chromosome 9 fused (arrows) together with other areas of different chromosomes: the centromere of chromosome 1 (Figure 3a); the centromere of chromosome 4 (Figure 3b); the centromere of chromosome 5 (Figure 3c); the centromere of chromosome 12 (Figure 3d); and the satellites of an acrocentric chromosome 15 (Figure 3e).

Fourth, because the heterochromatic qh variants of chromosome 9 are built of millions of positively charged histones wrapped with negatively charged DNA. Therefore, the charge of chromosomes is one of the main suspected factors responsible for the development of breaks, translocations and fusions that are found in the qh areas of chromosome 9.

Based on the images and facts presented above we suggest that breaks, translocations, fusions and other abnormalities occur at the qh areas of chromosome 9 under the influence of charge interactions between positively charged histones and negatively charged DNA.

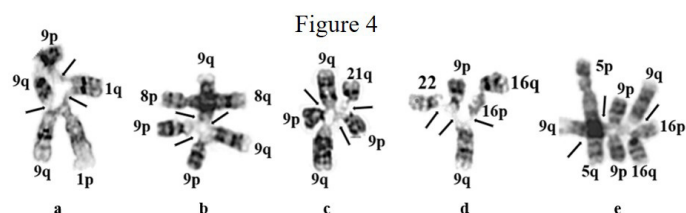


Figure 4a-e. Microphotographs of the qh area of one chromosome 9 fused (arrows) together with two or more chromosomes at: the centromere of chromosome 1 and the short (p) arm and long (q) arm of chromosome 9 (Figure 4a); the long arm of chromosome 8 and the qh area of chromosome 9 (Figure 4b); the qh area of chromosome 9 and the satellites of an acrocentric chromosome 21 (Figure 4c); the short arm of chromosome 16 and the satellites of an acrocentric chromosome 22 (Figure 4d); and the long arm of chromosome 5, the qh area of chromosome 9, and the short arm of chromosome 16 (Figure 4e).

2. We use charge of chromosomes to study the mechanism responsible for the development of breaks, translocations, fusions and other structural abnormalities of chromosomes that occurred at the area possessing important oncogenes and tumor suppressing genes, proteins and enzymes

In our long time clinical diagnostic work, structural abnormalities of oncogenes and tumor suppressing genes, were studied by using high resolution karyotypes, fluorescence in situ hybridization – FISH and molecular microarray. Presented here are selected results for breaks, translocations, fusions and other structural abnormalities that occurred at the oncogenes (BCR-ABL1 gene fusion) of Philadelphia chromosome [t(9;22)(q34.1;q11.2)]. This abnormality was selected because it is the most commonly distributed structural abnormality of human chromosomes causing a specific blood cancer – CML [23] and because the translocation causes a one of the most variable and diverse blood cancers in both chromosomal abnormalities and clinical

symptoms known as Philadelphia-negative CML.

Philadelphia-negative CML patients show a number of clinical and hematological features of CML with negative chromosomal and FISH studies. As shown in Figure 5a-b, these studies show no visible breaks or translocations at this resolution. We suggest that this variant form of CML develops when the fragile site is not as weak or the electric charge effect is not strong enough to break and then fuses chromosomes 9 and 22 together. However, we propose that the charge is strong enough to cause small, invisible cracks that cause DNA to “switch off” and silence the expression of the ABL gene located on the long arm of chromosome 9 and/or the BCR gene that is located on the long arm of chromosome 22.

Figure 5

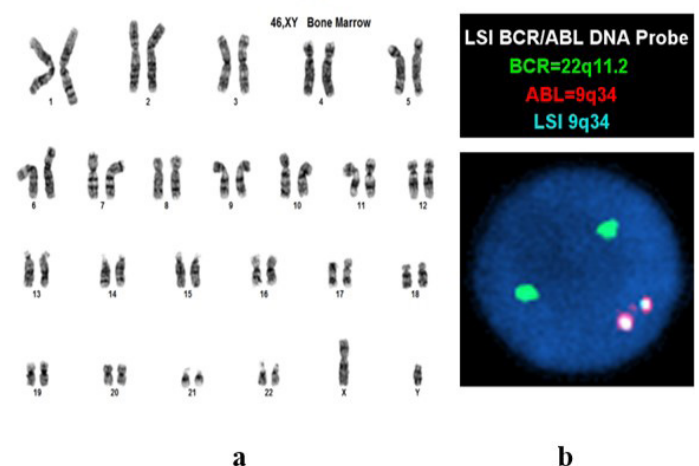


Figure 5a-b. Microphotograph of a Philadelphia-negative CML with normal chromosomes (Figure 5a) and normal locations for the ABL/BCR genes from FISH analysis (Figure 5b).

The typical (classical) form of Philadelphia-positive CML presents the characteristic abnormal karyotype with the translocation involving the long arms of chromosomes 9 and 22 and is also visible utilizing FISH analyses (Figure 6a-b). We suggest that this typical form of CML develops when the fragile site is strong or the disturbing charge is strong enough to break, translocate and fuse chromosome 9 in band q32 (ABL gene) and chromosome 22 in band q11.2 (BCR gene).

Figure 6

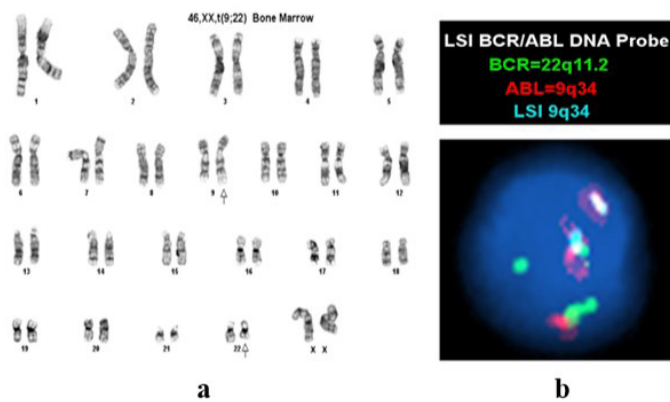
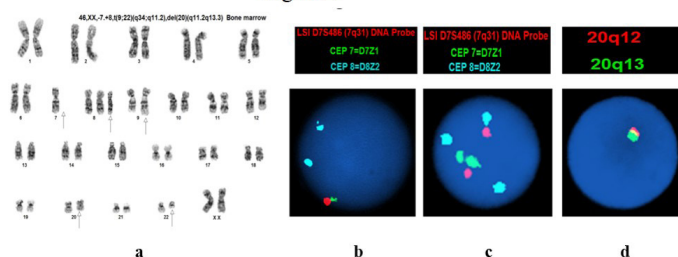


Figure 6a-b. Microphotograph of a classic Philadelphia-positive CML karyotype, showing an abnormal (translocated) chromosome 9 and 22 (Figure 6a) and abnormal FISH studies with a fusion in the ABL and BCR genes (Figure 6b).

The complicated (blast) form of Philadelphia-positive CML typically presents an abnormal karyotype presenting translocations and fusions that involve not only chromosomes 9 and 22 but also other chromosomes. Translocations, deletions and fusions are visible in both the karyotype and the FISH studies of these patients (Figure 7a-d). We suggest that this variant form of CML develops when the fragile site is very strong and unstable or the disturbing charge is strong enough and capable of causing breaks, deletions, translocations, inversions and fusions not only in chromosomes 9 and 22, but also in other chromosomes.

We suggest that the same charge-based mechanism that is described and illustrated above for CML plays a role in the development of many other breaks, translocations and fusions found in cancer cells with an array of chromosomal aberrations.

Figure 7



This fact has been known since World War II when researchers reported chromosome aberrations and cancer of survivors of the atomic bombs in Hiroshima and Nagasaki in 1945 [32, 33]. Later the same findings were reported by researchers who studied chromosomes and cancer in victims of the Chernobyl accident in USSR in 1986 [34] and the Fukushima Daiichi nuclear power plant accident in Japan in 2011 [35].

Clinical studies revealed that charge in the form of X-rays is causing both – structural abnormalities of human chromosomes and cancer. Structural abnormalities of chromosomes caused by exposure to X-rays were reported by Lloyd et al. [36], Bhatti et al. [37] and many others. Cancer caused by X-rays has been known since 1895 when doctors and researchers suggested that X-rays were harmless for humans. Work without adequate protective equipment from these doctors and researchers ultimately caused the development of cancer. They were described by Sansare et al. [38] as victims of cancer who died after exposure to X-rays. Clarence Dally and Elizabeth Ascheim are considered to be the first victims. Dally died in 1904 of cancer at only 39 years old. He was experimenting with X-rays in Thomas Edison's laboratory at General Electric (GE) in New York. Ascheim died in San Francisco the next year in 1905.

Based on the facts presented above, we suggest that without understanding and using charge it is difficult to understand the mechanism that is responsible for the development of structural abnormalities that are causing cancer.

3.2. Understanding, preventing and treatment

The treatment of cancer and other diseases with a chromosomal etiology are far behind in comparison to other human diseases. Compared with the treatment of infectious diseases, those diseases with a chromosomal etiology are difficult to cure. For example, human diseases with viral, microbial and parasitic origins have been well studied, understood and oftentimes put under control. Plague, smallpox, rabies, malaria, anthrax and others are primarily eliminated in Europe, North America and other parts of the world. In contrast, cancer is still difficult to cure even though it was discovered many centuries ago.

One of the main problems is in the unpredictable results of treatment. Some patients are responding positively in treatment while others have no visible effect and some develop fatal complications shortly after treatment. Another problem is in the fact that many of the factors claimed to cure cancer did not provide the results that were promised and expected. We have studied the history of 100 of the best known chemical, physical, biological and genetic factors that have been claimed to cure cancer. In all cases, the history started with strong and enthusiastic promise for the discovery of the cure for cancer. In all cases, the history ended with results that were different from those that were promised and expected.

Problems also exist with the methods that claim to cure cancer

successfully. Time has shown that that not one method has provided the promised and expected level of cure. This includes: “chemotherapy”, introduced over 100 years ago by the Nobel Prize laureate Paul Ehrlich in 1908; “electrotherapy” developed in 1855 by Guillaume Duchenne to cure the genetic disorder Duchenne muscular dystrophy; “radiation therapy” used for the first time by Emil Grubbe to cure breast cancer in 1896; “immunotherapy” introduced in 1891 by William Coley to cure patients with tumors; “hormone therapy” which was used in 1942 after the Food and Drug Administration approved the hormone estrogen product “Premarin”; and “homeopathic therapy” that embraces a natural approach to cure cancer by using selected products of minerals, plants and animals.

The same problems exist with the treatment of Alzheimer, Parkinson, and many other human diseases and health conditions with a chromosomal etiology. Therefore, we suggest that all these problems would not exist and the therapy of cancer could be more effective if electric charge effect of chromosomes was taken into consideration during the development of treatments of human diseases and health conditions caused by abnormal chromosomes. Our understanding is that it is impossible to cure diseases that are caused by the electric charge effects without acknowledging and identifying that electric charge effects are in fact causing the disease.

3.3. Correlations

The correlation between cancer and heterochromatic variants of human chromosomes was suggested, supported, doubted and rejected. The suggestion was first made by Sandberg [39] who noticed that the heterochromatin was found in increased sizes in the chromosomes of cancer cells. This is especially true for the qh heterochromatic variant regions of human chromosomes 1, 9, 16, and Y. Based on this fact, they suggested that there is a correlation between the heterochromatic variants of chromosomes and the development of human diseases with a chromosome etiology. Unfortunately, the majority of clinical specialists in genetics have doubted and rejected the existence of such a correlation. They argue that this correlation is impossible because the qh heterochromatic regions of chromosomes 1, 9, 16 and Y do not have any coding genes that might cause cancer. Based on this fact, they considered the increased size of the qh heterochromatic variant regions in cancer cells as coincidental that had nothing to do with the mechanisms responsible for the development of cancer.

Our studies on the structural abnormalities of heterochromatic qh area of chromosome 9 described above is in support of Sandberg's correlation between cancer and heterochromatic variants of chromosomes. More heterochromatin is correlated with more abundance of positively charged histones wrapped with more negatively charged DNA, which leads to more charge interactions and more charge destabilization effects on the construction and function of chromosomes.

3.4. Preventing

The idea of curing and preventing cancer was developed in 1921 when the President of the United States, Warren Harding, rewarded the double Noble Prize winner to Marie Curie and presented her with one gram of radium for her novel program for treating, curing and preventing cancer. This attempt failed because treatment of cancer with radium was found to be far from what was expected.

The next idea for curing cancer was presented officially in 1971, with the signing of the National Cancer Act by President Richard Nixon. In this Act, cancer was recognized to be an extraordinarily complex disease that involves many factors that requires special attention and approaches. The aims of this Act were to: find an effective cure for cancer by the development of new visions, methods and techniques; prevent the spread of cancer by using new programs; and eradicate cancer as a major cause of health problems. Generally, in the scientific cancer community, these three aims were viewed as the beginning of the “War on Cancer”.

The research arsenal for this “war” included new and inspiring ideas, visions, programs, strategies and approaches for the fight against cancer. These tools have been developed and applied as: new funding programs and foundations; new modern cancer clinics, hospitals, and centers; cutting edge technologies and methods; and interdisciplinary consortiums.

In spite of all the inspiring visions, cutting edge technologies, brilliant computer programs and internationally organized interdisciplinary consortiums, the “war on cancer” has not been won. The initial aims have not been completed after years of study and billions in spending. The mechanism which is responsible for the development of cancer has yet to be revealed. The promised effective cure for cancer has not been found. Cancer is still considered to be the “Emperor of All Maladies” [25].

The same problem exists in the present day knowledge concerning the prevention and possible cure of Alzheimer, Parkinson and other human diseases with a chromosomal etiology along with other health conditions caused by numerical and structural abnormalities of chromosomes. We suggest that these problems could be eliminated and solutions for the prevention and cure could be more effective if electric charge effect of chromosomes was studied, accepted and used in the research.

Conclusions

This study reveals that after many years of study and billions in spending, cancer is still not fully understood and difficult to predict, cure, and prevent. This is because charge of chromosome that is responsible for the development of structural abnormalities of DNA and genes causing cancer is doubted and ignored in genetics and molecular biology where cancer causing chromosomes are primarily studied. The century old issues concerning cancer could be solved if the electric charge properties of chromosomes were not ignored but instead utilized in genetics, molecular biology, oncology, hematology and other disciplines where the origin,

predicting, curing and preventing cancer are studied and applied.

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Conflict of Interest: None to report.

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