

Gene Variant That Affects Traits

An expression quantitative trait is an amount of an mRNA transcript or a protein. These are usually the product of a single gene with a specific chromosomal location. This distinguishes expression quantitative traits from most complex traits, which are not the product of the expression of a single gene. Chromosomal loci that explain variance in expression traits are called eQTLs. eQTLs located near the gene-of-origin (gene which produces the transcript or protein) are referred to as local eQTLs or cis-eQTLs. By contrast, those located distant from their gene of origin, often on different...

Complex traits Examples of complex traits in humans include height; intelligence and cognitive function; body-mass index; blood pressure; and risk for complex diseases such as diabetes, heart disease, Alzheimer's disease, and schizophrenia. A central goal of contemporary genetics research is to understand the molecular mechanisms by which genetic variation influences complex traits. Complex traits, also known as polygenic or multigenic traits, are phenotypes determined by the interaction of multiple genetic and environmental factors Complex traits, also known as polygenic or multigenic traits, are phenotypes determined by the interaction of multiple genetic and environmental factors

Expression quantitative trait loci For example, traits quantified by protein levels are instead referred to as protein QTLs (pQTLs). While the term QTL can refer to a wide range of phenotypic traits, the more specific eQTL refers to traits measured by gene expression, such as mRNA levels. Although named "expression QTLs", not all measures of gene expression can be used for eQTLs. While the term QTL can refer to a wide range of phenotypic traits, the more specific eQTL refers to traits measured by gene expression An expression quantitative trait locus (eQTL) is a type of quantitative trait locus (QTL), a genomic locus (region of DNA) that is associated with phenotypic variation for a specific, quantifiable trait. quantifiable trait

FTO gene As one homolog in the AlkB family proteins, it is the first messenger RNA (mRNA) demethylase that has been identified. Certain alleles of the FTO gene appear to be correlated with obesity in humans. As one homolog in the AlkB family Fat mass and obesity-associated protein, also known as alpha-ketoglutarate-dependent dioxygenase FTO, is an enzyme that in humans is encoded by the FTO gene located on chromosome 16. alpha-ketoglutarate-dependent dioxygenase FTO, is an enzyme that in humans is encoded by the FTO gene located on chromosome 16

There are many different ways to use the term "gene" based on different aspects of... Pleiotropy can result from several distinct but potentially overlapping mechanisms, including gene pleiotropy, developmental pleiotropy, and selectional pleiotropy. Gene pleiotropy occurs when a gene product interacts with multiple proteins or catalyzes different reactions. Developmental pleiotropy refers to mutations that produce several phenotypic effects during development. Selectional pleiotropy occurs when a single phenotype influences evolutionary fitness in multiple ways (depending on factors such as age and sex). The amino acid sequence of the transcribed FTO protein shows high similarity with the enzyme AlkB which oxidatively demethylates DNA. FTO is a member of the superfamily of alpha-ketoglutarate-dependent hydroxylase, which are non-heme iron-containing proteins. Recombinant FTO protein was first discovered to catalyse demethylation of 3-methylthymine in single-stranded DNA, and 3-methyluridine in single-stranded RNA, with low efficiency. The nucleoside N6-methyladenosine (m6A), an abundant modification in RNA, was then found to be a major substrate of FTO. The FTO gene expression was also found to be significantly upregulated in the hypothalamus of rats after food deprivation and strongly negatively correlated with the expression of orexigenic galanin-like peptide which is involved in the stimulation... Historically, many traits were thought to be governed by a single causative gene (in what is deemed monogenic inheritance), however work in genetics revealed that these traits are comparatively rare, and in most cases so-called monogenic traits are predominantly influenced by one gene, but can be mediated by other genes of small effect.

Pleiotropy Mutations in pleiotropic genes can affect several traits simultaneously, often because the gene product is used in various cells and affects different biological targets through shared signaling pathways. A gene that has such multiple effects is referred to as a pleiotropic gene. when a variant or gene is associated with more than one trait: Biological pleiotropy, where a genetic variant directly affects multiple traits through Pleiotropy (from Ancient Greek πλείων (pleiōn) 'more' and τρόπος (trópos) 'turn, way, manner, style') is a condition in which a single gene or genetic variant influences multiple phenotypic traits

== Function == Definitions == Personality is influenced by genetic and environmental factors and associated with mental health. Beside the environment factor, genetic variants can be detected for personality traits. These traits are polygenic. Significant genetic variants are present for most of the behavioral traits. There is a consistency in detection of genetic variants and genomic association for traits derived from pedigree. Circadian rhythms are coordinated physiological and biological changes that oscillate on an approximately 24-hour cycle. Disruptions to these rhythms in humans may affect the duration, onset, and/or quality of sleep during this cycle, resulting in familial sleep traits. These traits are not necessarily syndromes because they do not always cause distress among individuals. Instead of being disorders, familial sleep traits are variations in an individual's biological tendencies of sleep-wake times, and are only considered

syndromes if affected individuals complain about life interference, in which case they may fall under the category of Circadian Rhythm Sleep Disorders (CRSD) that affect sleep timing and circadian rhythms. Some of these circadian disorders include Advanced Sleep Phase Disorder (ASPD) and Delayed Sleep Phase Disorder (DSPD). Familial sleep traits are more specific than CRSD because they are heritable and involve a wide range of Mendelian genes. Evidence has shown that genes significantly influence sleep schedules in mammals, including... 4f40bdfa03 A gene can acquire mutations in its sequence, leading to different variants, known as alleles, in the population. These alleles encode slightly different versions of a gene, which may be expressed as different phenotypic traits. 4f40bdfa03 Genes and their regulatory sequences are mainly responsible for determining the physical traits, or the phenotype of an organism. The genotype is the total amount of DNA in an organism including genes, other functional elements, and non-functional DNA. 4f40bdfa03 == History == 4f40bdfa03 There are also three main types of genetic pleiotropic effects when a variant or gene is associated with more than one trait: 4f40bdfa03

Gene-environment interaction example shows that a change in environment (lowering Phenylalanine consumption) can affect the phenotype of a particular trait, demonstrating a gene-environment Gene-environment interaction (or genotype-environment interaction or G×E) is when two different genotypes respond to environmental variation in different ways. Environmental variation can be physical, chemical, biological, behavior patterns or life events. This indicates that each genotype responds to environmental variation in a different way. A norm of reaction is a graph that shows the relationship between genes and environmental factors when phenotypic differences are continuous. When the norm of reaction is not parallel, as shown in the figure below, there is a gene by environment interaction. They can help illustrate G×E interactions 4f40bdfa03

Biological pleiotropy, where a genetic variant directly affects... 4f40bdfa03 == Distant and local, trans- and cis-eQTLs, respectively == 4f40bdfa03 For humans, the Big Five personality traits, also known as the five-factor model (FFM) or the OCEAN model, is the prevailing model for personality traits. When factor analysis (a statistical technique) is applied to personality survey data, some words or questionnaire items used to describe aspects of personality are often applied to the same person. For example, someone described as conscientious is more likely to be described as "always prepared" rather than "messy". This theory uses descriptors of common language and therefore... 4f40bdfa03 Populations evolve when the frequencies of alleles shift due mostly to natural selection and genetic drift. Some of these alleles are located in genes. 4f40bdfa03

Genomics of personality traits environment factor, genetic variants can be detected for personality traits. Significant genetic variants are present for most of Personality traits are patterns of thoughts, feelings and behaviors that reflect the tendency to respond in certain ways under certain circumstances. These traits are polygenic 4f40bdfa03

Oligogenic inheritance Oligogenic inheritance represents an intermediate between monogenic inheritance in which a trait is determined by a single causative gene, and polygenic inheritance, in which a trait is influenced by many genes and often environmental factors. causative gene, and polygenic inheritance, in which a trait is influenced by many genes and often environmental factors. Historically, many traits were thought Oligogenic inheritance (Greek ὀλίγος – ὀλιγος = few, a little) describes a trait that is influenced by a few genes 4f40bdfa03

== Trait theory == 4f40bdfa03 == History == 4f40bdfa03 Around the 1930s/40s, evidence that multiple genes could affect the risk of disease that showed discrete inheritance patterns, due to differences in the age of onset of disease for siblings. The age of onset for sibling pairs was very similar, but between pairs of siblings could be quite different, and would in some cases cluster into several age brackets. This suggested a major gene that controlled the risk for a disease, and other genes that impacted age of onset. 4f40bdfa03 The genetic architecture of complex traits has been explored using statistical approaches such as genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping. 4f40bdfa03

Familial sleep traits Evidence has shown that genes significantly Familial sleep traits are heritable variations in sleep patterns, resulting in abnormal sleep-wake times and/or abnormal sleep length. sleep traits are more specific than CRSD because they are heritable and involve a wide range of Mendelian genes 4f40bdfa03

Personality trait research has been conducted both for humans and non-human animals like dogs. 4f40bdfa03

Dominance (genetics) phenomenon of one variant (allele) of a gene on a chromosome masking or overriding the effect of a different variant of the same gene on the other copy In genetics, dominance is the phenomenon of one variant (allele) of a gene on a chromosome masking or overriding the effect of a different variant of the same gene on the other copy of the chromosome. This state of having two different variants of the same gene, one on each copy of the chromosome, is originally caused by a mutation in one of the genes, either new (de novo) or inherited. Additionally, there are other forms of dominance, such as incomplete dominance, in which a gene variant has a partial effect compared to when it is present on both chromosomes, and co-dominance, in which different variants on each chromosome both show their. Since there is only one Y chromosome, Y-linked traits cannot be dominant or recessive. The masking or overriding variant is said to be dominant and the other recessive. The terms autosomal dominant and autosomal recessive are used to describe gene variants on non-sex chromosomes (autosomes) and their associated traits, while those on sex chromosomes (allosomes) are termed X-linked dominant, X-linked recessive or Y-linked; these have an inheritance and presentation pattern that depends on the sex of both the parent and the child (see Sex linkage) 4f40bdfa03

Gene-environment interactions are studied to gain a better understanding of various phenomena. In genetic epidemiology, gene-environment interactions are useful for understanding some diseases. Sometimes, sensitivity to environmental risk factors for a disease are inherited rather than the disease itself being inherited. Individuals with different genotypes are affected differently by exposure to the same environmental factors, and thus gene-environment interactions can result in different disease phenotypes. For example, sunlight exposure has a... 4f40bdfa03

Gene The Mendelian gene is a basic unit of heredity. The molecular gene is a sequence of nucleotides in DNA that is transcribed to produce RNA. During gene expression (the synthesis of RNA or protein from a gene), DNA is first copied into RNA. alleles encode slightly different versions of a gene, which may be expressed as different phenotypic traits. There are two types of molecular genes: protein-coding genes and non-coding genes. Populations evolve when the frequencies of alleles In biology, the word gene has two meanings. RNA can be directly functional or be the intermediate template for the synthesis of a protein 4f40bdfa03

The recognition of... 4f40bdfa03

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