HOW YOUR GENETICS CAN INFLUENCE YOUR BEHAVIOR

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Genetics is the study of how genes and genetic variations are transmitted from one generation to another. Genes were first discovered by Gregor Mendel back in the 19th century (1). He used garden peas to first identify the patterns by which a single gene can be passed from one generation to the next, now known as classic Mendelian genetics (1). Since then, a new era of modern genetics emerged with the identification of the DNA and its underlying genetic code as well as the establishment of a plethora of molecular methods allowing to identify gene sequence and how it influences overall traits. This progress led to the identification and publication of the whole human genome sequence in the early 21st century also known as the Human Genome Project.

The Human Genome Project revolutionized biology and medicine as it enabled the identification of most human genes, their expression, products, variations across distinct populations and their downstream effects on health, physical traits and personality (2,3). With such knowledge at hand, modern genetics is nowadays crucial across most medical disciplines and helps understand and cure many diseases including obesity, cancer, diabetes, and cardiovascular diseases. It also allows us to better understand ourselves including our personality, longevity, and our athletic and artistic predispositions. New approaches to identify and understand our genetic differences are constantly emerging paving the way for personalized medicine and well-being for each individual.

The critical material of heredity, DNA

The Deoxyribonucleic acid molecule, shortly known as **DNA**, carries the genetic instructions and forms the genes. DNA is a polymeric macromolecule made of 4 distinct nucleotides which are guanine (G), cytosine (C), adenine (A), and thymine (T) (4). These nucleotides polymerize into long polynucleotide chains to form a DNA double helix (4). The genetic information is inscribed in the distinct sequences of the 4 nucleotides forming the DNA and determines most of our physical and character traits.

A ***Gene*** is the functional unit of inheritance and consists of a specific segment of the DNA (5). At the molecular level, a gene needs to be first transcribed into a messenger RNA (mRNA) and then translated into an amino-acid chain known as a protein (6). Both RNAs and Proteins can influence and shape final traits. Thus, a gene contains both the code for the amino acid sequence forming a protein and the regulatory sequences responsible for its expression (4). Genes consist of exons (coding regions) and introns (non-coding regions) and the vast majority of human genes have one or more non-coding regions (1).

The information stored in the DNA/gene is transferred to RNA and/or protein to reveal a phenotype. This process is called ***gene expression*** and includes several steps such as transcription of DNA to an RNA, translation of RNA to a polypeptide chain, and formation of the mature protein (6). Sometimes this stream ends just after RNA synthesis when the single RNA molecule itself is required as the final product.

Whole human DNA is packaged into the structures called chromosomes and kept in the nucleus of the cell (7). A human has 46 chromosomes consisting of 22 pairs of **autosomes** (non-sex chromosomes) and 1 pair of sex chromosomes, XX or XY (7). Every individual has two copies of each gene located on each chromosome pair, one inherited from each parent. The genetic sequence is very similar across people, but a small number of differences that are less than O.1 per cent of the genome is responsible for the differences we see across humans (8). The alternative form of a gene is named ***allele*** (9). An allele is one of the versions of a gene (9). A person inherits two alleles of each autosomal gene (autosomes: the chromosomes numbered from 1 to 22; autosomal gene: the genes located on autosomes, one from each parent (10). When the two alleles are the same, the individual is called “homozygous” for that gene (9). When the alleles are different for a person, the individual is called “heterozygous” (9). The allele term is used for defining variation among genes including variation among non-coding DNA regions.

Genotype and phenotype

The term ***genotype*** simply refers to the complete set of genes, the genetic makeup, of an organism (11). The genotype is responsible for the unique trait or characteristics and is composed of each pair of alleles passed between generations. The ***phenotype*** is an

observable and measurable characteristic and a trait of an individual, such as the physical appearance, behaviours, or disorders (11). Specifically, hair colour, eye shape, blood group, and height are some examples of our phenotype (11). In summary, the knowledge we have in our nucleus is the genotype, and the characteristics we display is our phenotype.

However, a phenotype is influenced both by its genotype and the environment. While some traits are affected by the genotype, others are more likely affected by environmental factors (12). ***Phenotypic expression****,* the observable expression of *a* gene, is an outcome of the interaction between human genes and the environment (6). Environmental factors, such as lifestyle, diet, geography, past experiences, exposure to sunlight, finding the one and falling in love, can all influence gene expression with the help of additional biological/neurobiological factors.

Single Nucleotide Polymorphisms (SNP)

During cell division, the genetic material of the cell is replicated (13). Though the DNA replication machinery has high accuracy, some mistakes can result in changes to the original DNA sequence, such as substituted or included nucleotides in the original sequence or even missing ones (1). These mistakes are defined as mutations or genetic variants. When there is a change in a single nucleotide (adenine, cytosine, guanine or thymine) in the DNA sequence, it is called a single nucleotide polymorphism (SNP) (4). SNPs occur approximately one in a thousand base pairs which means that there are three million differences between two human genomes (4). To date, thousands of SNPs have been identified and catalogued, and this number is constantly increasing.

The clinical utility of the Human Genome Project has expanded with the determination of the high density of genetic polymorphisms and the identification of SNP patterns. SNPs and their ***effects on gene function*** are subjects of active research (4). Most SNPs may not alter the functionality of the DNA sequence and may not show any effect on health or development. However, this is not always the case as SNPs may occur within the regulatory region of genes and affect protein function, which, in turn, may affect the phenotype (4). This phenotype may be due to a different protein produced, an observable trait compared to the wildtype (the original and prevalent genotype in a population) (1). The SNPs may be responsible for the diversity, familial traits, and common diseases such as diabetes, psychiatric disorders, cancer, and obesity (14). Overall, identification of gene variants and analysis of the effects of these variations may help us understand their impact on human biology.

The improved knowledge about SNPs and their effects on human biology, characteristics and welfare led the researchers to develop new and helpful SNP markers for genetic testing. Most frequent SNPs are already in use for this purpose.

Soon, by the ongoing development of new SNP markers, personal SNP profiles will be used as genetic signatures for personalised care.

Hormones

Hormones, which are secreted by specific cells, act as messengers especially for distant organs and can regulate overall physiology and behaviour (15). They are secreted into the blood or extracellular fluid, and their functions are tightly regulated via bodily feedback mechanisms (16). Most hormones that are not derived from cholesterol or phospholipids are proteins and thus gene products. Peptide/protein hormones are **expressed** via translation although some post-translational modifications are made (16). The synthesis of hormones and their functional activities are regulated by transcription and other biological pathways involving other hormones themselves (16). Hormones play a pivotal role in psychological and behavioural status in humans as they regulate our emotions and mental well-being (17). Scientific evidence suggests that exogenous manipulation of hormones may alter our behaviours in various conditions such as stress response, aggressiveness, and decision making (18). The association between hormones and our behavioural activity is bidirectional, and various psychological states may affect our hormone levels and their activities (17).

The cognitive functions such as sensation, perception, motor skills and construction, attention and concentration, memory, executive functioning, processing speed, and language/verbal skills are also closely related to numerous hormonal activities (19). Hormones usually need their respective (target) receptors to initiate the hormone-specific cascade of events. As various brain regions are specialised for certain cognitive domains, the hormone receptors for these cognitive activities also vary in terms of localization within the brain (19). Since the hormonal function is based on two components, namely, hormone and its receptor; The abundance or absence of the receptor defines the cell's response abilities. The response abilities of hormone receptors, their localizations, and hormonal functions vary in different sexes and developmental stages, which, in turn, may be attributable to certain behavioural patterns (20).

Neurotransmitters

Our behavioural patterns are not only affected by hormones. Human behaviour is a result of the communication among brain cells, namely, neuron and glial cells. The communication of brain cells with each other is established by small agents called **neurotransmitters**, and they constitute the basis of brain functions via signalling (21). The neurotransmitter released from one neuron to the next may activate, modulate, or inhibit the communication (22).

The neurotransmitters acetylcholine, dopamine, gamma-aminobutyric acid (GABA), glutamate, histamine, norepinephrine, and serotonin carry out most of the brain

functions (23) and are the main ones associated with learning and memory (24). **Acetyl-choline**, the most common neurotransmitter, is involved in learning and recall and enhances memory (24). It also acts as a messenger between axons and muscles. **Dopamine** affects motivation and movement and is also of importance in the perception of reality (25). **Norepinephrine** helps to determine motivation and reward (26). **Serotonin** helps with regulating mood, sleep and appetite, and prevents pain (27).

Many substances have been discovered that can mimic a neurotransmitter, increasing or decreasing its function in several ways. Such substances have a wide range of uses in modern medicine, and many neurotransmitter functions are also targets of drugs that modulate the concentration of neurotransmitters (28). In this way, various psychiatric drugs prevent mental illnesses by regulating the amount of these chemical messengers in the brain.

Taken together, our perceptions, mood, and life experiences are all shaped by the key contributions of neurotransmitter functions.

Behavioural genetics

Behavioural genetics, also defined as psychogenetics, genetic psychology, or behavioural biology, is the field of research on how an organism's genetic makeup influences its behaviour (29,30). Genetic psychologists explore the effect of specific genes on human behaviour and personality and the interaction between inheritance and environment. In this instance, **the “nature-nurture” controversy** should be involved in discussion. Plato (380 BC) first introduced the terms, Nature and Nurture, into the behavioural biology glossary. In simple words, our genetic background (nature) and the circumstances we grew up in, including nutrition, sport motivation, a happy family, and all good and bad experiences passed through etc. (nurture) both have an undeniable impact on who we are.

Behavioural genetics has a history going back to the 19th century. Sir Francis Galton, officially introduced the notion of **"Nature vs Nature"** in his book Hereditary Genius (1869). After John L. Fuller and William Robert Thompson published the textbook “Behavior Genetics” taking attention to the era of discoveries in 1960, behavioural genetics gained an acceleration as a research discipline. Meanwhile, Irving Gottesman revealed the scientific data and publications highlighting the important levels of inheritance in the scales related to the genetics of personality in his PhD thesis. T.J. Bouchard's work (1989), known as the Minnesota Study of Identical Twins Reared Apart (MISTRA), indicated that shyness, political conservatism, dedication to hard work, orderliness, intimacy, extroversion, conformity, leadership, and a host of other social traits are largely heritable. A study aiming to measure individual differences in reading ability was also conducted on samples from the USA, Australia, and Scandinavia (31).

In this study, genetic effects were evident in both the USA and Australia, while in Scandinavia, environmental effects were also observed along with genetic effects (31).

The Swedish Registry of Twins Reared Apart was established in the 1960s to study how smoking affects human health. There is, at present, information on approxi- mately 85,000 twin pairs, both monozygotic and dizygotic (32). There are currently around 30 ongoing behavioural studies based on the Swedish twin registry (32). As per above, **twin studies** are widely used in behavioural genetics research. To learn more about the role of inheritance of traits, monozygotic (identical) twins can help researchers since they have identical genetic compositions (33). If the same trait is exhibited by each of the co-twins, one can say that the trait is under genetic influences. The Minnesota researchers found that twins raised apart tend to be similar in intelligence, so there is a correlation between IQ and genetics (34). The findings of twin studies determined that human behaviours are under a significant genetic influence.

On the other hand, **adoption studies** can demonstrate the influence of the environment (1). Adopted people grow up in a shared environment and do not have an identical genetic makeup. Therefore, similarities among adoptive siblings or between children and adoptive parents are due to the environment (4).

The main principle of adoption and twin studies is to understand the variable contribution of the genes and the environment on the phenotype. Because the methodology of adoption and twin studies are quite different, the results from these two methods converging on the same conclusion provide higher confidence.

Although behavioural biology is an old discipline, today it is one of the most intriguing areas of human biology. The effect of genetic composition has a role in personality, behaviour, social attitudes, preferences, and intellectual ability. Research has shown that genetic influence on personality traits, such as openness to new, conscientiousness, extraversion, and neuroticism is about 40 to 50% (will be mentioned later). That means genes do not directly determine behaviour. Instead, genes affect behaviour by influencing brain function first.

Connection between our DNA and Behaviours

Several decades after Mendelian Genetics has been applied to behavioural traits, quantitative Genetics has emerged as a new discipline to analyse behavioural traits with complex modes of non-Mendelian inheritance, where multiple alleles are involved (30). Quantitative Genetics is the study of the genetic basis underlying phenotypic variations (33). Quantitative genetic approaches aim to understand the inheritance of quantitative or complex traits that take a continuous ranpe of values (33,35). Behaviours have a polypenic basis (under the influence of many penes) and are also subject to environmental influences, therefore using classical Mendelian Genetics falls short of identifying the penes involved.

The intriguing parts of behavioural genetics are what the genes do; how they interact; how the brain function and signalling are affected, why is there so much genetic variations, the link of specific genes to specific behaviours, what turns genes on or off, and how genes and SNPs provide indicators to a more comprehensive picture of what makes us who we are. At the molecular level, remarkable progress has been made in addressing these problems. Underlying causes of quantitative trait effect, such as responsible genes, the specific nucleotide change in each gene are widely known.

Some well-known examples of hormones and neurotransmitters affecting behaviour through their SNPs

The neuropeptides oxytocin and vasopressin are mediators of social behaviours, including social recognition, attachment, and aggression (41). In particular, Oxytocin is an important hormone that controls some behaviours and social interaction (42). It reduces neuroendocrine and behavioural responses to social stress and enables to inhibit defensive behaviour, thereby facilitating approach behaviour (41,42). Oxytocin triggers the bond between mother and infant and plays a role in trust, sexual arousal, recognition, and anxiety (43). Research reveals that Oxytocin may affect addiction and stress, as wel‌l (42). The SNPs rs237887, rs2268493 in the oxytocin receptor gene were associated with behaviours such as empathy, social skills, trust, and bonding (44).

Vasopressin is a hormone that regulates social behaviours such as aggression and pair-bond formation (romantic relationships) and increases the tendency to cooperate for mutual benefit (41,45). The polymorphic regions of AVPR1A (arginine vasopres- sin receptor 1A) gene is associated with altruism, bonding, and generosity (43).

Catechol-0-methyltransferase (COMT) protein has been demonstrated to have a strong effect on **dopamine** neurotransmission in the prefrontal cortex (the brain region) playing a key role in several cognitive functions, including cognitive control and IQ (46), rs468O on the COMT gene was shown to be effective on executive cognition, handling stress, and reward learning (47).

Serotonin is an important modulator of the nervous system and has impacts on cognition and behaviour including learning and memory, mood, behavioural flexibility, social interactions, aggressiveness, and anxiety (48). The SNPs rs25531 and rs25532 on SLC6A4 (serotonin transporter protein) gene affect optimism, handling stress, and emotional behaviour (49).

Genetic polymorphisms, a few samples of which have been shared above, have significant importance on human personality. Since the completion of the human genome project; expanding genetic knowledge, rapidly developing gene screening technologies and easy access to genetic laboratories, and most importantly, the high specificity and sensitivity of DNA tests, provide a great opportunity for society to access

personal data for a qualified lifestyle in terms of education, health and care. Obtaining genomic data is more accurate, faster, and cheaper than ever before.

Approach and Methodology

Meet Yourself™ collaborate with a DNA sequencing laboratory and data analysis algorithm to enable behavioural analysis combining psychology (perception) and DNA (objectivity), combining nature and nurture.

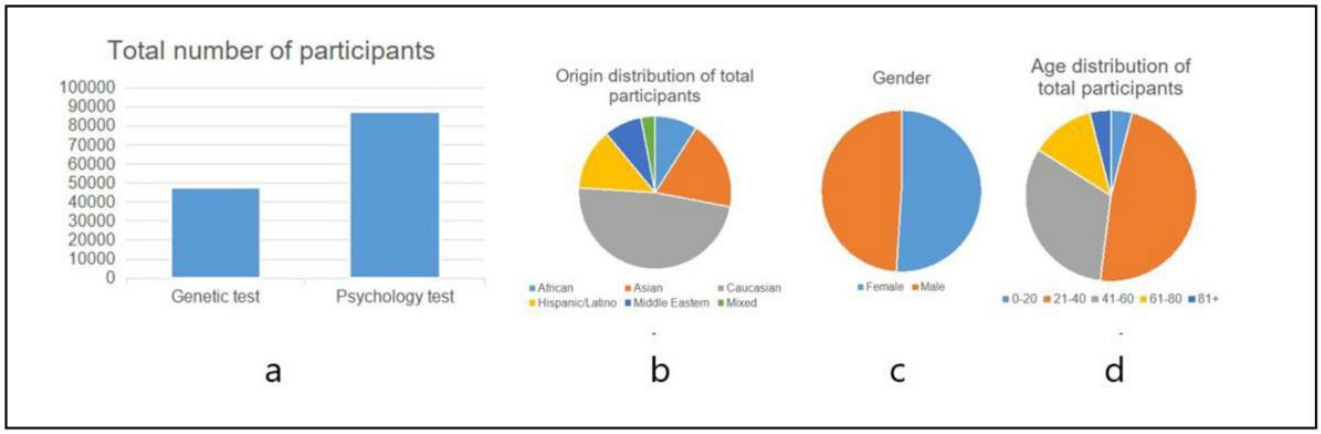
We extract your DNA from your salivary epithelial cells (SWAB), then we sequence your DNA in an ISO certified (ISO 17025:2017) Swiss laboratory. We use bioinformatics to analyse and identify your SNPs, then we apply a proprietary algorithm constructed on a polygenic approach that links multiple SNPs and genes with each of the behavioural characteristics to compute the values and generate the results.

The technology has consisted of two parts:

***Part I**: Polygenic Approach*

The adopted polygenic approach involves linking each trait with multiple SNPs from various genetic loci. To build the architecture, an extensive literature search was initially conducted covering 29,000 human behavioural genetics studies. Then, 700 sifted out peer-reviewed scientific articles that span the SNPs of interest. Finally, 150 key papers were selected for quality, multiethnicity, and the strength of measured impact on personality, originating from different scientific teams. Fourteen personality traits were matched with at least 6 SNPs, and traits were normalised to the population.

The algorithmic analysis based on data sets are shown below in the demographic graphs (Figure 1).



The strength was scored for each SNP linked to each characteristic. Finally, the scores were normalized and a final score was determined as: Low; Mid-Low; Mid-High; High. The information extracted from the client DNA sample is only for the specific regions linked to the scope of analysis. Only the regions of interest that link DNA to behaviour

were checked. The data analysis (the scores linking DNA to each behavioural characteristic) is only used anonymously for statistical purposes and further improvement of the genetic test outcome. Your DNA sample is destroyed after analysis.

The method provides/guarantees increased effectiveness with multivariate and multi weighted analysis per trait, high internal consistency (0.90-0.91) for the traits examined, test-retest reliability with 90%-97% results stability, for a re-test within a 2-year interval. New scientific studies are consistently monitored, and the target is to add every 18-24 months any new SNP(s) related to a specific trait and enhance the trait scores based on new scientific discoveries.

Part II: *3-dimentional analysis+ clever algorithm*

The approach aims:

· to make the most of your strengths and work-related potential and to develop the parts of your personality, crucial for your professional advancement.

· to enhance your self-awareness and improve your relationships.

· to uncover what drives your emotions, live up to your values and enjoy a happier life.

Since the environment plays an important role in shaping our behaviour, both a thinking preferences and psychology models link the DNA findings with two-dimensional findings. Fifty-four quantified key personality traits such as leadership, EQ, innovation, etc. are identified.

To this end, genetic analysis of the traits is performed, including spelling abilities, educational attainment, short-term memory performance, spatial learning, word reading, working memory, cognitive function, delayed recall performance, reading abilities, verbal memory, learning ability, aerobic capacity / VO2, non-word repetition, language processing, learning from errors, elite endurance athlete, power-based athlete, muscle strength, athletic performance. Further deductions are made for **combined genetic, neuroscience, and psychological analysis** of the traits including **leadership, consciousness, team player, trustworthiness, stress-tolerant, emotional, EQ, agreeableness, risk-taker, spontaneous, self-aware, confident, driven, innovative, execution, neuroticism, communication skills, self-discipline, calm, imagination, bon vivant, decisive, dutifulness, flexibility, creativity, generosity, friendliness, strategic, openness, optimist, relatedness, social, and extraversion.**

In compliance with GDPR and genetic data protection guidelines, ubiquitous Amazon S3 infrastructure is used for storage, record keeping, archival, and information recovery. Once the analysis work with any dataset is finished, a strong cryptography is applied locally before storing files to the server. The record is archived for one year for quality

assurance reasons. The record-keeping period can be prolonged upon client-specific requests.

This approach brings together nature (DNA and objectivity) and nurture (environment and perception) by providing its DNA based personality test combined with neuroscience and psychology findings. The vision is to bring science and genetics into people's daily life in a positive, accurate, and scientific way.

For this purpose,

• Polygenic approaches, DNA sequence processed by Unique Algorithm,

• Neuroscience analysis,

• Psychology analysis.

DNA Sequencing

In the late 1970s, researchers discovered new methods for analysing DNA sequences. To date, research continues at full speed to make this technology more effective, faster and more economical. In the beginning, manual methods in usage that could only analyse a very small part of the genome and were very time-consuming. Today, however, thanks to high-throughput automated systems, it has become possible to analyse the entire genome at once and in less than one day (50). Today, third generation sequencing technologies are becoming widespread and promising. However, there are still situations where the third-generation sequencing cannot be used fully and requires the use of 1st or 2nd generation sequencing technologies. Although each generation of sequencing technology brings advantages, all technical and cost problems have not been resolved yet. For example, new methods sometimes fail at repetitive regions of DNA and 1st generation sequencing may be required for such regions (51).

Today, the genomic region of interest, the entire genome, or only the DNA regions involved in protein synthesis can be sequenced using high-throughput systems.

Modern sequencing systems utilize bioinformatics tools. Although the bioinformatic analysis of sequences starts with instrument-specific processes, the overall processes are common. At first, the obtained raw data is analysed and scored for reading quality. Then, short sequence reads are placed on a given reference. Certain features are filtered out and raw data becomes meaningful.

Currently, most common technologies require amplification of target sequences before sequence analysis. However, some 3rd generation technologies allow conducting analysis using only a single DNA molecule without the need for pre-amplification. Where such applications become widespread, it will be possible to analyse individual cells

rather than clusters of cells. However, today such applications are still not cheap enough, but they will be widespread and become accessible shortly.

Obtaining pure and intact DNA in the cell is the most important quality target for sequence analysis. In humans, DNA can be obtained from all cell types with cell nuclei or all bodily fluids containing free DNA.

Isolation of the DNA sample without purifying it from protein or other intracellular components reduces the experimental efficiency and may cause inaccurate results. In addition, the obtained DNA must be intact. An informative and repeatable sequencing analysis may not be possible if DNA is sheared. Special conditions and methods are required to maintain the stability of the DNA sample obtained in pure, excellent quality, and unfragmented state. On the other hand, it is cardinal to prevent cross-contamination of the samples before, during, and after the analysis. Every step of this process is meticulously fulfilled by an expert team, which requires expertise from beginning to end.

To understand how specific genes contribute to a phenotype, or a disease, many genomic samples from different ethnic origins are scanned by sequencing techniques and compared. The genetic markers that can be helpful to predict a particular phenotype are screened throughout the genome. The SNPs which are consistently different are statistically significant. This approach, aiming to associate specific genetic variations with certain phenotypes, is called **genome-wide association study (GWAS)** (8).

As behaviours result from complex interactions between several genetic loci, the same approach is used to associate the statistically significant SNPs in these loci with behaviours. Due to the complexity of the essential statistical estimations of several variants affecting the risk for a certain condition, this data is processed via bioinformatic calculations enabling the computation of which variants tend to exist more frequently within a given personality trait. In this manner, polygenic risk scores are obtained. Polygenic risk scores have become the standard to estimate the genetic liability of traits. These values are calculated by a weighted sum of risk alleles using risk allele effect sizes derived from GWAS data.

The relative risk for a disease is calculated using polygenic risk scores (52,53). Relative risk is used to compare the data from large-scale genomic studies of distinct groups of people with a particular disease with a group of people without the disease (52). Absolute risk is different from relative risk. Absolute risk is the probability of developing a disease (52).

Since we are not focused on disease-based analyses, we apply the polygenic risk scores for traits instead and integrate them into the technology. According to the multi weighted polygenic analysis, each SNP that is included in the test has a specific value

based on several factors including p-Value, peer-reviewed publications, demographics, and scientific repeatability (Table 1).

Table 1 Specific values of each allele of SNPs. Negative values represent a negative effect on being Innovative (the individuals with negative scores of specific alleles are likely less innovative)

SNPs scoring for a given trait e.g. Innovative			Value of both alleles	Absolute value (final scoring 0-100)
SNP #	Allele 1	Allele 2		
1	-5	-5	-10	10
2	-8	-8	-16	16
3	-6	-6	-12	12
4	-6	-6	-12	12
5	-2	-2	-4	4
6	7	7	14	14
7	2	2	4	4
8	-4	-4	-8	8
9	4	4	8	8
10	-3	-3	-6	6
11	3	3	6	6

The latest information on human genetics has led to many advances in behavioural genetics. This data contributes to progress, but sometimes it also brings about some potential problems. The **multiple comparisons problem** or **multiplexing** is one of these problems (54). The large amount of data obtained in recent high-throughput genetic research can cause multiplexing making the analysis difficult. The challenge herein is to isolate the valuable and accurate result from the noise in the data, avoiding the effect known as the **look-elsewhere effect** (55).

Cluster analysis is one of the methods used in raw data analysis. Robust approaches, calculations and algorithms should be used when performing cluster analysis to match known genetic differences to behavioural patterns. Additionally, there is an absolute need for interdisciplinary collaboration in statistics, genomics, psychiatry, mathematics, psychology, computer science, and many other fields in recent neuroscience research.

The usage of advanced technologies such as machine learning and artificial intelligence in behavioural genetics research facilitates the discovery of new data and saves time for researchers (56).

In addition to making use of dry-lab applications, alternative wet-lab methodologies are being developed today. Genomic information itself is a static syntax on DNA sequences and carries critical information regarding cellular events. However, intracellular dynamics is based on the functional products of genomic sequences and several other functional components are involved in each step of this dynamic process. Any

behaviour pattern that appears phenotypically is the result of the interaction of complex intracellular biological systems and cellular networks, including gene products, namely the **interactome** (57).

Interactome analysis is a holistic and modern research approach that aims to understand biological events by considering all intracellular interactions. In this way, not only based on DNA sequences, but also the results of the interaction of gene products such as various types of RNA and protein and all other functional cellular components can be understood, and more reliable information can be obtained (58).

Alterations in the genomic sequences may alter the functions of some genes and may cause behavioural changes. On the other hand, behaviours may affect the way our genes work without changing the sequences of the genome. **Epigenetics** deals with differences in gene function that are not due to changes in DNA sequence (59). Attachment or removal of a chemical group to DNA, modifications of DNA-bound proteins, and the functions of RNA subtypes not used as a template in DNA synthesis are the major components of epigenetic mechanisms and are natural members of the interactome as well.

A process is in place to make continuous updates to the genetic approach and analyses considering the rapid developments in science and biomedical technology regarding the genetic and epigenetic components of the behavioural interactome.

Conclusion

Having discussed the behavioural genetics approach to identifying innate potentials, it is important to highlight the following:

We are a combination of talents and potentials inherited through our DNA, the way our brains are wired after years of experience, and our infinite ability to experiment, learn, and adapt our behaviours.

MEET YOURSELF is the first test to combine the latest DNA-based testing, Neuroscience research and Behavioural assessment.

The approach aims to provide more comprehensive indicators from the different aspects of what makes us who we are and put them all in a single report.The report, although rich, is easy to read and focuses mostly on what makes you unique as a human being.

This is just the beginning. Assessments are only useful if the information provided is used and shared.

Meet Yourself encourages participants to appreciate their uniqueness while addressing the environmental requirements to develop and grow. It is a call to initiate the healthy conversations with your closest people to share the information you now have about

Yourself. You will be surprised that a lot of them were eager to know more about your true self.

GLOSSARY

Allele: Different versions of a gene inherited from each parent or alternative variants of a gene that has changes in the same locus.

Autosome: Chromosomes other than sex chromosomes, numbered as 1-22 in humans.

Big 5: Taxonomy of five personality traits consisting of Openness, Conscientiousness, Extraversion, Agreeableness, Neuroticism.

Cascade: Sequential cellular reactions that give rise to biological events.

Chromosome: The threadlike packaged forms within a eukaryotic nucleus that include DNA.

DNA: Deoxyribonucleic acid; the genetic material of most organisms. It is double stranded and contains deoxyribose sugar.

Epigenetics: It refers to heritable changes in gene expression that do not result from changes in gene sequences. Epigenetic changes are reversible and do not change the DNA sequence, but they can change how a DNA sequence is processed.

GDPR: General Data Protection Regulation is an EU law regarding the privacy and data protection of citizens of EU.

Gene: A functional unit of heredity. Specific DNA regions responsible for RNA and protein production.

Genome: Complete set of genetic sequences within an organism.

Genotype: The genetic constitution of an individual.

Glial cell: Cells that hold nerve cells together and help their functions.

Hormone: Hormones are chemical messengers produced by the endocrine glands to stimulate certain activities such as growth regulation, reproduction, digestion, and behaviours, etc.

Interactome: Network of molecular interactions. Gene-gene interactions, protein-protein interactions, or complex interactions in a cell.

Mendel: The founder of single gene inheritance, known as the father of genetics, lived in the 19th century.

Neuron: Key information carrier type of cells in human brain.

Neurotransmitter: A chemical substance that transmits nerve impulses across a synapse and carries messages between different nerve cells or between nerve cells and muscles.

Nucleic acid: Long chains of chemical compounds mainly used for preserving heritable patterns.

OCEAN: The first letters of each; Openness, Conscientiousness, Extraversion, Agreeableness, Neuroticism.

Phenotype: The observable traits of an individual.

Sequencing: Detection of building blocks line-up of DNA, RNA, or protein sequences.

Sex chromosomes: They are X and Y chromosomes, take part in gender determination. While females have two Xs, males have X and Y in humans.

Trait: Characteristic/property of an individual, e.g., curly hair, innovative personality.

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