dnamind

optimal health for life

Welcome

SUMMER

to your dna mind report

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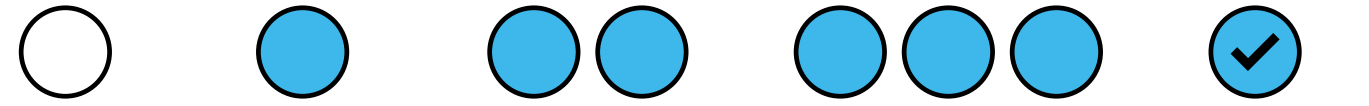
Referring Practitioner:		

Introduction

From your buccal swab sample we have used a process called the Polymerase Chain Reaction (PCR), which copies the DNA of your genes many times over so that we can generate sufficient quantities to analyse your genetic material. We then identify unique DNA sequences in some of your genes. Certain changes (polymorphisms) in these genes have been studied in detail, with evidence that correlates these polymorphisms with an individual's risk of developing certain chronic disease conditions or altered metabolic processes. Having identified the presence or absence of these polymorphisms, we are able to qualitatively assess particular areas of health risk related to the specific genes. To make a holistic assessment of health risks, environmental factors (diet and lifestyle) need to be considered in conjunction with the accompanying genetic profile.

How to read your results

You will find your genetic results in the following pages. On the left side you will see the gene name and description as well as your specific result and an explanation. The impact can be identified by the following:



No Impact | Low Impact | Moderate Impact | High Impact | Beneficial Impact

Introduction to DNA Mind

DNA Mind tests for genetic variations associated with changes in key biological areas that affect mental health. Weaknesses in these areas, together with environmental factors, increase risk for development of disorders related to mental health. The areas of mental health reported in DNA Mind include: Neurodegenerative disorders, mood regulation, and addictive behaviour.

Neurodegenerative disorders

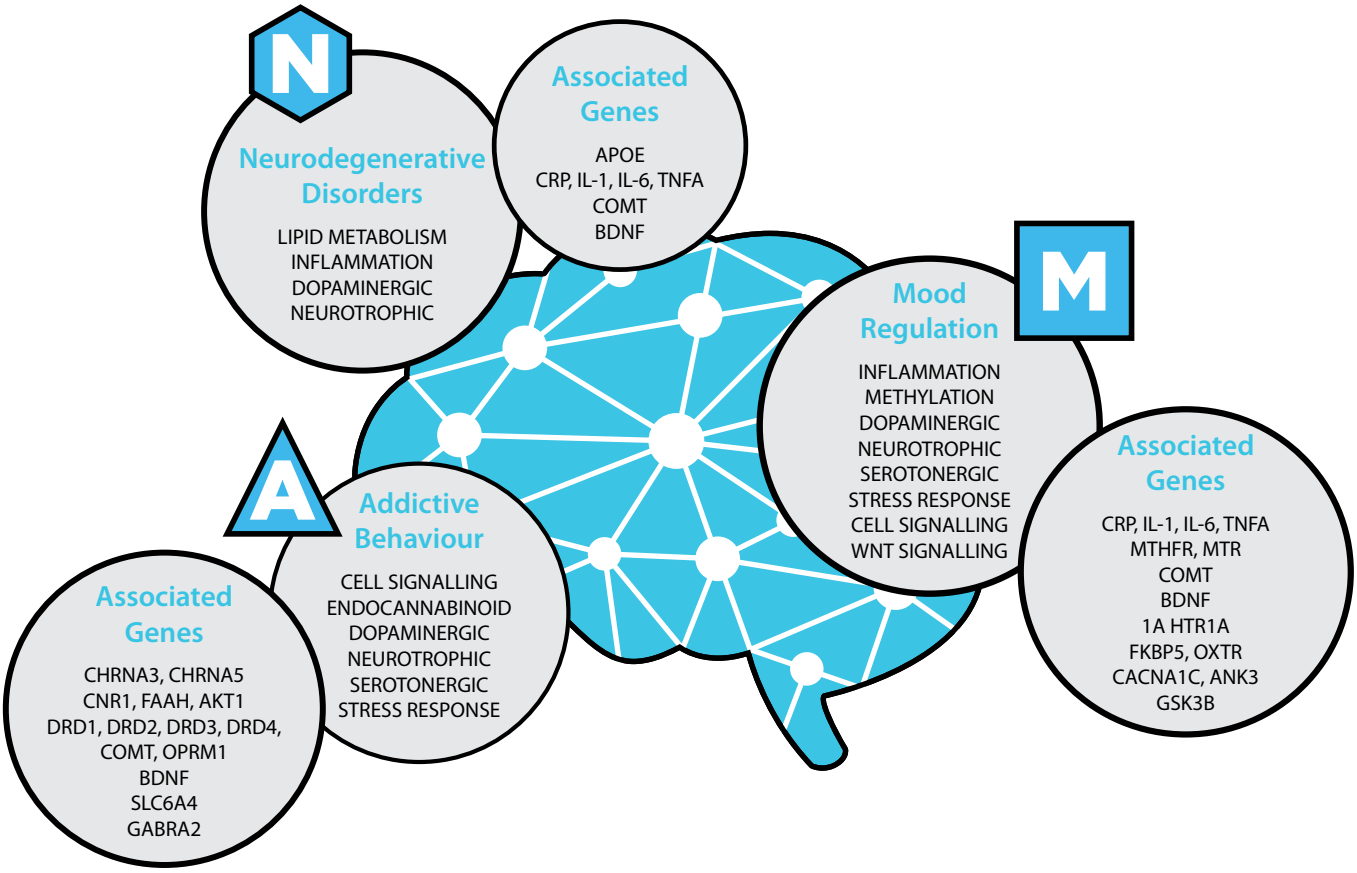
Mild cognitive impairment (MCI) causes a slight, but noticeable and measurable decline in cognitive abilities, including memory and thinking skills. Individuals with mild cognitive impairment are at an increased risk of developing Alzheimer's Disease (AD) or another dementia. Altered functioning of specific biological areas have been related to increased risk of MCI as well as late-onset AD.

Mood regulation

Mood disorders are psychological disorders that are characterized by the elevation or lowering of an individual's mood, to the extent that it can interfere with everyday life for an extended period of time. The specific mood areas reported on include bipolar, depression, anxiety and post-traumatic stress disorder.

Addictive behaviours

Addictive behaviour can manifest in a number of disorders, which are complex in their aetiology and are influenced by both genetic and environmental factors. Genetics and addictive areas of association include behavioural disorders such as eating disorders (binge eating), 'adrenaline seeking', and risk-taking behaviour. Substance use disorders include risk for alcohol, nicotine, cannabis and opioid dependence. This area will also report on psychosis response from cannabis use.



Summary table of results

Biological Area	Gene Name	Genetic Variation	Your Result	Impact N	Impact M	Impact A
Lipid metabolism	APOE	E2/E3/E4	E3/E3			
Inflammation	CRP	G>A	GA			
	IL1-A	4845 G>T	GG			
		-889 C>T	CC			
	IL1-B	3954 C>T	CC			
		-511 A>G	AA			
	IL1-RN	2108 C>T	CT			
	IL-6	-174 G>C	GG			
	TNFA	-308 G>A	AG			
Methylation	MTHFR	677 C>T	CT			
		1298 A>C	CA			
	MTR	2756 A>G	AA			
Wnt Signalling	GSK3B	C>G	CC			
		A>C	AC			
		G>A	AG			
Stress Response	FKBP5	C>T	CC			
	OXTR	G>A	AG			
Cell Signalling	AKT1	T>C	CT			
	ANK3	A>G	AA			
		C>T	CC			
	CACNA1	G>A	GG			
	CHRNA3	G>A	GG			
	CHRNA5	Asp398Asn	GG			
Dopaminergic	COMT	Val158Met	AG			
	DRD1	T>C	CT			
		C>T	CC			
	DRD2	Taq1A/2A	CC			
	DRD3	Ser9Gly	TT			
	DRD4	-521 C>T	CT			
	OPRM1	Asn40Asp	AG			
Endocannabinoid	CNR1	T>C	TT			
	FAAH	385 C>A	CC			
GABAergic	GABRA2	T>C	TT			
Neurotrophic	BDNF	Val66Met	CC			
Serotonergic	1A HTR1A	-1019 C>G	CG			
	SLC6A4	A>C	AC			

Lipid metabolism

Apolipoprotein E is an important protein in the lipid metabolism pathway and has been implicated as the major gene target for risk of Late Onset Alzheimer's Disease (LOAD). ApoE plays multiple roles in the pathogenesis of LOAD; affecting Aβ deposition, Tau phosphorylation and neurofibrillary tangle formation, as well as neuro-inflammation. It should be noted that environmental factors are also important risk mediators of LOAD.

APOE E2/E3/E4

APOE encodes Apoliprotein E, a lipid-transporting protein functioning in both the periphery and the central nervous system. It is involved in multiple biological processes related to AD development and progression. Two SNPs on APOE results in three possible isoforms. The isoform affects the structure and function of apoE including binding to lipids, receptors and Aβ.

YOUR RESULT: **E3/E3**

The APOE E3/E3 genotype is the most common in the general population and encodes a 'normal' protein.

Carriers of the APOE E3/E3 genotype are considered to have the 'neutral' genotype, and are not associated with increased risk for cognitive decline.

Inflammation

Neuroinflammation is recognised as one of the potential mechanisms mediating the onset of a broad range of psychiatric disorders, where studies have shown that abnormal inflammatory responses can result in altered behavioural responses and cognitive deficits. Variations in genes encoding pro-inflammatory cytokines, together with environmental factors, may increase risk for chronic low- grade inflammation and development of psychiatric diseases, including neurodegenerative and mood disorders.

Considering inflammation plays a key role in the pathogenesis of psychiatric disorders, anti-inflammatory therapies may play a critical role in their management.

CRP rs1205 G>A

CRP, encoding C-reactive protein, is an acute phase protein and a marker of inflammation. It's levels are increased with IL-6 secretion by macrophages and T cells.

YOUR RESULT: **GA**

The G allele increases expression of CRP, which is associated with higher levels of CRP in the serum. The G allele has also been associated with AB deposition in the brain.

The G allele increases predisposition to disorders related to chronic inflammation. The G allele has been associated with an increased risk for cognitive decline.
Focus on lifestyle interventions to decrease inflammation, including increasing intake of omega 3 fatty acids.

IL-1: IL-1A, IL1-B & IL-1RN

IL-1 has been increasingly implicated as an important leverage point in the inflammatory cascade, and IL-1 expression is therefore key in the pathogenesis of several chronic diseases. The biological activity of IL-1 involves the two agonists – IL-1alpha (IL-1A) and IL-1beta (IL-1B), specific IL-1 receptors, and an IL-1 receptor antagonist (IL-1RN), which is a negative regulator of the pro-inflammatory response. Certain genetic variations in IL-1A, IL-B and IL-1 RN lead to a more active inflammatory response, and have been associated with increased risk for a number of chronic diseases.

YOUR RESULT:

This specific IL-1 genotype combination is not associated with increased risk for chronic, low-grade inflammation.

This specific IL-1 genotype combination has not been associated with increased susceptibility to neurodegenerative or mood disorders.

IL-6 -174 G>C

Interleukin 6 is a pro-inflammatory cytokine that plays a crucial role in inflammation and regulates expression of CRP.

YOUR RESULT: GG

No variant was detected at the -174 G>C locus. The IL-6 GG genotype is the wild type, and has been associated with normal expression of IL-6 and therefore no increased risk for chronic, low-grade inflammation.

Individuals carrying the GG genotype have not been associated with increased risk for mental health disorders such as cognitive decline and depressive disorder.

TNFA -308 G>A

Tumour necrosis factor-α (TNFα) is a proinflammatory cytokine, secreted by both macrophages and adipocytes and has been shown to alter whole body glucose homeostasis.

YOUR RESULT: **AG**

The A allele results in a two-fold increase in TNFA transcription, which leads to elevated levels of the circulating TNFα protein, and has been associated with increased risk for inflammation.

Individuals with the A allele has been associated with an increased susceptibility for cognitive decline and depressive disorder, including treatment resistant depression. In the presence of the A allele, increase intake of n-3 fatty acids and moderate n-6 fatty acid and saturated fat intake. If dietary intake of n-3 fatty acids is inadequate, supplementation may be required. Weight management is also imperative in managing inflammation. It is also important to consider psychosocial stressors and manage accordingly.

Methylation

Methylation involves the process of creating methyl groups that can be added to a molecule, or substrate, and plays an essential role in the production of neurotransmitters. In order for methylation reactions to be completed, specific amounts of B-vitamins are required. B-vitamins are nutrients that are derived from the diet. Poor methylation function due to enzymatic deficiencies as well as low levels of B-vitamins have been associated with increased risk of mood disorders.

MTHFR

Methylene tetrahydrofolate reductase, encoded by MTHFR, catalyzes the conversion of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which is a co-substrate for homocysteine remethylation to methionine. Reduced enzyme activity, due to function-reducing polymorphisms, results in the impairment of homocysteine metabolism and the folate cycle, leading to a decreased ability to synthesise important neurotransmittors.

MTHFR 677 C>T

YOUR RESULT: **CT**

The MTHFR 677 CT genotype results in a 30% reduction in enzyme function and is associated with risk of higher homocysteine levels and a decreased ability to synthesise neurotransmitters.

The MTHFR 677 CT genotype results in a 30% reduction in enzyme function and is associated with risk of increased homocysteine levels and mood disorders, including depressive disorder, when B-vitamin intake, and folate levels, are low. T allele carriers may have increased B-vitamin, specifically folate, requirements. Consider the use of methyl folate if clinically indicated.

MTHFR 1298 A>C

YOUR RESULT: **CA**

The MTHFR 1298 CA genotype results in altered enzyme function and is associated with risk of higher homocysteine levels and a slight decreased efficiency for neurotransmitter synthesis.

The MTHFR 1298 CA genotype is associated with increased susceptibility to mood disorders, including depressive and bipolar disorders, especially when B-vitamin intake, and folate levels, are low. MTHFR 1298 C allele carriers may have increased B-vitamin requirements, and methyl folate may be especially beneficial. Extra emphasis should be placed on this SNP when the MTHFR 677 CT heterozygous

MTR 2756 A>G

MTR encodes methionine synthase, which is responsible for the regeneration of methionine from homocysteine, using 5-methyltetrahydrofolate as its essential co-factor. This enzyme is dependent of methylcobalamin, and forms part of the S-adenosylmethionine (SAMe) biosynthesis and regeneration cycle.

YOUR RESULT: **AA**

No variant was detected at the 2756 A>G locus, and is associated with normal enzyme capacity.

The AA genotype has no association with increased risk for mood disorders.

Wnt Signalling

Wnt signaling pathways are a group of signal transduction pathways made of glycoproteins that pass signals into a cell through cell surface receptors. The Wnt signaling pathway regulates critical aspects of cell fate determination, cell migration, cell polarity, neural patterning and organogenesis during embryonic development.

GSK3B

GSK3B encodes the B-isoform of glycogen synthase kinase 3, which is expressed abundantly in the central nervous system and has been implicated in several neuropsychiatric disorders, including bipolar and major depressive disorder. It is an important target protein of several anti-depressants, including lithium, and upregulation of GSK3B is associated with increased risk for mood disorders.

GSK3B rs334555 C>G, rs11925868 A>C, rs11927974 G>A

YOUR RESULT: **Neutral**

The genotype combination is associated with normal regulation of GSK3B.

Individuals carrying this combination of gene variations on GSK3B are not at an increased risk for bipolar disorder.

Stress response

Stress exposure is known to precipitate mental disorders, however, even though stress is part of daily life, there is large interindividual variability that exists in the development of stress-related psychopathology. An important marker of stress sensitivity is hypothalamus–pituitary–adrenal (HPA)-axis function, and variation in stress-induced cortisol responses may predict differences in neural vigilance processing during stress exposure.

Oxytocin also plays an important role in stress a management, and genetic variation in the oxytocin receptor gene (OXTR) has been implicated in anxiety, depression and related stress phenotypes.

FKBP5 rs1360780 C>T

The FK506 binding protein, encoded by FKBP5, acts as a co-chaperone that modulates not only glucocorticoid receptor activity in response to stressors but also a multitude of other cellular processes in both the brain and periphery. Notably, the FKBP5 gene is regulated via complex interactions among environmental stressors, FKBP5 genetic variants, and epigenetic modifications of glucocorticoid-responsive genomic sites.

YOUR RESULT: **CC**

The CC genotype has been linked to normal FKBP5 expression and an unaltered glucocorticoid receptor activity.

Individuals with the CC genotype may have a better stress management ability compared to those with the CT or TT genotype and, are not at increased risk for post traumatic stress disorder.

OXTR rs53576 G>A

Oxytocin is a peptide hormone and neuropeptide that is involved in the regulation of mood, anxiety and social biology. It plays a role in social bonding, sexual reproduction in both sexes, and during and after childbirth. The protein encoded by the OXTR gene belongs to the G-protein coupled receptor family and acts as a receptor for oxytocin. Its activity is mediated by G proteins which activate a phosphatidylinositol-calcium second messenger system.

YOUR RESULT: **AG**

The A allele is associated with a change in OXTR function such that there is decreased sensitivity to social cues, especially in a stressful environment.

Individuals with the AG genotype may have a lower empathetic ability and a decreased ability to manage stressful situations, with an increased risk for post-traumatic stress disorder, especially with exposure to adverse child events.
Individuals who carry the risk variant may require more intensive follow up after exposure to an environmental stressor.

Cell signalling

Genes encoding proteins involved in cell signalling are important in ensuring normal cell-to-cell communication among nerve cells (neurons), neuronal survival, and the formation of memories. Cell-signalling proteins also serve important roles in activating the release of specific neurotransmitters and hormones.

Calcium and sodium signalling controls many neurological functions, including neurotransmitter release and regulation of excitatory signalling in the brain. Disruptions in these pathways have been linked to altered mood regulation, specifically bipolar disorder.

AKT1 rs2494732 T>C

AKT1 encodes one of 3 closely related serine/threonine-protein kinases (AKT1, AKT2 and AKT3) and is important in regulating many processes including metabolism, proliferation, cell survival, growth and angiogenesis. AKT1 SNPs have been linked to paranoia and psychosis with cannabis use.

YOUR RESULT: **CT**

The AKT1 TC genotype is possibly associated with altered gene function.

Individuals with the TC genotype may have a slightly increased risk for paranoia in response to cannabis use.

ANK3

ANK3 encodes Ankyrin-3, which plays a key role in sodium channel functioning and regulation of excitatory signalling. The gene has been linked to conditions characterised by mood instability.

ANK3 rs1938526 A>G

YOUR RESULT: **AA**

The ANK3 AA genotype has been linked to normal cell signalling capacity.

The AA genotype is considered to be the low risk genotype. Individuals carrying the ANK3 AA genotype are not at increased risk for mood disorders.

ANK3 rs10994336 C>T

YOUR RESULT: **CC**

The ANK3 CC genotype has been linked to normal cell signalling capacity.

The CC genotype is considered to be the low risk genotype. Individuals carrying the ANK3 CC genotype are not at increased risk for mood disorders.

CACNA1C rs1006737 G>A

The CACNA1C gene belongs to a family of genes that provide instructions for making calcium channels. CACNA1C encodes a subunit of L-type voltage gated Calcium Channel, involved in excitatory signaling in the brain, and has been linked to conditions characterised by mood instability.

YOUR RESULT: **GG**

The CACNA1 GG genotype is associated with an unaltered brainstem volume and regular CACNA1 excitatory signalling.

The GG is not associated with any increased risk to depressive and/or bipolar disorder.

CHRNA3 rs16969968 G>A

CHRNA3 encodes the nicotinic acetylcholine receptor alpha 3 subunit. The encoded protein is a ligand-gated ion channel that likely plays a role in neurotransmission and release of neurotransmittors after exposure to a stimulant such as with nicotine intake.

YOUR RESULT: **GG**

The GG genotype is associated with normal receptor function.

This genotype shows no increased risk for a high number of cigarettes smoked per day.

CHRNA5 Asp398Asn / D398N

CHRNA5 encodes the nicotinic acetylcholine receptor alpha 5 subunit. The encoded protein is a ligand-gated ion channel that likely plays a role in neurotransmission and release of neurotransmittors after exposure to a stimulant such as with nicotine intake.

YOUR RESULT: **GG**

The GG genotype is associated with normal receptor function.

Individuals with the GG genotype do not show an increased susceptibility for nicotine dependence.

The dopaminergic pathway and dopamine response

Dopamine is an excitatory neurotransmitter in the catecholamine family that is synthesized in the brain, and is responsible for modulating reward and pleasure. Dopamine actions include areas of reward, cognition, working memory, and motor coordination. Alterations in dopamine production, breakdown, and receptor function may increase susceptibility to cognitive decline, altered mood regulation and addictive behaviour disorders, including risk for substance abuse, risk-seeking behaviour and binge eating disorders.

COMT Val158Met

COMT, encoding the catechol-O-methyl transferase enzyme, is responsible for methylation of catecholamines, thereby regulating dopamine (DA) levels primarily in the prefrontal cortex. The COMT Val158Met SNP strongly determines enzyme function, and has been associated with differences in neural processes underlying cognitive output and breakdown of excitatory neurotransmittors.

YOUR RESULT: **AG**

The COMT AG genotype is associated with intermediate enzymatic activity.

The COMT AG genotype is associated with low risk for cognitive function disorders, as well as a low risk for addictive behaviour. Due to the slightly slower catecholamine breakdown, individuals with the GA genotype may be slightly susceptible to anxiety-related disorders.

DRD1

DRD1 encodes the D1 subtype of the dopamine receptor, which is the most abundant dopamine receptor in the central nervous system. D1 receptors regulate neuronal growth and development, mediate some behavioral responses, and modulate dopamine receptor D2-mediated events. Dopamine D1 Receptor is involved in regulation of dopamine release in accumbens.

DRD1 rs4532 T>C

YOUR RESULT: **CT**

Due to the C to T substitution that occurs on this SNP, it may act in inhibiting it receptor translation, changing the functionality of the DRD1 receptor.

This CT genotype may be mildly associated with alcohol dependence and associated disorders including bipolar disorder and novelty seeking, as well as behavioural persistence and harm avoidance behaviour characterized as anticipatory worry, fear of uncertainty, and shyness.

DRD1 rs5326 C>T

YOUR RESULT: **CC**

The CC genotype is associated with an unaltered DRD1 translation.

Individuals with the CC genotype have not shown an increase in risk to addictive behaviours.

DRD2 Taq1A/2A

DRD2 encodes the D2 subtype of the dopamine receptor, which is integral in the reward-circuitry pathway. The gene has been linked to co-morbid substance use disorders as well as risk seeking and binge eating behaviour.

YOUR RESULT: **CC**

The CC genotype is associated with normal dopamine receptor function.

Carriers of the CC genotype do not show increased susceptibility for addictive behaviours and co-morbid substance use disorders.

DRD3 Ser9Gly

DRD3 encodes the D3 subtype of the dopamine receptor. This receptor is localized to the limbic areas of the brain, which are associated with cognitive, emotional, and endocrine functions.

YOUR RESULT: **TT**

The TT genotype is linked to normal DRD3 activity.

The TT genotype has not been linked to increased risk for addictive behaviour.

DRD4 -521 C>T

DRD4 encodes the D4 subtype of the dopamine receptor, which is integral in the reward-circuitry pathway. The gene has been linked to novelty seeking, substance dependence vulnerability, as well as ADHD.

YOUR RESULT: **CT**

The T allele leads to a reduction of dopamine D4 receptors at the synapse, altering dopaminergic response.

The DRD4 T allele, but more so the TT genotype, may predispose to increased risk for opioid dependence. The C allele is associated with novelty seeking behaviour.
Having insight to risk for opioid dependence may assist with early intervention and therapeutic management.

OPRM1 Asn40Asp (118 A>G)

OPRM1 encodes the mu opioid receptor (MOR), which is the principal target of endogenous opioid peptides and opioid analgesic agents such as beta-endorphin and enkephalins. MOR also has an important role in dependence to other drugs of abuse, such as nicotine, cocaine, and alcohol via its modulation of the dopamine system.

YOUR RESULT: **AG**

The G allele alters μ opioid receptor availability and is associated with a threefold increase in β-endorphin binding affinity and potency.

OPRM1 G allele carriers are associated with increased risk for alcoholism and opioid dependence and may also experience stronger cravings. Carriers of the G allele may also have increase pain sensitivity.
Having insight to risk for opioid and alcohol dependence may assist with early intervention and appropriate therapeutic management.

Endocannabinoid pathway

Cannabinoids, principally delta-9-tetrahydrocannabinol (Δ9-THC) & synthetic analogs, are psychoactive ingredients of marijuana. Cannabinoids bind to central cannabinoid (CB1) receptors where they mimic the effects of endogenously produced cannabinoids. Studies suggest that cannabinoids increase dopamine (DA) activity in the nucleus accumbens (Nac) and prefrontal cortex (PFC) by activating CB1 receptors in the ventral tegmental area (VTA), which increase DA neuronal firing and burst rates.

In this panel, genetic variants will be reported on that have been shown to increase risk for dependence on cannabis as well as other illicit substances.

CNR1 rs2023239 A>G

CNR1 gene encodes 1 of 2 cannabinoid receptors. Cannabinoids, principally delta-9-tetrahydrocannabinol (THC) bind to central cannabinoid, or CB1, receptors, in which it mimics the effects of endogenously produced cannabinoids. The gene has a role in modulating endocannabinoid and DA-mediated reward signaling.

YOUR RESULT: **TT**

The TT genotype is associated with normal CNR1 function and thus normal reward signalling in this area.

The TT genotype does not confer increased risk to addictive behaviour or dependence on comorbid substances and cannabinoids.

FAAH 385 C>A

FAAH encodes Fatty Acid Amide Hydrolase, which is an enzyme that is expressed in the brain and liver.

It de-activates N-arachidonoyl-ethanolamine, an endogenous central cannabinoid 1 agonist. FAAH plays an important role in pain, depression, appetite, and inflammation, and has been shown to be associated with risk for substance abuse.

YOUR RESULT: **CC**

The CC genotype individuals appear to show greater activation in widespread areas within the reward circuit as compared with the FAAH A-allele carriers after a stimulus.

The FAAH CC genotype is not linked to increased risk for addictive disorders. Even though there is less risk for addiction, it is important to note that there may be more difficulty with withdrawal for CC genotype carriers compared to AA individuals.

The GABAergic pathway

Externalising behaviour is considered to be a strong predictor of early-onset substance use and substance use disorder in adulthood and, the GABAergic pathway has been implicated in this behaviour.

Gamma-aminobutyric acid (GABA) is a neurotransmitter that is expressed predominantly in the central nervous system and is the major inhibitory neurotransmitter. Neuronal activity in the brain is regulated by excitatory inputs and inhibitory activity, including GABAergic inhibitory activity. Stimulation of the inhibitory GABAergic activity, either by endogenous ligands or certain drugs such as benzodiazepines, results in sedation, amnesia and ataxia, while attenuation of the GABAergic system leads to arousal, anxiety, restlessness, insomnia and exaggerated reactivity.

GABRA2 rs279858 T>C

GABRA2 encodes the gamma-aminobutyric acid receptor subunit alpha-2. GABA is the major inhibitory neurotransmitter in the mammalian brain where it acts at GABA-A receptors, which are ligand-gated chloride channels. Chloride conductance of these channels can be modulated by agents such as benzodiazepines (BZDs) that bind to the GABA-A receptor, where stimulation of the inhibitory GABAergic activity results in sedation, amnesia and ataxia.

YOUR RESULT: **TT**

The TT genotype is associated with normal receptor function, and does not have an altering effect GABA-ergic pathway.

The TT genotype is has not been linked to externalising behaviour or increased risk for addictive disorders.

The neurotrophin pathway

Neurotrophins are a family of trophic factors involved in differentiation and survival of neural cells. The neurotrophin family consists of nerve growth factor (NGF), brain derived neurotrophic factor (BDNF), neurotrophin 3 (NT-3), and neurotrophin 4 (NT-4). Function and signalling of neurotrophin plays an important role for neural development and additional higher-order activities such as learning and memory.

BDNF Val66Met

BDNF, encoding brain derived neurotrophic factor, is a member of the nerve growth factor family of proteins. It is believed to promote many aspects of brain development, such as neuronal cell survival, differentiation, migration, dendritic arborization, synaptogenesis, and plasticity. It is proposed that this gene may take part in the regulation of the stress response and in the biology of neurodegenerative and mood disorders. The gene has also been linked to a number of addictive behaviours, including binge eating disorder.

YOUR RESULT: **CC**

The BDNF CC genotype leads to normal expression of BDNF.

The CC genotype is the wild type and is considered to have normal BDNF expression and function, with an unaltered risk for mental health disorders.

The serotonergic pathway

Serotonin, or 5-hydroxytryptamine, is a monoamine neurotransmitter that is derived from tryptophan. Serotonin is primarily found in the gastrointestinal tract, as well as blood platelets, and the central nervous system (CNS) and is an important modulator of mood; contributing toward feelings of well-being and happiness. The involvement of serotonin neurotransmission in learning and memory formation via the serotonin receptors may play a modulatory role in the behavioural effects induced by many psychostimulants, providing further understanding of the mechanisms underlying the formation and retrieval of drug-associated memories. Low levels of serotonin are associated with mood disorders, including depression.

1A HTR1A -1019 C>G

Serotonin 1-A (5-HT1A) receptors are critical regulators of the serotonin system. Serotonin receptor HTR1A is a G protein coupled receptor that mediates negative feedback inhibition of serotonergic neurons and signalling in limbic brain regions, including the amygdala.

YOUR RESULT: **CG**

The G allele blocks transcriptional repression, upregulating 5-HT1A activity and increasing auto-receptor expression. This is associated with increased negative feedback and reduced serotonin signalling at post-synaptic sites.

The G-allele confers increased stress reactivity and reduced stress coping that may predispose individuals to depression. The CG genotype has been associated with major depressive disorder and bipolar disorder. The G allele may also be related to increased impulsivity-related behavior.
Consider stress management strategies, improving gut health, as well as including tryptophan-rich foods.
G-allele carriers may also associate with reduced responses to therapies that modify the 5-HT system.

SLC6A4 -rs1042173 A>C

SLC6A4 encodes Solute Carrier Family 6 Member 4, which is an integral membrane protein that transports the neurotransmitter serotonin from synaptic spaces into presynaptic neurons, terminating the action of serotonin and recycling it in a sodium-dependent manner. This protein is a target of psychomotor stimulants, such as amphetamines and cocaine.

YOUR RESULT: **AC**

The AC genotype may lead to higher SLC6A4 expression.

C-allele carriers do not confer increased risk to addiction related disorders and are also not associated with a heavier alcohol consumption status.

Notes for practitioners

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