Chapter

Genetic Polymorphisms

Dhafer A.F. Al-Koofee and Shaden M.H. Mubarak

Abstract

It is amazing to know that around 99.9% of the individuals genome among persons is alike, and only 0.1% of it differs in chromosome. This variance is accountable for the diversity in phenotypes and receptiveness of them to environmental effects. DNA variants are happening in numerous formulas. Mutations might be definite as order variants which happen in less than 1% of the populace, whereas the extra prevalent variant is identified as polymorphisms. More than 1% of the greatest public hereditary variants are known as single nucleotide polymorphisms (SNPs). In human genome, SNPs considered as plentiful figure of genetic variation, and their importance in contribution to many disease, drug efficacy, and side effects in addition to may represent a prophylaxis. SNPs represent a specific location at which more than one nucleotide is established and only two alleles at a SNP locus. More than 100 million SNPs have been recognized in human, in average each 300 nucleotide on usual. The gene which has more than one allele is a normal result of SNP. SNPs are not restricted to coding sequence, but may be associated with non-coding region. Many techniques are used to analyze SNPs and involve two phases, one for allele recognition and another for detection.

Keywords: SNP, allele frequency, point mutation, VNP, chromosome, gender, gene, VNTR, CNV, STR

1. Introduction

Genetics terms returns to origin from Greek genetikos meaning "genitive," which in turn derives from genesis meaning "origin" [1, 2]. Genetics in general is a branch of biology related to survey of genes, genetic variation, and even heredity in living systems [3–5]. The study of inheritance pattern that influences genes on human nature and occurs in human beings is called human genetics. Human genetics represents an original aspect that encompasses a variety of overlapping fields like the structure of gene and organization; the study of mutation detection; genetic mapping and linkage analysis; molecular diagnostics; gene expression; cytogenetics assessment; biomedical genetics; disease association studies; tumorigenesis of molecular levels; developmental genetics; and genetic epidemiology, in addition to genetics of complex disease [6, 7]. In general, genes can be considered as a key of most human inherited lesions. So, the benefit study of human genetics can be helpful to answer many questions concerning human diseases and invent effective drugs [8]. The passing of a certain genes from parents to offspring by biological process is called heredity. Each baby carries genes from their biological parents and some of these genes express particular trait or lesion [9]. Various traits may be physical like color of eyes, hair, skin, and other phenotypic matter. In other direction, some genes may play a key role in the risk of certain disorders and increase incidence of disease, or prophylaxis from it [10]. Several disorders occur and arise from multiple factors such as genetic, lifestyle, and environmental [11]. Many previous studies revealed facts for the hereditability of main neuropsychiatric disorders, for example, depression, bipolar disorder, and schizophrenia [12, 13]. In all these behavioral disorders, a specific genetic fault is transported from parents to children and will enhance a progeny susceptibility risk of inheriting a specific disorder [11, 12, 14, 15].

Neurological and mental diseases cannot be related to genetics science alone, so it is significant to seek implicated one's genetic composition material that possibly affects various direction of human behavior [16]. The relationship between genes and behavior leads to development of highly prevalent responses and disorders throughout a new biological factors. About 30–50% of the risk for anxiety and depression is genetic, while the other 50–70% of the risk may be attributed to environmental factors, such as substance use, stress, diet, and childhood experiences [17]. A comparison between genetic and environmental factors, demonstrated about 30–50% of the risk for anxiety and depression and 50–70% of substance uses, stress, and diet, respectively [17, 18].

2. Genes in the cell

Not each living cell of the human body have nucleus. Skin, hair, and red blood cells contain no nucleus [19, 20]. Nucleus contains a genetic material that is responsible for information. Half of these information of the genetic materials come from each parent [20].

2.1 Chromosome

All nuclei of human cell contain 23 pairs of small thread-like structures called chromosomes. Genes are localized within these 23 pairs chromosomes. About 23 out of 46 chromosomes come from the father and others like them come from the mother [21]. These chromosomes contain genes and some of them carry thousands of important genes while some carry only a few [22]. In addition to these, genes are made up of a chemical substance named deoxyribonucleic acid (DNA). The chromosomes are very long thread strands of DNA, coiled up tightly and compacted [23].

Along every chromosome, there is a constriction point called centromere, the numbering and divided packages of chromosome started from it [24]. The centromere separates the chromosome into two arms: long called "q arm" and short called "p arm" as in **Figure 1**. Chromosomes are numbered from 1 to 22 in both sexes and called autosomes, while the last one remaining take letters X and Y which are responsible for the gender. In female, X chromosome is duplicated, whereas Y chromosome is combined with X chromosome in male [24, 25] (**Figures 2** and **3**).

2.2 Nitrogenous bases

The nitrogenous bases are organic molecule with a nitrogen atom that bears chemical prosperities of a base and involves four letters in addition to fifth letter used in ribonucleic acid (RNA), and classified into two main compounds: pyrimidine cytosine (C), thymine (T), and uracil (U); and purine guanine (G) and adenine (A), respectively [27]. They were arranged in unique position in genes, which makes up combinations with permutations and combinations. It is worth mentioning (AT and GC) that bases pair is always found together, and there are different sequences

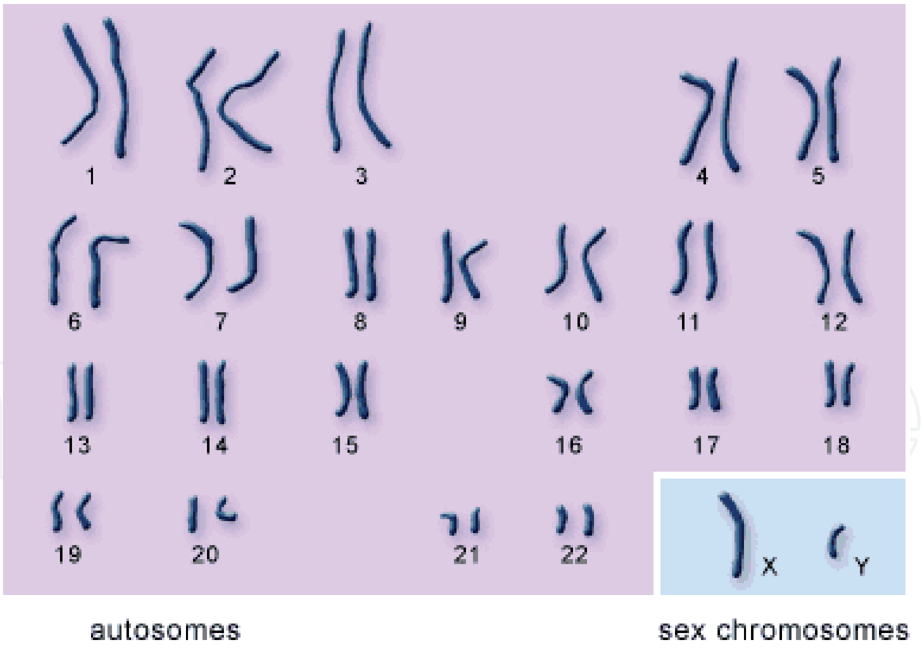

Figure 1.
Autosomes and sex chromosomes of Homo sapiens from US National Library of Medicine, National Institutes of Health, Department of Health & Human Services. June 4, 2012.

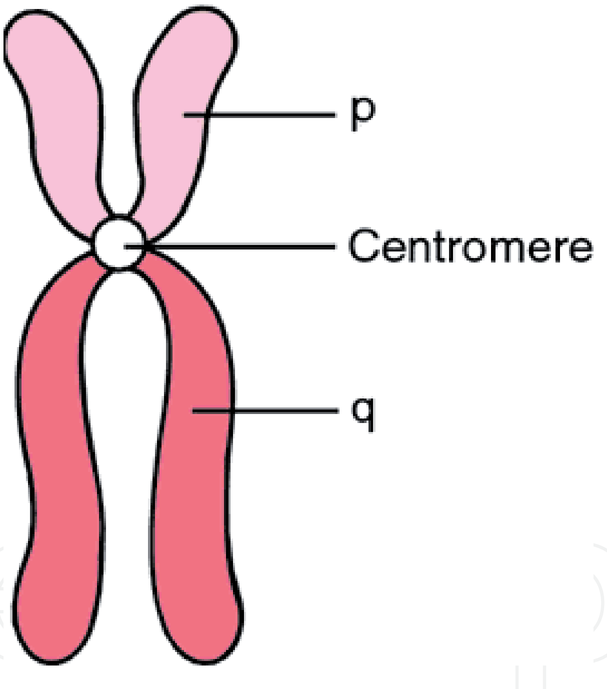

Figure 2.
Chromosome structure explained long and short arms [26].

of bases pairs in DNA coded messages [28]. These bases are part of DNA, and constitute a language when arranged together acting as a guide telling cells what need to do such as growing, division, maturity, and variety functions [29].

2.3 Gender

Both gender have 46 paired chromosomes (44 autosomes), numbered from 1 to 22 chromosome pairs according to size, chromosome number 1 being the biggest one. In addition to autosomes, there are other two copies of sex chromosomes X and Y responsible for determination of gender. In female, two copies of X chromosome

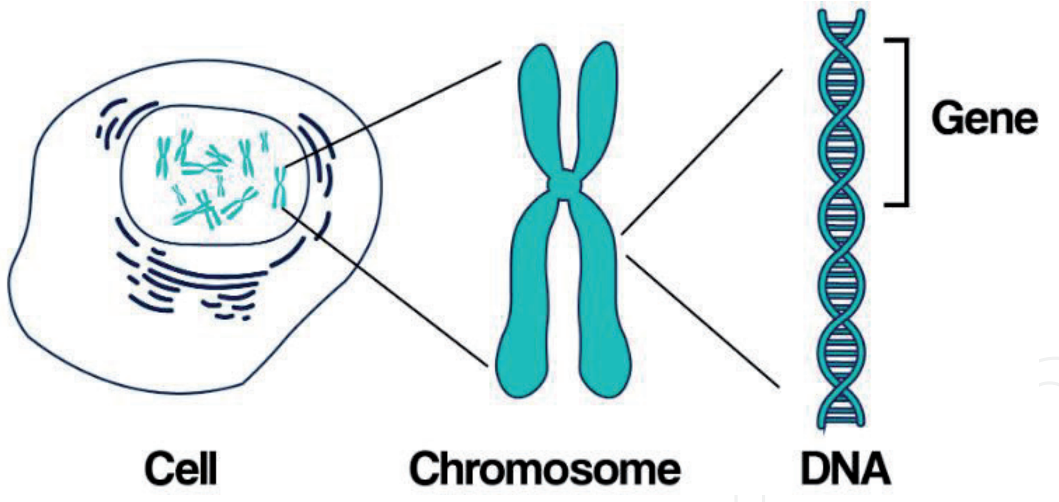

Figure 3.
Distribution of gene in the chromosome within human cell from U S National Library of Medicine, National Institutes of Health, Department of Health & Human Services. June 4, 2012.

are present, while in male, one X copy and one Y copy in their body cells. In female, 22 autosomes paired chromosomes in addition to X sex chromosome present in the egg cells, while in male, the same number of chromosomes are present and the difference only X or Y chromosome in their sperm cells. The combination egg with sperm gives 46 chromosomes regarding the sex chromosome (XY in male and XX in female babies) [30, 31].

2.4 Human genes and genetics

The whole DNA in the cell makes a genome which contains both the exon (coding regions) and intron (non-coding region) that represent large sequences that do not encode any protein and their function is exactly not known yet [32, 33]. In genome, the gene is a basic biological functional unit of heredity that contributes to phenotype/function. A segment of DNA that encodes instruction is needed for a certain protein or enzyme. In other side, a lot of genes do not encode any protein. Only a fraction of DNA of the gene in the cell is expressed through transcription process that involves copy of chemical bases into messenger RNA (mRNA) in order to produce protein according to central dogma [33]. After that it will be translated by using ribosomes organelles, and mRNA migrates toward cytoplasm from nucleus to create polypeptide that folds in a certain configuration to make the protein. A range of human genes are between hundred to more than two millions of nitrogen bases. About 20,000–25,000 genes are located on the 23 pairs of chromosomes within nucleus according to human genome project [34]. The human genome project completed officially in April 2003, and only 12,800 genes and numerous other genes have been well mapped to loci on each of the chromosomes. On the other hand, the correct number of human gene is still unknown [35, 36].

In human being, any individual has two copies from each gene, one copy comes from father and second copy comes from mother [32]. In all people, most genes are similar, excluding small number of genes that are little a bit diverse between people (<1%). The alternative form of a gene that occurs at the same locus on homologous chromosomes called allele bears a small variation in their DNA sequences and participates to every person's single physical features. A single allele for each gene is inherited from each parent (e.g., at a locus for hair or eye color and blood type). About 2% only of genome represent the DNA in genes and full information is stored in a database that is publicly accessible [37].

2.5 Inherit characteristics

Genes are considered as building blocks of inheritance [38]. The traits pass from parents to their offspring and are controlled by some genes; these are carried out by either sexual or asexual reproduction [39]. The genetic information and characteristics are acquired in the progeny cells from their natural parents. However, most of them are affected by mixing the environmental effect and genes. Many traits are observed simply like tongue rolling, dimples, freckles, hands clasping, etc. [40].

2.6 Dominant, recessive, and co-dominant genes

The cell works via coded messages that send from both alleles of genes that involved in every set of chromosomes. Some of these genes appear dominant more than other in works [41]. The dominant occurs when one allele of gene is dominant, while the recessive appears in opposite to dominant within the pair. However, there is present other situation neither dominant nor recessive called homozygous [32]. Homozygous is an equal weight carrier combination of each allele in the gene pair and demonstrates phenotypic and physical characteristics between them [42].

2.7 The genetic keys

The genetic information that endures on the genes order to produce specific protein will be converted to "switched on" position in a few specific specialized cells, and at the same time, other genes may be "switched off" position [43]. Cells differ in differentiation, so genes "switched on" in liver cells are completely different to those that at same position in brain cells [44].

Numerous cases are born with a defect in particular gene which related to a specific illness, and this does not mean you are more susceptible to it. At the same time, this raises the risk of appearing of the disease. So, the predisposition genetic effects such as occurrence of many types of cancer may be need to be triggered by environmental factors, and to reducing the risk achieved through decreasing or avoiding such triggers [45, 46].

In each gene, non-coding regions (introns) account more than 98% and as suggested previously, they do not have any function "junk," and do not involve any information of gene output in cells. The previous opinion about non-coding DNA regions is rejected despite that role is still unknown and appears to have very important roles to do in through gene expression and regulation in each cell [47].

2.8 Genes, mutation, and single nucleotide polymorphism

As mentioned previously, about 23,000 genes in the human cell act as leader in growth and general health, which are responsible for everything in human life; in which the genetic code is a set of rules used by human being and every living system to translate the information encoded within DNA or RNA sequence to protein. Every three nucleotides called codon encode a certain amino acid in protein [48].

In this direction, any changes in the genetic code can lead to each person is exceptional in his behavior and health, that is to say, the alteration in the sequences of nucleotide in DNA can give a uniqueness characteristic for person. Mainly these changes are risk free, while others may have embroiled in proteins production either not properly, wrong sequence, or not produced totally [49]. Hence, the changes in genetic material cause inactive or disturbed gene called mutation. These mutations occur in DNA sequence either by mistake during copy process or by environmental effectors. Sometimes mutations affect individuals directly or indirectly and are prone more susceptible to certain disease circumstances [50].

3. Polymorphism

A brief glance across a time: the beginning of the human genetic polymorphism was belonging to the b globin gene in 1978, which utilized to recognize a heredity disease. After 2 years, in 1980, short distinctions in DNA discovered were spread over the whole human genome. It was described by utilized restriction fragment length polymorphisms (RFLPs) method. Further complicated interesting information of DNA polymorphisms was reported in 1985. They were named minisatellites. The empirical arguments about DNA fingerprinting remained to the 1990s. With the trial of OJ Simpson in the USA in 1995, the DNA proofs play a very important role in forensic medicine history presented by the prosecution; OJ Simpson was acquitted. This event call attention to the proofs of DNA has great significance [51].

When we see the great diversity of human ethnicities, really we find it shocking that all of these different ethnicities share a genetically identical sequence at 99%. The range of their variances is only within limits 0.1% of sequence genetic that differs between double chromosomal threads, **Figure 4**, [52, 53]. It is a small ratio of variances (1%) indeed, but it is accountable for the multiplicity in person's phenotypes and receptiveness of them to ecological contacts [53, 54].

Polymorphism at the DNA grade contains a broad domain of variations from single base pair alteration, numerous unite pairs, and frequent sequences [55]. One of the most famous types of genetic variations is the genetic mutation. Genetic mutation can be definite as order variants which happen in a smaller than 1% of the populace, whereas the extra prevalent variants are identified as polymorphisms. The greatest public hereditary variants than 1% are single nucleotide polymorphisms (SNPs) [53, 54].

Generally, genetic polymorphism can be available in numerous designs, comprising: single nucleotide polymorphisms (SNPs), tandem repeat polymorphisms which include a variable number of tandem repeats (VNTRs) and short tandem

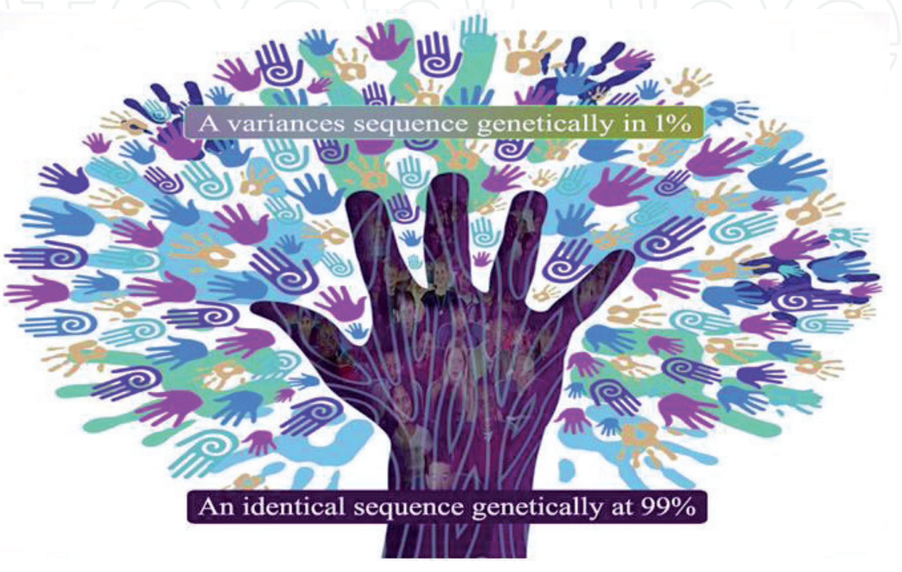

Figure 4.
Human genetic polymorphism is identical in sequences at 99% and variation sequences only about 1% [52].

repeats (STRs), insertion/deletion polymorphisms, transposable elements (TE) or Alu repeats also known as "jumping genes," structural alterations, and copy number variations (CNV) [55].

For the studying diverse kinds of DNA polymorphisms, different techniques can be utilized, such as restriction fragment length polymorphisms (RFLPs) accompanied by southern blots, polymerase chain reactions (PCRs), hybridization methods (southern and northern blotting) utilizing DNA microarray chips, and whole genome sequencing (WGS) [55]. The following is an illustration of the most famous polymorphism (**Figure 5**).

3.1 Single-nucleotide polymorphism (SNP)

Single nucleotide polymorphisms (SNPs) (pronounced: snip) are an alteration in a lone DNA order structure building block unit: (A, T, C, or G) which termed a nucleotide, **Figure 2** [56]. It is the simplest formula of genetic difference among persons. SNPs are the most frequent occurrence from all genetic variants, which happen usually in a person's DNA. It is a ratio of occurrence near 90% of human genomic variants [57, 58].

They may be occurring one time in each 300 nucleotides on usual, that is, average is about 10 million SNPs in the individual's genome. Greatest frequently, those SNPs are set between genes or within genes. They may perform as living signs and/or hereditary indicators, aiding experts find sequence, which are linked with disease. As soon as SNPs happen inside a gene or in an adjusting area nearby a gene, they might show an additional strong impact in disease via stirring the gene's role. However, the SNPs generally have no influence on the general state of health. Moreover, investigators have instituted that SNPs might assist and guess a person's reaction to definite medications. Additionally, they are utilized for a pathway of genetic factors of malady inside relatives [59–62].

3.2 Polymorphic repetitive sequences

The extension of the human genome threads that include gene sequences or intergenic and include retro (pseudo) genes and transposons are composed of small sequences of nitrogen bases that have repeated in tandem. It can consist of more two-thirds of human DNA. The number of units of these tandems in a specified site is extremely variable between separated persons. Tandem repeat polymorphisms include a variable number of tandem repeats (VNTRs) minisatellites and short tandem repeats (STRs) microsatellites. Both of VNTRs and STRs are the same in the total grounds. The difference between different alleles is consequence to a difference in the number of repeat bases that exist in alleles that are of various lengths, and later, tandem repeat polymorphisms have been identified as length polymorphisms. So, widely distinguished types from mini- and microsatellites

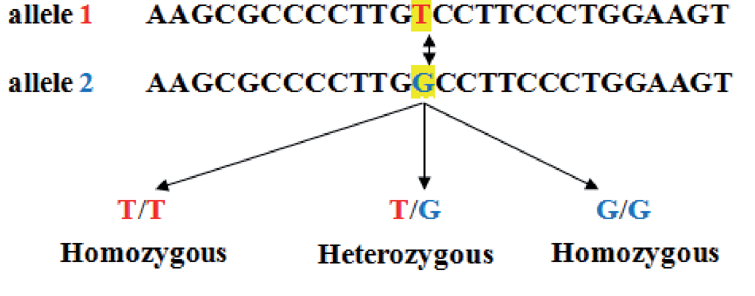

Figure 5.
Single nucleotide polymorphism for two alleles.

depend on the distance of the repeated blocks. In microsatellites, the order repeat base composes between 2 and 9 units; while mini-satellites composes between 9 and 100 units [63–65].

3.2.1 Variable number of tandem repeats (VNTRs)

VNTR is among the earliest DND markers in the application. It is a kind of tandem repetitions in which a small order of bases (10–60 base pairs) are frequented changeable times in a certain position. Therefore, VNTR is additionally familiar as minisatellites. Minisatellites are scattered everywhere in the humane DNA. Usually, the number of repeated bases in minisatellites differs among persons. Hence, the array extension shaped by VNTRs as well differs among persons. Accordingly, the variant number of chromosomes is familial from parents, so they can be applied in parental or individual identification. The techniques that use to determine this type are: routines PCR, gel electrophoresis, and amplicons of band designs by southern blotting. The utilization of VNTRs was, nevertheless, restricted by the kind of specimen that could give good results for the reason that a big quantity of DNA was needed. In addition, understanding VNTR profiles might be a difficulty. Their utilization in forensic genomics has been replaced at the present time by short tandem repeats (STRs) [66].

3.2.2 Short tandem repeats (STRs)

Short tandem repeats (STRs) give an extremely good method because of their great grade of polymorphism and a comparatively small length. Additionally, STRs are typical methods for genotyping in the identity of one's parents check and forensic identity check. A category of tandem repeats depended on presents a small order of bases (2–6 base pairs) are frequented a variable number of times in a certain site. STRs are a type of microsatellites, and they are furthermore recognized as short sequence repeats (SSRs) in plant DNA. The repeating bases consist of a single nucleotide that is familiar as a single nucleotide polymorphism (SNP) [66].

3.3 Insertion/deletion polymorphisms

It is a type of genomic difference in which a particular base order of different sizes ranging from one base to several 100 units is inserted or deleted. Indels are very extending across the DNA. Several writers consider one base pair as SNPs or frequent insertion/deletion as indels [55].

4. Genome-wide association studies (GWAS)

Genome-wide association studies (GWAS) are a new technique used worldwide in genetics research to identify inherited genetic risk variants linked with risk of prevalent disease. GWAS are the most inclusive way of genetic variation study. In general, this approach deals with full scan of genome for identifying genetic markers frequently are polymorphisms (SNPs) that appear more in patients relative to healthy individuals, and also understanding the contribution of genes in the diseases and developing better prevention and treatment approaches.

GWAS are the greatest complete way of research and contain skimming the whole genome of research members for polymorphisms and anomalies related with the sickness of attention. GWAS have the benefit of supplying a complete investigation of related genetical anomalies inside the genome, as the term "genome-wide"

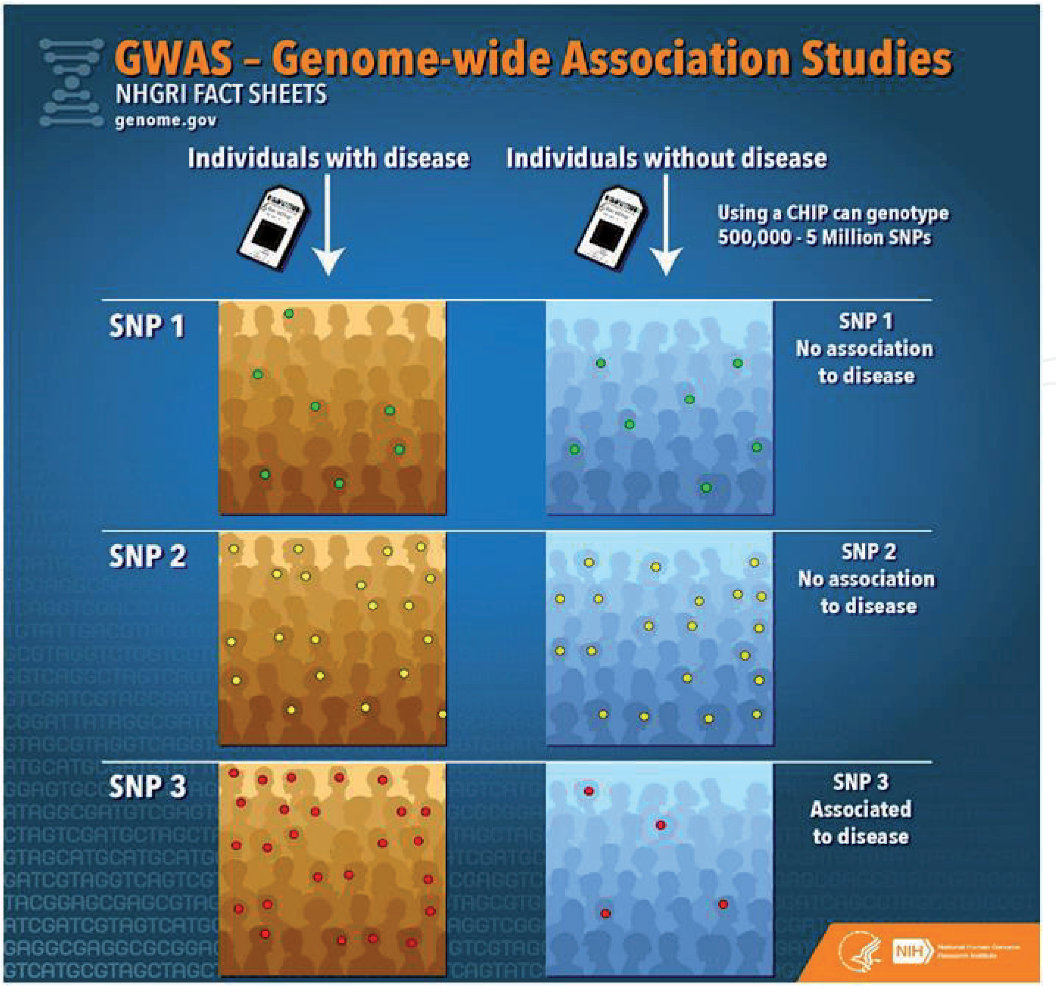

Figure 6.
Genome-wide association studies [71].

shows, in spite of that, GWAS are timing spender, costly, and yields a massive quantity of data that can/cannot actually be related to the illness of study. As of that, they are best beneficial as an initial mark pretty than a way for measuring accurate connotation [67]. In additional, GWAS are case-control study setup concentrating on obviously distinct participators geneticists who assume to find only proportionally brief extends of participate chromosomes **Figure 6** [67]. It includes comparison between two groups of individuals, one healthy and second patients or affected group with disease. Therefore, GWAS purpose is to recognize hereditary variations that convert danger of public maladies or touch additional phenotypes. The simple thought of it is: check hereditary variations (frequently SNPs), and phenotypes in haphazardly-tested persons, and view which SNPs are connected with phenotypes, while infrequent variations are inferiorly taken by GWAS method [68–70].

5. Discussion

All humans have variation in genetic material, even identical twins by the time of born, and this variation give us the uniqueness. We inherit our genes from our parents, so the members of the same family share majority of their genetic material involving its variations. The variation in DNA that cause wrong in required genetic code translates into a specific protein called pathogenic variant or mutation when linked to phenotypic particularly if they occur within the protein coding sequence of the gene. Variations are caused by the environment and genetic factors. Several disorders arise from multiple effectors like environmental, lifestyle, and genetic factors. From these diseases is behavioral genetics neuropsychiatric, such as schizophrenia, depression in which a genetic fault transferred from parents to sons through familial genes causing elevated the risk of a particular disease. SNPs can affect more than 90% of genetic variation and are responsible for the occurrence of differences between the humans. Despite the presence of SNPs, there is no relation to modify or change cellular function that is to say have no effects, and at the same time, many SNPs were found to participate in the initiation of disease like cancer or act as prophylaxis against a certain disease or even impact the responses to medications. Depending on the SNPs' position in the genome, we can classify them into that happen with exome (coding region), intron (non-coding region), and between adjacent genes (intergenic region). Because there is much of non-coding DNA (99%) that lead to harboring majority of SNPs occurring in these segments. However, only small part (1%) of genome is considered important to represent exome that can contribute existing mutations, and SNPs that have a big outcome on several diseases. Non-coding genome includes many categories of regulatory factors such as promoters, enhancers, silencers, and insulators. Each one of them provides binding sites for proteins, carries out transcription, activates transcription, suppresses transcription, and controls transcription process, respectively.

SNPs are very important and used in various studies such as estimating the tendency to disease and predicting genetic lesion; and are also used as biomarkers since they can occur near disease genes for complicated diseases, but not always. In complex disease, which means a pathological circumstance of the body due to a defect in a number of genetic and environmental aspect, SNP can affect that person has toward a specific disease. Nowadays, various methods have been established and assembled to identify known or unknown SNPs through two categories which are genotyping and scanning sequence, respectively.

Acknowledgements

I am grateful to my family, father, mother, sisters, and brothers, for always being the person I could turn to during those dark and desperate years. They sustained me in ways that I never knew that I needed.

I have to start by thanking my wife, and my daughter awesome, from reading early drafts to giving me the support. Thank you so much. "Thanks to everyone in my publishing team."

Conflict of interest

We would like to declare there is no conflict for this work.

DOI: http://dx.doi.org/10.5772/intechopen.88063

Author details

Dhafer A.F. Al-Koofee* and Shaden M.H. Mubarak
University of Kufa, An Najaf, Iraq

*Address all correspondence to: dhafera.faisal@uokufa.edu.iq

References

[1] Ekure IA. Genetic epistemology: An examination. J. Intergative Humanism. 2015;**6**(1)

[2] Liang P, Xu Y, Zhang X, Ding C, Huang R, Zhang Z, et al. Research article Crispr/Cas9-mediated gene editing in human tripronuclear zygotes. Protein & Cell. 2015;**6**(5):363-372

[3] Chakravarti A. Perspectives on human variation through the lens of diversity and race. Cold Spring Harbor Perspectives in Biology. 2015;**7, a023358**:1-14

[4] Griffiths E, Anthony JF, Miller JH, Suzuki DT, Lewontin RC, Gelbart. Human genetics. In: An Introduction to Genetic Analysis. 7th ed. 2000

[5] Zhang W. Genetics: Analysis of genes and genomes, sixth edition. Neuro-Oncology. 2005;**7**(2):204-205

[6] Fraga Sandra Rodríguez-Rodero MF, Fernández-Morera JL, Menéndez-Torre E, Calvanese V, Fernández AF. Aging genetics and aging. Aging and Disease. 2011;**2**(3):186-195

[7] Prescott KR, Wilkie AOM. Genetics aspects of birth defects: New understandings of old problems. Archives of Disease in Childhood. Fetal and Neonatal Edition. 2007;**92**:308-314

[8] J. K. J. G. T. A. G. R. M. T. M. M. D. L. R. A. Cardiac anesthesia. Journal of Cardiothoracic and Vascular Anesthesia. 2017

[9] Zhang X, He ÃP, Liang ÃY, Yang S, Yuan ÃW, Xu S. A gene for freckles maps to chromosome 4q32–q34. The Journal of Investigative Dermatology. 2004;**122**(2):286-290

[10] Jackson M, Marks L, May GHW, Wilson JB. The genetic basis of disease. Essays in Biochemistry. 2018;**62**(December):643-723

[11] Van Loo KMJ, Martens GJM. Genetic and environmental factors in complex neurodevelopmental disorders. Current Genomics. 2007;**8**:429-444

[12] R Assessment. 3. Risk assessment. Safety Engineering. **19**:13-21

[13] Crous-Bou M, Harrington LB, Kabrhel C. Environmental and genetic risk factors associated with venous thromboembolism. Thieme E-Journals-Seminars in Thrombosis and Hemostasis. 2017;**42**(8):808-820

[14] Singh M, Tyagi SC. Ocular disorders. Genes and genetics in eye diseases: A genomic medicine approach for investigating hereditary and inflammatory ocular disorders. International Journal of Ophthalmology. 2018;**11**(1):117-134

[15] Melaiu O, Gemignani F, Landi S. The genetic susceptibility in the development of malignant pleural mesothelioma. Cancer Chemotherapy and Pharmacology. 2018;**10**(Suppl. 2): 246-252

[16] Maccoby EE. Parenting and its effects on children: On reading and misreading behavior genetics. Annual Review of Psychology. 2000;**51**:1-27

[17] Manuscript A. Overview of the genetics of major depressive disorder. Current Psychiatry Reports. 2011;**12**(6):539-546

[18] Lesch KP. CRSN symposium : Focus on depression, Part I [Symposium du CRSN : le point sur la dépression , première partie]. Gene – Environment Interaction. 2004;**29**(3):174-184

[19] Baker BJR. The cell-theory: A restatement, history, and critique

part V. The Multiplication of Nuclei. 1955;**96**:449-481

[20] Pederson T. The nucleolus. Molecular Biology of the Cell. 2011;**3**:1-15

[21] Alberts B, Johnson A, Lewis J, Raff M, Roberts K, Walter P. Copyright © 1983, 1989, 1994. Alberts B, Bray D, Lewis J, Raff M, Roberts K, Watson JD. Copyright © 2002

[22] O'Connor C, Miko I. Developing the chromosome theory. Nature Education. 2008;**1**(1):44

[23] Molecular Biology of the Cell. 2002

[24] Chueh AC, Wong LH, Wong N, Choo KHA. Variable and hierarchical size distribution of L1-retroelement-enriched CENP-A clusters within a functional human neocentromere. 2005;**14**(1):85-93

[25] Receptor E, Liehr T, Imbalances PC. Learn More about Human Chromosome Human Chromosomes Hematological Cancers. 2001

[26] Encyclopedia and Dictionary of Medicine

[27] Structural Organization of DNA

[28] Majuri I, Rautanen A. 582319 Molecular Genetics and Gene Mapping for Methodological Sciences 3 CP Course Assistants. Organizers

[29] Molecular Biology of the Cell, 4th ed

[30] Cleary MA. Autosome Learn More about Autosome Autosomes Chromosomes in the Cell. 2001

[31] Ross MT, Grafham DV, Coffey AJ, Scherer S, Mclay K, Muzny D, et al., Europe PMC Funders Group. The DNA sequence of the human X chromosome. 2009;**434**(7031):325-337

[32] Jürgen B. The fragment gene. Annals of the New York Academy of Sciences. 2009;**1178**:186-193

[33] Jo B, Choi S. Introns: The functional benefits of introns in genomes. Genomics & Informatics. 2015;**13**(4):112-118

[34] Human Genome Project Information Site Has Been Updated. Ornl.gov. 23 July 2013. Retrieved: 6 February 2014

[35] Just as reading the words on the page of a book allows an understanding of the author's message. 2016;**June**:1-5

[36] Human Genome Project Information. Genomic Science Program

[37] Allele meaning in the Cambridge English Dictionary. Dictionary.cambridge.org. [Retrieved: 29 October 2017]

[38] Genes. (n.d.). [Retrieved from: http://www.genomenewsnetwork.org/resources/whats_a_genome/Chp1_3_1.shtml#genedet8]

[39] Genetic testing. (n.d.). [Retrieved from: https://www.caregiver.org/genetic-testing]

[40] Ben-Shahar Y, Robichon A, Sokolowski M, Robinson G. Influence of gene action across different time scales on behavior. Science. 2002;**296**(5568):741-744

[41] Jirtle RL, Weidman JR. Imprinted and more equal. American Scientist. 2007;**95**:143-149

[42] Conley D, Rauscher E, Siegal ML. Beyond orchids and dandelions: Testing the 5-HTT 'risky' allele for evidence of phenotypic capacitance and frequency-dependent selection. Biodemography and Social Biology. 2013;**59**(1):37-56

[43] Takumi Takizawa TM, Meaburn KJ. The meaning of gene positioning. Cell. 2012;**135**(1):9-13

[44] Different genes are active in different kinds of cells

[45] Findlay GM, Daza RM, Martin B, et al. Accurate classification of BRCA1 variants with saturation genome editing. Nature. 2018;**562**(7726):217-222. [PubMed Abstract]

[46] Hampel H, Bennett RL, Buchanan A, et al. A practice guideline from the American College of Medical Genetics and Genomics and the National Society of genetic Counselors: Referral indications for cancer predisposition assessment. Genetics in Medicine. 2015

[47] Maston GA, Evans SK, Green MR. Transcriptional regulatory elements in the human genome. Annual Review of Genomics and Human Genetics. 2006;**7**:29-59

[48] Nirenberg M. Historical review: Deciphering the genetic code—A personal account. Trends in Biochemical Sciences. 2004;**29**(1):46-54. DOI: 10.1016/j.tibs.2003.11.009

[49] Griffiths AJF, Gelbart WM, Miller JH, et al. Modern Genetic Analysis. New York: W. H. Free; 1999

[50] Mutation learn science at scitable. Available from: www.nature.com. [Retrieved: 24 September 2018]

[51] Trent RJ. Forensic medicine and science. In: Molecular Medicine. Vol. 3. Amsterdam; Boston: Elsevier; 2005. pp. 221-236

[52] Faith and Service: 3 Simple Ways to Do Something—The Giving Net [Online]. Available: http://thegivingnet.com/faith-and-service-3-simple-ways-to-do-something/. [Accessed: 20 May 2019]

[53] Kruglyak L, Nickerson DA. Variation is the spice of life. Nature Genetics. 2001;**27**(3):234-236

[54] Stenson PD et al. The human gene mutation database: 2008 update. Genome Medicine. 2009;**1**(1):1-6

[55] Teama S. DNA polymorphisms: DNA-based molecular markers and their application in medicine. In: Genetic Diversity and Disease Susceptibility, i, Number Tourism. InTech; 2018. p. 13

[56] Mapping Your Health through SNPs: Your unique QR code | BioViva. [Online]. Available from: https://bioviva-science.com/blog/mapping-your-health-through-snps-your-unique-qr-code/ [Accessed: 21 May 2019]

[57] Palmer LJ, Cardon LR. Shaking the tree: Mapping complex disease genes with linkage disequilibrium. Lancet. 2005;**366**(9492):1223-1234

[58] Komar AA. Single Nucleotide Polymorphisms. Vol. 578. Totowa, NJ: Humana Press; 2009

[59] UN Library of Medicine; NIH. What are single nucleotide polymorphisms (SNPs)?—Genetics Home Reference. NIH; U.S. National Library of Medicine. [Online]. Available: https://ghr.nlm.nih.gov/primer/genomicresearch/snp

[60] Yousefi S et al. A SNP panel for identification of DNA and RNA specimens. BMC Genomics. 2018;**19**(1):1-12

[61] Huang E et al. Genome-wide screen for universal individual identification SNPs based on the HapMap and 1000 genomes databases. Scientific Reports. 2018;**8**(1):1-6

[62] Balding DJ, Martin Bishop CC. Handbook of Statistical Genetics. 3rd ed. Vol. 1. Chichester, England; Hoboken, NJ: John Wiley & Sons; 2007 Retrieved from https://www.cambridge.org/core/product/identifier/CBO9781107415324A009/type/book_part

[63] The Science of Forensic Genetics [Online]. Available from: http://www.

councilforresponsiblegenetics.org/geneticprivacy/DNA_forensics_1.html [Accessed: 23 May 2019]

[64] The Science of Forensic Genetics

[65] Panneerchelvam S, Norazmi MN. Forensic DNA profiling and database. Malaysian Journal of Medical Sciences. 2003;**10**(2):20-26

[66] Schichman SA, Suess P, Vertino AM, Gray PS. Comparison of short tandem repeat and variable number tandem repeat genetic markers for quantitative determination of allogeneic bone marrow transplant engraftment. Bone Marrow Transplantation. 2002;**29**(3):243-248

[67] Rosenfield RL, Ehrmann DA. The pathogenesis of polycystic ovary syndrome (PCOS): The hypothesis of PCOS as functional ovarian hyperandrogenism revisited. Endocrine Reviews. 2016;**37**(5):467-520. DOI: 10.1210/er.2015-1104

[68] Schwartz AG. Genetic epidemiology of cigarette smoke–induced lung disease. Proceedings of the American Thoracic Society. 2012;**9**(2):22-26

[69] Dai J. Clinical and Genetic Associations Between Lung Cancer and Chronic Obstructive Pulmonary Disease. University of Sheffield; 2017

[70] Stephens M. Statistical Genetics. 2012

[71] Genome-Wide Association Studies Fact Sheet | NHGRI. [Online]. Available from: https://www.genome.gov/about-genomics/fact-sheets/Genome-Wide-Association-Studies-Fact-Sheet [Accessed: 21 May 2019]