Journal of Molecular and Genetic Medicine

ISSN: 1747-0862

Koriem, J Mol Genet Med 2019, 13:2

Review Article Open Access

# The Impact of Genomics in Different Fields of Medicine

**Koriem KMM***

*Department of Medical Physiology, Medical Research Division, National Research Centre, Dokki, Cairo, Egypt*

## Abstract

All characteristics of genomes such as their structure, method of evolution and arrangement are covered in genomics. This science includes a complete DNA double strand which covers all DNA genes. Genetic is completely different from genomics where genetic is dealing with individual gene and its role in heritage while genomics covers quantification and qualification of genes which incorporates in protein production. This review aims to discuss in detail the role of genomics application in different medical fields such as genomic medicine, medical biotechnology, molecular medicine, biomedical engineering, medical anthropology, social medicine, conservative medicine and pharmacology and biomarkers discovery. Genomics controls social life around the world in research and health. Genomics helps to understand ourselves as individuals and as members of the family or society. Genomics is the investigation of an organism's genomics at the functional condition of various parts that cover the blueprint of the living cell to reveal the physiology of the cell and its basic, developmental, and tissue-specific processes. Genomics new techniques measure the behaviour of genes inside the cell as well as the analysis and the management of biological data and this concept plays a major role in recent molecular biology. Genomics used also to develop the next generation of antimicrobials against harmful strains of bacteria and viruses. Genomics gives a map about the biological cells under physiologic and pathologic conditions which help in the progress of disease diagnosis, therapy and drug development. The biomedical engineering reproduces the recent progress in genomics arrangement data which leads to the huge progress in drug detection, biomarkers discovery and disease treatment. Consequently, future genomics researches are the basis for detecting the initiation of many human diseases which help in therapy advances in the future.

**Keywords:** Genome; Disease; Health; Medicine; Biomarkers; Therapy

## Introduction

All characteristics of genomes such as their structure, method of evolution, final effects that is meant when two or more genes combined to produce the final phenotype, or when alleles of a single gene combine to produce their combined effects which equal the sum of their individual effects, arrangement and final genomics map are covered in genomics. This science includes a complete DNA double strand which covers all DNA genes. Genetic is completely different from genomics where genetic is dealing with individual gene and its role in heritage while genomics covers quantification and qualification of genes which incorporates in protein production. These proteins form different tissue and organs inside the human body. Genomics includes also DNA sequences and next generation techniques. Genomics is very important to biological system health state and to understand the complexity of biological system integrity, such as a brain complex system [1]. Genomics has a different and complexity studies such as: (1) effect one gene on another gene, (2) effect of many regions or loci on the same chromosome, (3) gene hybridization and (4) interaction between different loci and alleles [2]. Genomics is the investigation of an organism's genomics at the functional condition of various parts that cover the blueprint of the living cell to reveal the physiology of the cell and its basic, developmental, and tissue-specific processes. Genomics new techniques measure the behaviour of genes inside the cell as well as the analysis and the management of biological data and this concept plays a major role in recent molecular biology (Figure 1). Genomics explains the framework of molecular medicine and gives a map about the biological cells under physiologic and pathologic conditions which help in the progress of disease diagnosis, therapy, and drug development [3]. Thus, the study of the genomics has been subdivided into several research areas as follows:

1. Human genomics focus on the genomics in the field of human genomics until the entire human DNA sequence of the Human Genomics Project and this field helps in treating and preventing diseases.
2. Bacteriophage genomics focus on the study of bacteriophages or bacteria which infect the viruses.
3. Cyanobacteria genomics focus the study of cyanobacteria such as blue-green algae and this field plays an important role in shaping the Earth's atmosphere and biodiversity of life.
4. Metagenomics focus on the study of metagenomics of the material obtained directly from the environmental samples.
5. Metagenomics focus on the revolution of both microbes and entire living world.
6. Functional genomics focus on understanding the data formed by genomics to describe the functions and interaction of a gene where the functional genomics is dealing with the DNA on the levels of the genes consequently it describes genomics-wide method.
7. Pharmacogenomics focus on pharmacology and the relationship between drug response and genetic variation to develop drug therapy, which gives high drug effect and decreases the side effects in the patient's genotype and this field, is useful in treating cancer, cardiovascular disease, diabetes, asthma and depression.

***Corresponding author:** Dr. Khaled Mohamed Mohamed Koriem, Department of Medical Physiology, Medical Research Division, National Research Centre, 33 El-Buhouth Street, Dokki, Cairo, P.O. Box. 12622, Egypt, Tel: 20233371433, Fax: 20233371930; E-mail: kkoriem@yahoo.com

**Received** March 10, 2019; **Accepted** April 11, 2019; **Published** April 18, 2019

**Citation:** Koriem KMM (2019) The Impact of Genomics in Different Fields of Medicine. J Mol Genet Med 13: 416

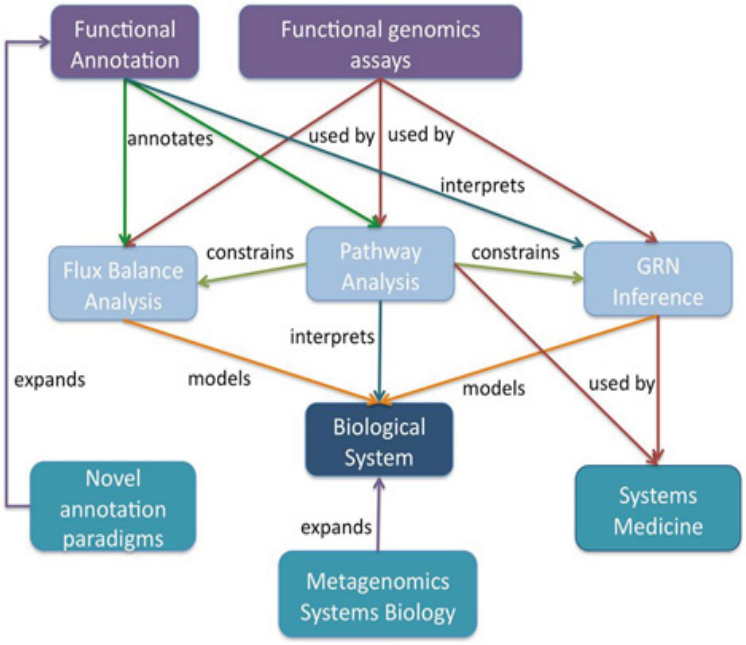
The most recent application used in the last decade in genomics to identify various and common respiratory diseases such as occupational asthma is a genomics-wide association study method. The identification and analysis methods of single nucleotide polymorphisms in genomics-wide association technique in occupational asthma are help in the development and produce of new genetic markers to accurately identify asthma-infected patients [4]. Genomics is connected with hybridization to comparison between pairs of whitefish species occurring in contrasting ecology. There are four genomics loci between those white fish pairs by using genomics technique [5]. The genomics data collected provides information about the serious damage of *Rhodococcus* genus bacteria by hydrocarbon contamination. These data are collected through DNA, RNA, protein, and metabolite levels to give a complete vision about catabolic process of *Rhodococcus* genus bacteria by hydrocarbon contamination. There are many genes are included in catabolic process of *Rhodococcus* strains such as aliphatic, aromatic, phthalate, polyethylene and polyisoprene genes [6].

## Literature Review

This review inspects the importance of genomics application on different medical fields, especially in clinical application, biomarkers discovery and therapeutic process.

### Role of genomics in genomic medicine

The DNA isolated from 491 samples reveals genetic variation in chemokine ligand 5 (*CCL5*) and chemokine receptor type 5 (*CCR5*) in metastatic colorectal cancer patients by genomic analysis applied in a recent research [7]. In another study, the control of DNA phosphorothioate levels is increased by ATPase activity of DNA sulfur modification, protein in *Methanoregula boonei 6A8* (DndB). The binding of ATP-ase in DndB is followed by destruction of DNA complex in DndB and these leads to increase transcriptional process. On the other hand, ATP hydrolysis increases the conversion of DndB-ATP to free DndB which binds again to DNA for transcriptional inhibition [8]. The obesity degrades sperm damage increases with age. Increased Sperm DNA fragmentation and changed protamine. Changes in seminal plasma miRNA expression lead to the characteristic molecular signature of the ageing with new biomarker for male reproductive function [9]. The genomics analysis communicates with transcriptomics method applied to natural killer T-cell lymphoma obtained from Epstein-Barr virus and both are closely related. The transcriptomcs analysis reveals less latent and lytic gene activities and higher changes occurs in T-cell epitope in natural killer T-cell lymphoma comparing with other Epstein-Barr virus-related cancers [10]. The genomics method of next-generation ribonucleic acid (RNA) sequence (RNA seq) technology is applied to the mechanism of varicose veins and its new genes occurred. The results obtained found that hyaluronan synthases 2 gene (*HAS2*) plays an important role in the varicose veins mechanism. Also, the *HAS2* expression decreases in the venous samples of patients with varicose veins [11]. The recent technique of genomics method such as microRNA (miRNA) profile of splenocytes in mice has experimental autoimmune encephalomyelitis (a model of human multiple sclerosis). A miRNA-microarray reveals increases in the expression of 9 miRNAs (let-7e, miR-23b, miR-31, miR-99b, miR-125a, miR-146b, miR-155, miR-193b and miR-221) experimental autoimmune encephalomyelitis where the serum levels of miR-99b, miR-125a, and miR-146b are high in experimental autoimmune encephalomyelitis mice compared to normal mice [12]. The genomics analysis reveals that claudin 10 expression level




**Note:** Functional genomics assays like gene expression profiling, metabolomics and proteomics are used as input data by different systems-level analysis approaches such as Gene Regulatory Network (GRN) inference, Pathway Analysis (PA) and Flux Balance Analysis (FBA). Functional annotation, a core activity of genomics, is a prerequisite in PA and FBA, and helps in the interpretation of GRNs. GRN and FBA generate models of the biological system based on genomics data and can also use pathway databases as a priori information to help building models of the system. Alternatively, PA can be directly employed as an interpretative tool of the system. Systems Medicine relies on GRNs and pathways to develop personalized genomic diagnosis tools. Metagenomics expands the system under study to a supraorganismal level, whereas novel systems-level annotation paradigms such as transcript annotation expand the scope of functional annotations.

**Figure 1:** Relationships between systems biology and genomics (Conesa and Mortazavi, 2014).

decreases in breast cancer cases compared with normal breast cases by using the cancer genomics atlas through gene expression profiling interactive analysis method [13]. The effects of both senescence and senescence-related secretory phenotype have been connected in age-related bone loss, but their roles in radiation-related bone damage are still indefinable. Clinical radiotherapy is used in the treatment of many cancers that include long-term mortality and lifelong distress [14]. In newly published data, the recent genomics 4Tran technique combined both capture-based chromosome conformation capture (3C) assay and PCR method is applied to determine endogenous retrovirus various copies in human and animal models. The 4Tran method focus on transposons occurs in chromosome and detects target genes and their transposable elements control [15]. The genomics method such as microRNAs (miRNAs) have a significant role in cell formation, differentiation and cancer development through controlling the expressions of protein-coding genes by breaking down the messenger RNA in a sequence-specific method. The miRNAs in cancer gives informative data about the current status of the disease and this help prostate cancer prognosis and diagnosis [16].

## Role of genomics in medical biotechnology

In a recent study, the metagenomics analysis is used and proved that the microorganisms like bacteria have not been having the extracellular electron transfer ability and these results are very important in microbial physiology, microbial ecology and biotechnology studies [17]. In other research, a direct correlation was established between the gold aggregating gold assay and the qPCR in the detection of the Topoisomerase 1 and DNA phosphodiesterase 2 mRNA transcripts so the gold aggregating gold assay is applied as a fast, easy and sensitive tool for the determination of RNA [18]. The genomics researches detected 482 and 433 pentatricopeptide repeat genes in *Gossypium raimondii* and *Gossypium arboreum* genomics, respectively. Also, there are 8 pentatricopeptide repeat genes were found in mitochondrion coding protein, which have protein binding activity [19]. Genomics studies are very suitable to detect the resistance ability of living organisms such as bacteria to toxic materials such as cadmium. The bacteria can be used for bio-remediating more efficiently environments highly polluted with metals [20]. The genomics research is applied also to determine the resistance to *Macrobrachium rosenbergii nodavirus* infection in adult prawn is due to an increase immune factors and the acceleration of hemocyte homeostasis by the dual roles of the hematopoietic tissue organ in *Macrobrachium rosenbergii nodavirus* [21]. Another benefit of genomics study is to role of fibronectin in nasopharyngeal cancer cell motility and proliferation in concerted action with hypoxia-inducible factor-1α and transforming growth factor-β1 possibly through linking molecules such as Src proto-oncogene (protein-tyrosine kinase) and protein kinase B or Akt. Fibronectin expression has potential prognostic value in patients with nasopharyngeal cancer cell [22]. The genomics play a potential role with proteomics in the adaptive response to hypoxia-reoxygenation stress and serve as an important benchmark to understand the mechanisms underlying mitochondrial sensitivity to hypoxia (ischemia) and reoxygenation [23]. The genomics and proteomics studies communicate together to investigate the autophagy. Autophagy is active during nail keratinocyte cornification and its substrate specificity depends on the accessibility of the proteins outside of the cytoskeleton and their presence in large complexes [24]. The genomics researchers are recently applied in the gene regulatory network analysis where genomics study explores the role of the non-starch polysaccharide pathway in the diminishing glycemic index [25]. The results obtained from genomics and proteomics researches revealed that plant RNA viruses utilize chloroplast membranes to collect viral replication processes. Furthermore, the viral proteins were connected with chloroplast-related proteins and prompt of viral proteins was occurring. Consequently, the viral replication process is stimulated by chloroplasts [26]. The recent plant genomics method such as genomics sequencing help to understanding of plant stress biology and improve the worldwide food production [27].

## Role of genomics in molecular medicine

The genomics application in molecular medicine helps to progress the precision of drug-target interactions and play a vital role in the new drug studies and objective protein progress [28]. In other research, the necessity for fertilization in rice embryogenesis is interceded by male- genomics factors. The genomics technique applied to mitosis for meiosis in rice egg cell, clonal offspring obtained have of parental heterozygosity. The synthetic asexual-propagation quality is genetically through multiple generations of clones. This work establishes the probability of asexual reproduction in crops increasing rates [29]. The genomics method is applied to detect the serine/arginine protein kinase 1 (a moonlight protein involved in many cellular activities such as cell cycle progression, immune response, chromatin reorganization, controlling of viral genomics replication, protein amino acid phosphorylation, controlling of many mRNA paths, germ cell growth and inflammation). There are many diseases such as cancer is associated with dysregulation of serine/arginine protein kinase 1 that controls by various transcription factors and signaling pathways [30]. In a recent research, the genomics assay is used to identify the role of folate-controls one-carbon metabolism that incorporated in mitochondrial methylenetetrahydrofolate dehydrogenase 2 and purine synthesis pathways. The mitochondrial methylenetetrahydrofolate dehydrogenase 2 decreases cancer progress and also their processes related with purine nucleotide deficit that induces accumulation of 5-aminoimidazole carboxamide ribonucleotide [31]. The molecular medicine communicates with synthetic gene circuits to give a great progress in medicine, biology and chemistry. The application of genomics technique such as clustered regularly interspaced short palindromic repeat system helps in cancer biology and therapy field. The use of synthetic gene circuits is used to treat cancer [32]. The genomics technique is also used in synthetic double-stranded RNA (polyinosinic:polycytidylic acid). This synthetic DNA causes increases of viral signal transition and increases of transcription 1 and decreases of inflammatory chemokines. Exposure to PIC increases chromatin-bound inflammatory activity (IFNβ) activity. This effect on IFNβ inhibits in beta cells [33]. The genomics field is applied in synthetic consortia, biophysical theory and simulations the role of the spatial interference ecosystem organization. The results obtained reveals at growing fronts and the elimination time of toxin-sensitive species is equal to the spatial interference balance. In bidirectional interfering, their structures separate into monoculture colonies with the corresponding separatrix set by the spatial interference balance. The ecosystem progress becomes high and yields differing structures. So, spatial interaction balance plays an important and significant role in microbial extension, microbial organization and synthetic ecosystem environment [34]. Another application of genomics in molecular medicine is a transcription activator-like effector (TALE) induces another TALE protein from DNA. The polar translation by TALEs is based on its bind to DNA. The polar TALE plays an important and significant role in gene expression and enriching the molecular medicine [35]. Another benefit of genomics is its application in the

design of artificial bone and formation of novel bone. The micropores play a significant and important role in both refining bone growth in the macropores and in providing extra space for bone growth [36]. In a recent research, the genomics assay also used in genes programming in cytochrome P450 and ATP-dependent RNA. The results obtained in this research leads to the development of lentinus tigrinus (wood-decaying fungi, Polyporales) and other fungi researches [37].

## Role of genomics in biomedical engineering

Genomics application is preferred also in biomedical engineering where the highest expressions of pyruvate dehydrogenase kinase 2 (PDK2) and pyruvate dehydrogenase kinase 3 (PDK3), especially the latter, were prognostic factors of acute myeloid leukemia [38]. In another recent research, genomics application new technique (MeDEStrand tool) to detect the whole- genomics arrangement in the DNA double strand with more accurate and high-resolution way [39]. Another use of genomics in medicine is its use to maintain of cellular protein homeostasis. Protein hemostasis in cell is needed for cell growth, maintanance, function, adaptation and responses to environmental stress. Protein hemostasis in the cell is controlled by proteostasis networks. The proteostasis networks composed of protein synthesis and autophagy-lysosomal processes. The proteostasis networks control by autophagy-lysosomal processes such as macroautophagy, microautophagy and mitophagy in tumor development and progress [40]. The application of the new and most recent genomics technique (the novel two-amplicon method) provides an accurate and well-defined tool on the role of microbiota in both health and disease [41]. Cancer stem cells are a key trigger for the initiation, development and chemo-resistance of liver cancer. They are novel targets for the treatment of liver cancer. The microRNAs-486-Sir1 is being incorporated in suppressing cancer stem cell initiation and tumor development [42]. The accumulation of visceral fat is direct proportional obesity mortality. The B cell lymphoma 6 is a key trigger in the immunity in visceral fat accumulation. The genomics application, including both RNA and DNA analyses revealed that B cell lymphoma 6 controls gene networks in cell growth and fatty acid biosynthesis. Consequently, B cell lymphoma 6 conversely related to visceral fat accumulation and metabolic health [43]. Another application of genomics in medicine has been its use recently to investigate the mitochondrial role, such as mitochondria movement and divide to maintain mitochondrial number and shape. Also, mitochondria play an important role in ATP-generating energy, reactive oxygen species, and $Ca^{2+}$ buffering system. Mitochondria play a significant role in various neurodegenerative disorders. So, mitochondrial dysfunction is proportional to neurodegenerative diseases [44]. Another application of genomics is the use of novel micro RNAs and microRNA Expression in *Medicago truncatula* plant which effect on plant growth and productivity. The genetic basis of salt-alkali resistance in the plant explains the significant role of miRNAs in plant stress resistance to saline-alkaline stress [45]. The novel and recent genomics technique such as *CRISPR-Cas9* gene is used in medicine to investigate the human genomics and this is very important in medical application. This method provides an accurate and well-identified of HIV patients by using $CD4^+$ T cells the detection period by using this technique range from 2-3 weeks [46]. Another important role of genomics is it's used in medicine through the identification of omega-3 polyunsaturated fatty acid level in brain tissues. The nutrition plays an important role in brain structure through the development of gray matter and maintenance of white matter through the whole human life. Consequently, omega-3 polyunsaturated fatty acids have an important role in brain tissue and cleverness, human health and disease [47].

## Role of genomics in medical anthropology

The genomics application is used also in the specimens chosen in allopatry and sympatry correlated with reproductive segregation using natural selection. There are various and different forms of selection that depend on reproductive method. This reproductive method determined first by allopatry method, then detected by sympatry method [48]. The genomics communicates with microarray application to detect a novel esophageal squamous cell carcinoma hypermethylation biomarker (*ZNF132* gene). The *ZNF132* gene is controlled by hypermethylation and found in both normal tissues and cancer cell lines. Consequently, the *ZNF132* gene plays an important role in the development of esophageal squamous cell carcinoma as a tumor suppressor gene and this gene is controlled by the DNA hypermethylation [49]. In a recent research, the genomics field plays a significant role in the high-altitude variation among human groups. This study investigates the DNA methylation of the promoter region of EPAS1 and LINE-1. Human exposure to the high-altitude hypoxia has a significant role on both EPAS1 and LINE-1 methylation and this indicates that epigenetic variation plays an important role in high-altitude variation [50]. The usage of genomics in anthropology is explained through epigenetic where epigenetic is a bridge between the social factors of health and physiological appearance such as obesity. The epigenetics knowledge is employed in the social factors of the human health. This research leads to more advanced in health field specially preventing obesity [51]. The genomics field is communicated with gene expression to investigate DNA methylation levels in blood samples from five of the six extant species of the baboon genus Papio. So, the rate and distribution of DNA methylation changes across the genomics depend on hereditary basis. The DNA methylation levels depend on positive selection [52]. The genomics method can be applied in chromatin-bound dexamethasone-induced protein (DEXI) in the type 1 diabetes-associated 16p13 genomics region. This result can provide the bridge between DEXI and the regulation of local antiviral immune responses in pancreatic beta cells. Also, this result can provide an initial information on the function of DEXI [33]. The medical application of genomics in medicine is its application in Triatoma rubrofasciata which causes Chagas disease in the Americas. The total length of Triatoma rubrofasciata mitochondrial genomics was 17,150 base pairs with the base composition of 40.4% adenine, 11.6% genuine, 29.4% thymine and 18.6% cytosine. The Triatoma rubrofasciata mitochondrial genome contains 13 protein-coding genes, 22 tRNA genes, 2 rRNA genes and one control region [40]. The growth hormone controls the entire body phenotype and causes minor variations in cardiac trail. This hormone plays an important role. There is no other similar case of positive selection of genes correlated with growth or cardiac development was reported [53]. Another application of genomics in anthropology is its application of antibiotics and antimicrobial resistant bacteria which help to detect the maintenance and removing of antibiotic resistance genes. This antimicrobial resistance is very important to human health, food security, and the global economy. Consequently, the antimicrobial resistant bacteria within a wild animal population led to understand of how resistance genes are spread and maintained in natural ecosystems [54].

## Role of genomics in social medicine

The application of genomics in the social sciences is greatly observed in a recent research where this study recorded small support for foreign aid for social development amongst the Hong Kong public. This result contrasts similar surveys in other countries, but this observation related to the lack of a local data from official development assistance to foreign countries [55]. In another study, the childhood danger disturbs health

later on and this observation need to understand the genomics basis. In this regard, genomics communicates with DNA methylation levels. So, dangerous experience to childhood correlated with parental health and this dangerous pattern effects on peripheral DNA methylation later on the whole life [56]. The genomics field is also applied to the concept of frailty which described as a clinical state of the poor resolution of homeostasis following stress which increases the falls, delirium, disability and mortality. The GRIN2B gene plays an important role in brain development, synaptic plasticity and cognition. So, this gene plays a role in frailty [57]. The application of genomics in the social sciences is also involved in pre-mRNA process that responsible for protein diversity. The pre-mRNA process is also responsible for tumor pathology. In a tumor, this process controls proliferation, metastasis and apoptosis of tumor cells. Thus, this process is very important for cancer discovery and therapy [58]. The genomics test is increasing in the last decade in clinical practice and research. The genomics information can be transmitted to a specific product. In 2018, the Human Genetics Society of Australia updated its position statement on genetic testing and life insurance such as life, critical care, and income protection products. The above-mentioned genomics or genetic society takes more active role in regulating the use of genetic information in personal insurance [59]. The history of science (particularly the history of biology) is another field of genomics application in the social sciences. The function of the dissertations of biologists in the genomics field is to detect the bridge between a molecule and its function [60]. Another preferable application of genomics is its use for the detection of ghrelin level. Ghrelin is a gastric hormone involved in the neurobiology of alcohol intake. A significant decrease was recorded in gut-microbial variety in alcohol consumption. The ghrelin hormone involved in alcohol consumption that increased alcohol intake levels and that ghrelin receptor decreases alcohol consumption [61]. The human papillomavirus increases the cervical cancer incidence. The genomics study of cervical cancer is very important in the determination of genes which controls cancer incidence. The arrestin domain containing 3 (*ARRDC3*) gene is the gene responsible for cervical cancer. The *ARRDC3* gene suppression caused decreases in both cell growth and susceptibility to human papillomavirus infection and this mean that *ARRDC3* gene is involved in the human papillomavirus infection [62]. The specific application of genomics is its application in Yes-associated protein. Yes-associated protein is an important factor f *ARRDC3*or tissue homeostasis. The reduction of Yes-associated protein such as the tumorsphere-forming potential, cell motility and chemoresistance *in vitro* is sufficient to decrease tumor growth and cancer stem cell marker expression in esophageal squamous cell carcinoma [63]. The mothers in an angry case who take message ingested more fruit and vegetable for their child in the essential buffet while fathers in this group did not consume more fruit and vegetable but make more intention to improve future fruit and vegetable feeding. Consequently, regarding to parents, especially mothers, in an anger case are more effective for encouraging healthy dietary choices for children [64].

## Role of genomics in conservative medicine

Another application of genomics is its communication and integration with proteomics, metabolomics and lipidomics to form the complete picture of the application of the new recent techniques in medicine [65-67]. The genomics research is applied also in both mitochondrial DNA changes and maternal hypertension in China. Higher changes level of amino-acid and RNA alterations were observed in maternal hypertension than the control. There are also 40 changed heteroplasmicl/homoplasmic modifications in 4 genes: COXII, $tRNA^{Lys}$, ATP8 and ATP 6. So, new mitochondrial DNA changes are included in maternal hypertension the pathological cases and mitochondrial genetic changes were identified in maternally hypertension [68]. The genomics correlated with meta-analysis is applied to investigate the genetic basis of both coronary artery disease and periodontitis. There is a hereditary basis of both due to same environmental risk factors [69]. Genomics approach is used in medicine to detect a conservative bridge that allows viral DNA synthesis. The genomics application is also increasing complete virions secretion compared to empty virions secretion. Consequently, the ratio of complete virions to empty virions is increased. The hepatitis B virus core protein linker region plays an important and significant job at various stages of hepatitis B virus reproduction [70]. The genomics has a great step in the human metabolism and the obtained results shows that there are 5-10% of all genetic areas occur in the control of blood/urine metabolite levels plays an important and key-trigger role in body mass index and mental characters/disorders. The metabolomics researches reveal that the blood/urine metabolites provide new preventive and therapeutic agents [71]. The genomics method is an accurate good and valuable way to determine the complete list of biological functions of RNA inside the human and animal models. The genomics describes accurately the specific microRNA and its important role inside the biological system where circular RNA is an active regulatory transcription factor. Circular RNA has various functions such as continuous synthesis of RNA and protein molecules to be in a conservative way inside biological system. In addition, circular RNA expression is higher than that of RNA linear forms where the expression of circular RNA is tissue-specific. Circular RNA has a specific function and can be used as biomarkers for the diagnosis, prognosis, and evaluation of response to therapy [72]. Another unique application of genomics is its application in the pathogenesis of multiple sclerosis. The hereditary factors are related to multiple sclerosis in addition to environmental factors. Also, endogenous retrovirus has an important a role in multiple sclerosis. The genetic mutations on human chromosomes 6, 14 and 18 have been known as major biomarkers in multiple sclerosis. The obtained results give a relation between association between Endogenous retrovirus and multiple sclerosis [73,74]. The whole genomics data in 8 domesticated species such as cat, dog, pig, goat, sheep, chicken, cattle and horse are detected and compared these domesticates with their ancient relatives. The correlation analysis revealed that the most recent one (~ 10.000 years ago) is proportionally correlated with domesticated and wild animals [75]. Another genomics application was observed in Han Chinese essential hypertensive cases depend on clinical and molecular data. Phylogenetic analysis shows 4375 haplotype C is greatly conservative in 17 species. So, these alterations reported in hypertension and halop type C play a significant and initiated role on the phenotype in this hypertensive family [76].

## Role of genomics in pharmacology and biomarkers discovery

The genomics research is also used in pharmacology and biomarkers discovery where eosinophil-correlated diseases are rare diseases that characteristic of the presence of eosinophils in tissues and/or peripheral blood. The drug development and biomarkers detection for these diseases are limited. The application of eosinophil genomics, epigenomics and proteomics are better and suitable techniques to investigate the role of the eosinophil in tissues, detect the eosinophil biomarkers that activated the tissue and better understand of the role of eosinophils in human disease [77]. The genomics is better technique to detect the genetic diseases such as orphan diseases where these diseases found in < 1 in 2000 persons. In this disease, the specific mutations detect in patients reflect on patient's phenotype. The genomics technique helps to discover drug targets and drugs/drug-like molecules for treatment

of patients with genetic disease [78]. The genomics strategy by the examination of gene expression in human-induced pluripotent stem cell cardio-myocytes show the compound called cardioprotectant 312. This compound causes up-regulation of hemeoxygenase-1 (a marker of the antioxidant response) and this marker correlated with protection of cardiomyocytes from oxidative stress [79]. The genomics application explores the bridge between epigenetics of an individual and his/her environmental exposure record (exposome) and this gave rise to determinant factor that causes human malignancies. The epigenetic changes are risk fingerprints in the discovery of new biomarkers in the tumor [80]. The genomics method in obesity and diabetes explores that cannabinoid 1 receptor is correlated with obesity and type 2 diabetes. So, the identification of AJ5012 as a novel peripheral cannabinoid 1 receptor antagonist and this antagonist of the peripheral cannabinoid 1 receptor blockade breaks the correlation between insulin resistance and adipose tissue inflammation [81]. The genomics assay in cancer is very urgent and recent technique where the tumor suppressor gene is p53 programmed by TP53 gene. Many factors such as DNA damage, heat, hypoxia and over expression causes activation of p53 gene. Thus, p53 gene regulates many biological cycles that responsible for genetic stability by preventing genomics mutation. About 50% mutations in human cancers increases in expression of murine double minute 2 gene (mdm2) which represents one of the reasons for cancer progression [82]. The most recent genomics technique (*CRISPR-Cas9* gene-editing strategies) has been applied to investigate and follow the complex biological processes. This technique is used in primary human $CD4^+$ T cells for analyzing the role of host factors in HIV infection and pathogenesis. Consequently, this technique allows high-throughput detection of HIV host factors in primary $CD4^+$ T cells by gene knockout, validation, and HIV spreads infection in a very short time of 2-3 weeks (Hultquist et al., 2019). The estrogen receptor and human epidermal growth factor receptor 2 are essential biomarkers to endocrine and anti-HER2 therapies, respectively. The genomics technique in estrogen receptor and human epidermal growth factor receptor 2 which recorded mutations, amplifications, translocations and alternative splicing, emerging as new biomarkers [83]. Type 2 diabetes mellitus is the most common disease with endocrine and metabolic disorders. The proteomics, metabolomics and meta-genomics techniques have a significant role to understand the physiological processes and regulatory mechanisms of type 2 diabetes mellitus such as genetic regulation of blood glucose levels, intestinal microorganism, and inflammation. The modification of proteins can be investigated by proteomics while metabolomics identify the metabolites in living organisms [63]. The microRNAs are good specific biomarkers for cancer diagnosis**.** The miRNAs are not only predictive of cancer incidence but can be used for cancer classification also. The microRNAs are included in angiogenesis pathways and microRNAs are used to calculate cancer severity [84].

## Discussion and Conclusion

There are a lot of scientific thinking are opened when we discuss the role of genes, multiple functions in the biological system such as gene expression, mutations and alterations. Genomics is very important to the biological system health and to understand the complexity of biological system integrity. Genomics has a different and complexity studies such as:

1. Effect one gene on another gene,
2. Effect of many regions or loci on the same chromosome,
3. Gene hybridization and
4. Interaction between different loci and alleles. The most recent application used in the last decade in genomics is a genomics-wide association studies.

Genomics provides the scientific community with a better view about the role of genes inside the cell in health and disease states and future genomics researches help us to understand disease initiation and progress which helps us in biomarkers discovery and therapy advancement.

## Conflict of Interest

I declare that I have no conflict of interest.

### References

1. Kadakkuzha BM, Puthanveettil SV (2013) Genomics and proteomics in solving brain complexity. Mol Biosyst 9: 1807-1821.
2. Pevsner J (2009) Bioinformatics and functional genomics (2nd edn), Hoboken, New Jersey, Wiley-Blackwell Publication, USA.
3. Pattini L, Bertacco R, Candiani G, Masseroli M, Servi S (2011) Trends in biomedical engineering: Focus on genomics and proteomics. J Appl Biomater Biomech 9: 98-108.
4. Park JS, Son JH, Park CS, Chang HS (2019) Clinical implications of single nucleotide polymorphisms in diagnosis of asthma and its subtypes. Yonsei Med J 60: 1-9.
5. Feulner PGD, Seehausen O (2018) Genomic insights into the vulnerability of sympatric whitefish species flocks. Mol Ecol 1: 1-2.
6. Zampolli J, Zeaiter Z, Di Canito A, Di Gennaro P (2018) Genome analysis and -omics approaches provide new insights into the biodegradation potential of Rhodococcus. Appl Microbiol Biotechnol 103: 1069-1080.
7. Suenaga M, Stintzing S, Cao S, Zhang W, Yang D, et al. (2018) Role of CCL5 and CCR5 gene polymorphisms in epidermal growth factor receptor signalling blockade in metastatic colorectal cancer: Analysis of the FIRE-3 trial. Eur J Cancer 107: 100-114.
8. Xia S, Chen J, Liu L, Wei Y, Deng Z, et al. (2018) Tight control of genomic phosphorothioate modification by the ATP-modulated autoregulation and reusability of DndB. Mol Microbiol 111: 938-950.
9. Paoli D, Pecora G, Pallotti F, Faja F, Pelloni M, et al. (2018) Cytological and molecular aspects of the ageing sperm. Hum Reprod 34: 218-227.
10. Peng RJ, Han BW, Cai QQ, Zuo XY, Xia T, et al. (2018) Genomic and transcriptomic landscapes of Epstein-Barr virus in extranodal natural killer T-cell lymphoma. Leukemia 33: 1451-1462.
11. Hsieh CS, Tsai CT, Chen YH, Chang SN, Hwang JJ, et al. (2018) Global expression profiling identifies a novel hyaluronan synthases 2 gene in the pathogenesis of lower extremity varicose veins. J Clin Med 7: 537.
12. Venkatesha SH, Dudics S, Song Y, Mahurkar A, Moudgil KD (2018) The miRNA expression profile of experimental autoimmune encephalomyelitis reveals novel potential disease biomarkers. Int J Mol Sci 19: 3990.
13. Liao J, Li J, Cheng H, Chen Y, Mo Z (2018) CLDN10 single nucleotide polymorphism rs1325774 alters the risk of breast cancer in south chinese women. Medicine 97: e13187.
14. Chandra A, Park SS, Pignolo RJ (2018) Potential role of senescence in radiation-induced damage of the aged skeleton. Bone 120: 423-431.
15. Raviram R, Rocha PP, Luo VM, Swanzey E, Miraldi ER, et al. (2018) Analysis of 3D genomic interactions identifies candidate host genes that transposable elements potentially regulate. Genome Biol 19: 216.
16. Aghdam SG, Ebrazeh M, Hemmatzadeh M, Seyfizadeh N, Shabgah AG, et al. (2019) The role of microRNAs in prostate cancer migration, invasion, and metastasis. J Cell Physiol 234: 9927-9942.
17. Tanaka K, Yokoe S, Igarashi K, Takashino M, Ishikawa M, et al. (2018) Extracellular electron transfer via outer membrane cytochromes in a methanotrophic *Bacterium methylococcus capsulatus* (Bath). Front Microbiol 9: 2905.
18. Shawky SM, Awad AM, Abugable AA, El-Khamisy SF (2018) Gold nanoparticles

- an optical biosensor for RNA quantification for cancer and neurologic disorders diagnosis. Int J Nanomed 13: 8137-8151.

19. Zhao N, Wang Y, Hua J (2018) Genomewide identification of PPR gene family and prediction analysis on restorer gene in Gossypium. J Genet 97: 1083-1095.
20. Ramos-Zúñiga J, Gallardo S, Martínez-Bussenius C, Norambuena R, Navarro CA, et al. (2018) Response of the biomining Acidithiobacillus ferrooxidans to high cadmium concentrations. J Proteomics 198: 132-144.
21. Jariyapong P, Pudgerd A, Cheloh N, Hirono I, Kondo H, et al. (2018) Hematopoietic tissue of Macrobrachium rosenbergii plays dual roles as a source of hemocyte hematopoiesis and as a defensive mechanism against *Macrobrachium rosenbergii* nodavirus infection. Fish Shellfish Immunol 86: 756-763.
22. Wang WY, Twu CW, Liu YC, Lin HH, Chen CJ, et al. (2019) Fibronectin promotes nasopharyngeal cancer cell motility and proliferation. Biomed Pharmacother 109: 1772-1784.
23. Sokolov EP, Markert S, Hinzke T, Hirschfeld C, Becher D, et al. (2018) Effects of hypoxia-reoxygenation stress on mitochondrial proteome and bioenergetics of the hypoxia-tolerant marine bivalve Crassostrea gigas. J Proteomics 194: 99-111.
24. Jaeger K, Sukseree S, Zhong S, Phinney BS, Mlitz V, et al. (2018) Cornification of nail keratinocytes requires autophagy for bulk degradation of intracellular proteins while sparing components of the cytoskeleton. Apoptosis 24: 62-73.
25. Anacleto R, Badoni S, Parween S, Butardo VM, Misra G, et al. (2018) Integrating a genome-wide association study with a large-scale transcriptome analysis to predict genetic regions influencing the glycaemic index and texture in rice. Plant Biotechnol J 1: 1-2.
26. Budziszewska M, Obrępalska-Stęplowska A (2018) The role of the chloroplast in the replication of positive-sense single-stranded plant RNA viruses. Front Plant Sci 9: 1776.
27. Shameer K, Naika MBN, Shafi KM, Sowdhamini R (2018) Decoding systems biology of plant stress for sustainable agriculture development and optimized food production. Prog Biophys Mol Biol 1: 1-4.
28. Shi H, Liu S, Chen J, Li X, Ma Q, et al. (2018) Predicting drug-target interactions using Lasso with random forest based on evolutionary information and chemical structure. Genomics 1: 1-2.
29. Khanday I, Skinner D, Yang B, Mercier R, Sundaresan V (2018) A male-expressed rice embryogenic trigger redirected for asexual propagation through seeds. Nature 565: 91-95.
30. Patel M, Sachidanandan M, Adnan M (2018) Serine arginine protein kinase 1 (SRPK1): A moonlighting protein with theranostic ability in cancer prevention. Mol Biol Rep 46: 1487-1497.
31. Nishimura T, Nakata A, Chen X, Nishi K, Meguro-Horike M, et al. (2018) Cancer stem-like properties and gefitinib resistance are dependent on purine synthetic metabolism mediated by the mitochondrial enzyme MTHFD2. Oncogene 38: 2464-2481.
32. Zhou Q, Zhan H, Liao X, Fang L, Liu Y, et al. (2018) A revolutionary tool: CRISPR technology plays an important role in construction of intelligentized gene circuits. Cell Prolif 5: e12552.
33. Dos Santos RS, Marroqui L, Velayos T, Olazagoitia-Garmendia A, Jauregi-Miguel A, et al. (2018) DEXI, a candidate gene for type 1 diabetes, modulates rat and human pancreatic beta cell inflammation via regulation of the type I IFN/STAT signalling pathway. Diabetologia 62: 459-472.
34. Ozgen CV, Kong W, Blanchard AE, Liu F, Lu T (2018) Spatial interference scale as a determinant of microbial range expansion. Sci Adv 4: eaau0695.
35. Lebar T, Verbič A, Ljubetič A, Jerala R (2019) Polarized displacement by transcription activator-like effectors for regulatory circuits. Nat Chem Biol 15: 80-87.
36. Rustom LE, Poellmann MJ, Johnson WAJ (2019) Mineralization in micropores of calcium phosphate scaffolds. Acta Biomater 83: 435-455.
37. Wu B, Xu Z, Knudson A, Carlson A, Chen N, et al. (2018) Genomics and development of *Lentinus tigrinus*, a white-rot wood-decaying mushroom with dimorphic fruiting bodies. Genome Biol Evol 10: 3250-3261.
38. Cui L, Cheng Z, Liu Y, Dai Y, Pang Y, et al. (2018) Overexpression of PDK2 and PDK3 reflects poor prognosis in acute myeloid leukemia. Cancer Gene Ther 1: 1-2.
39. Xu J, Liu S, Yin P, Bulun S, Dai Y (2018) MeDEStrand: An improved method to infer genome-wide absolute methylation levels from DNA enrichment data. BMC Bioinformat 19: 540.
40. Dong L, Ma X, Wang M, Zhu D, Feng Y, et al. (2018) Complete mitochondrial genome of the chagas disease vector *Triatoma rubrofasciata*. Korean J Parasitol 56: 515-519.
41. Popovic A, Bourdon C, Wang PW, Guttman DS, Voskuijl W, et al. (2018) Parkinson J. design and application of a novel two-amplicon approach for defining eukaryotic microbiota. Microbiome 6: 228.
42. Yan X, Liu X, Wang Z, Cheng Q, Ji G, et al. (2018) MicroRNA-486-5p functions as a tumor suppressor of proliferation and cancer stem-like cell properties by targeting Sirt1 in liver cancer. Oncol Rep 1: 1-2.
43. Senagolage MD, Sommars MA, Ramachandran K, Futtner CR, Omura Y, et al. (2018) Loss of transcriptional repression by bcl6 confers insulin sensitivity in the setting of obesity. Cell Rep 25: 3283-3298.
44. Kausar S, Wang F, Cui H (2018) The role of mitochondria in reactive oxygen species generation and its implications for neurodegenerative diseases. Cells 7: 274.
45. Cao C, Long R, Zhang T, Kang J, Wang Z, et al. (2018) Genome-wide identification of microRNAs in response to salt/alkali stress in *Medicago truncatula* through high-throughput sequencing. Int J Mol Sci 19: 4076.
46. Hultquist JF, Hiatt J, Schumann K, McGregor MJ, Roth TL, et al. (2019) CRISPR-Cas9 genome engineering of primary CD4$^+$ T cells for the interrogation of HIV-host factor interactions. Nat Protoc 14: 1-27.
47. Talukdar T, Zamroziewicz MK, Zwilling CE, Barbey AK (2018) Nutrient biomarkers shape individual differences in functional brain connectivity: Evidence from omega-3 PUFAs. Hum Brain Mapp 40: 1887-1897.
48. Baiz MD, Tucker PK, Cortés-Ortiz L (2018) Multiple forms of selection shape reproductive isolation in a primate hybrid zone. Mol Ecol 28: 1056-1069.
49. Jiang D, He Z, Wang C, Zhou Y, Li F, et al. (2018) Epigenetic silencing of ZNF132 mediated by methylation sensitive Sp1 binding promotes cancer progression in esophageal squamous cell carcinoma. Cell Death Dis 10: 1.
50. Childebayeva A, Jones TR, Goodrich JM, Leon-Velarde F, Rivera-Chira M, et al. (2018) LINE-1 and EPAS1 DNA Methylation Associations with High-Altitude Exposure. Epigenet 14: 1-15.
51. Milliken-Smith S, Potter CM (2018) Paternal origins of obesity: Emerging evidence for incorporating epigenetic pathways into the social determinants of health framework. Soc Sci Med 1: 1-2.
52. Vilgalys T, Rogers J, Jolly C, Mukherjee S, Tung J (2018) Evolution of DNA methylation in Papio baboons. Mol Biol Evol 36: 527-540.
53. Bergey CM, Lopez M, Harrison GF, Patin E, Cohen JA, et al. (2018) Polygenic adaptation and convergent evolution on growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers. Proc Natl Acad Sci USA 115: E11256-E11263.
54. Miller EA, Johnson TJ, Omondi G, Atwill ER, Isbell LA, et al. (2018) Assessing transmission of antimicrobial resistant Escherichia coli in wild giraffe contact networks. Appl Environ Microbiol 85: 1-2.
55. Lee CH, Tse B, Lai N, Goggins W, Baum L, et al. (2018) Hong Kong's role in global health: Public opinion of official development assistance. PLoS One 13: e0207687.
56. Houtepen LC, Hardy R, Maddock J, Kuh D, Anderson EL, et al. (2018) Childhood adversity and DNA methylation in two population-based cohorts. Transl Psychiatry 8: 266.
57. Mekli K, Stevens A, Marshall AD, Arpawong TE, Phillips DF, et al. (2018) Frailty Index associates with GRIN2B in two representative samples from the United States and the United Kingdom. PLoS One 2018; 13: e0207824.
58. Di C, Syafrizayanti A, Zhang Q, Chen Y, Wang Y, et al. (2018) Function, clinical application, and strategies of Pre-mRNA splicing in cancer. Cell Death Differ 26: 1181-1194.
59. Newson AJ, Ayres S, Boyle J, Gabbett MT, Nisselle A (2018) Human genetics society of Australasia position statement: Genetic testing and personal insurance products in Australia. Twin Res Hum Genet 21: 533-537.
60. Sato N, Sato K (2019) Statistical analysis of word usage in biological publications since 1965: Historical delineation highlighting an emergence of

function-oriented discourses in contemporary molecular and cellular biology. J Theor Biol 462: 293-303.

61. Zallar LJ, Beurmann S, Tunstall BJ, Fraser CM, Koob GF, et al. (2018) Ghrelin receptor deletion reduces binge-like alcohol drinking in rats. J Neuroendocrinol 20: e12663.
62. Takeuchi F, Kukimoto I, Li Z, Li S, Li N, et al. (2018) Genome-wide association study of cervical cancer suggests a role for *ARRDC3* gene in human papillomavirus infection. Hum Mol Genet 28: 341-348.
63. Wang L, Zhang Z, Yu X, Huang X, Liu Z, et al. (2018) Unbalanced YAP-SOX9 circuit drives stemness and malignant progression in esophageal squamous cell carcinoma. Oncogene 38: 2042-2055.
64. Persky S, Ferrer RA, Klein WMP, Goldring MR, Cohen RW, et al. (2018) Effects of fruit and vegetable feeding messages on mothers and fathers: Interactions between emotional state and health message framing. Ann Behav Med 1: 1-2.
65. Koriem KMM (2018) Proteomic approach in human health and disease: Preventive and cure studies. Asian Pac J Trop Biomed 8: 226-236.
66. Koriem KMM (2017) Protective effect of natural products and hormones in colon cancer using metabolome: A physiological overview. Asian Pac J Trop Biomed 7: 957-966.
67. Koriem KMM (2017) A lipidomic concept in infectious diseases. Asian Pac J Trop Biomed 7: 265-274.
68. Zhu Y, Gu X, Xu C (2018) Mitochondrial DNA 7908-8816 region mutations in maternally inherited essential hypertensive subjects in China. BMC Med Genomics 11: 89.
69. Munz M, Richter GM, Loos BG, Jepsen S, Divaris K, et al. (2018) Genome-wide association meta-analysis of coronary artery disease and periodontitis reveals a novel shared risk locus. Sci Rep 8: 13678.
70. Liu K, Luckenbaugh L, Ning X, Xi J, Hu J, et al. (2018) Multiple roles of core protein linker in hepatitis B virus replication. PLoS Pathog 14: e1007085.
71. Hebebrand J, Peters T, Schijven D, Hebebrand M, Grasemann C, et al. (2018) The role of genetic variation of human metabolism for BMI, mental traits and mental disorders. Mol Metab 12: 1-11.
72. Belousova EA, Filipenko ML, Kushlinskii NE (2018) Circular RNA: New regulatory molecules. Bull Exp Biol Med 164: 803-815.
73. Emmer A, Brütting C, Kornhuber M, Staege MS (2018) Genetic determinants of antibody levels in cerebrospinal fluid in multiple sclerosis: Possible links to endogenous retroviruses. Int J Mol Sci 19: 786.
74. Brütting C, Narasimhan H, Hoffmann F, Kornhuber ME, Staege MS, et al. (2018) Investigation of endogenous retrovirus sequences in the neighborhood of genes up-regulated in a neuroblastoma model after treatment with hypoxia-mimetic cobalt chloride. Front Microbiol 9: 287.
75. Chen J, Ni P, Li X, Han J, Jakovlić I, et al. (2018) Population size may shape the accumulation of functional mutations following domestication. BMC Evol Biol 18: 4.
76. Chen H, Sun M, Fan Z, Tong M, Chen G, et al. (2018) Mitochondrial C4375T mutation might be a molecular risk factor in a maternal Chinese hypertensive family under haplotype C. Clin Exp Hypertens 40: 518-523.
77. Khoury P, Akuthota P, Ackerman SJ, Arron JR, Bochner BS, et al. (2018) Revisiting the NIH Taskforce on the Research needs of Eosinophil-Associated Diseases (RE-TREAD). J Leukoc Biol 104: 69-83.
78. Strynatka KA, Gurrola-Gal MC, Berman JN, McMaster CR (2018) How surrogate and chemical genetics in model organisms can suggest therapies for human genetic diseases. Genet 208: 833-851.
79. Kirby RJ, Divlianska DB, Whig K, Bryan N, Morfa CJ, et al. (2018) Discovery of novel small-molecule inducers of heme oxygenase-1 That protect human iPSC-derived cardiomyocytes from oxidative stress. J Pharmacol Exp Ther 364: 87-96.
80. Herceg Z, Ghantous A, Wild CP, Sklias A, Casati L, et al. (2018) Roadmap for investigating epigenome deregulation and environmental origins of cancer. Int J Cancer 142: 874-882.
81. Han JH, Shin H, Park JY, Rho JG, Son DH, et al. (2018) A novel peripheral cannabinoid 1 receptor antagonist, AJ5012, improves metabolic outcomes and suppresses adipose tissue inflammation in obese mice. FASEB J 33: 4314-4326.
82. Gupta A, Shah K, Oza MJ, Behl T (2019) Reactivation of p53 gene by MDM2 inhibitors: A novel therapy for cancer treatment. Biomed Pharmacother 109: 484-492.
83. Martínez-Pérez C, Turnbull AK, Dixon JM (2018) The evolving role of receptors as predictive biomarkers for metastatic breast cancer. Expert Rev Anticancer Ther 19: 121-138.
84. Bhowmick SS, Saha I, Bhattacharjee D, Genovese LM, Geraci F, et al. (2018) Genome-wide analysis of NGS data to compile cancer-specific panels of miRNA biomarkers. PLoS One 13: e0200353.