

dna health[®]

optimal health for life

Welcome

Sample Report

to your dna health[®] detoxification report

Date of Birth: 01 Jan 1980

Date Reported: 11 Nov 2018 11:11

Sample Number: #####-##

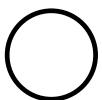
Referring Practitioner: Private

Introduction

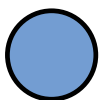
From your buccal swab sample we have used a process called the Polymerase Chain Reaction (PCR), which copies the DNA of your genes many times over so that we can generate sufficient quantities to analyse your genetic material. We then identify unique DNA sequences in some of your genes. Certain changes (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

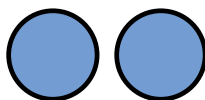
You will find your genetic results in the following pages. On the left side you will see the gene name and description. On the right side you will find your specific result and an explanation of the results, associated risks, and diet and lifestyle recommendations. The impact can be identified by the following:



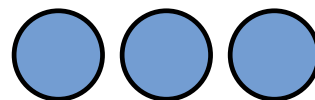
No Impact



Low Impact



Moderate Impact



High Impact



Beneficial Impact

Detoxification

The detoxification process in the body is governed primarily by the GST family of enzymes. Glutathione S-transferases are responsible for catalysing reactions in which the products of Phase I metabolism are conjugated with glutathione, thus making them more water soluble and more easily excreted from the body through sweat and urine. Cruciferous and allium vegetables help increase the activity of your detoxification system, which aids the removal of harmful substances from your body.

Gene Name	Genetic Variation	Your Result	Gene Impact
CYP1A1	Msp1 T>C	CT	
	Ile462Val A>G	GA	
GSTM1	Insertion/Deletion	Insertion	
GSTP1	313 A>G	AG	
GSTT1	Insertion / Deletion	Deletion	
NQ01	NQ01 C>T	TC	

Phase I Detoxification

CYP1A1 Msp1 T>C

The CYP1A1 gene encodes a phase I cytochrome P450 enzyme that converts environmental procarcinogens such as PAHs and aromatic amines to reactive intermediates having carcinogenic effects. In addition, CYP1A1 is involved in the oxidative metabolism of oestrogens, which may play a critical role in the aetiology of breast and prostate cancer.

YOUR RESULT: CT

The variant allele C is associated with increased enzyme activity resulting in elevated levels of activated metabolites and subsequently DNA damage. Many association studies have reported that this SNP increases the development of several types of cancer, especially amongst smokers. In the presence of the C allele it is important to reduce exposure to all diet and environmental procarcinogens such as PAH, aromatic amines, nitrates, and smoking of any kind. In addition attention should be paid to optimising phase 2 detoxification.

CYP1A1 Ile462Val A>G

The CYP1A1 gene encodes a phase I cytochrome P-450 enzyme that converts environmental procarcinogens such as PAHs and aromatic amines to reactive intermediates having carcinogenic effects. In addition, CYP1A1 is involved in the oxidative metabolism of oestrogens, which may play a critical role in the aetiology of breast and prostate cancer.

YOUR RESULT: GA

An A to G substitution leads to an amino acid substitution (ile to val) of its protein. The association between this SNP and cancer has been well documented.

The variant allele G increases enzyme activity resulting in increased rates of carcinogen activation and subsequently DNA damage. In the presence of the G allele it is important to reduce exposure to all diet and environmental procarcinogens such as PAH, aromatic amines, nitrates, and smoking of any kind. In addition attention should be paid to optimising phase 2 detoxification.

Detoxification continued

Phase II Detoxification

GSTM1 Insertion/Deletion

Glutathione S-transferase M1 is the most biologically active member of the GST super-family and is involved in Phase II detoxification in the liver. It is responsible for the removal of xenobiotics, carcinogens, and products of oxidative stress.

YOUR RESULT: **Insertion**

No deletion was detected.

GSTP1 313 A>G

Oxidative stress is a risk factor shared by most disorders implicating GST, and it appears that the efficiency of the GSTP1 enzyme may have an impact on the development and prognosis of diseases influenced by oxidative stress. GSTP1 is the most abundant GST subtype in the lungs and is known to metabolize many carcinogenic compounds.

YOUR RESULT: **AG**

The G allele decreases activity of the enzyme. Conjugation activity is around 80% for carriers of one G allele, and 70% for the GG genotype individuals.

GST enzyme activities are induced in part by the products of cruciferous and allium vegetables. These should be increased significantly in the diet to increase activity of other GST enzymes to compensate for decreased activity. Daily intake is recommended. When dietary intake is inadequate a high quality supplement containing DIM may be required.

GSTT1 Insertion / Deletion

GSTT1 is a member of a super family of proteins that catalyse the conjugation of reduced glutathione to a variety of electrophilic and hydrophobic compounds.

YOUR RESULT: **Deletion**

The deletion is associated with an increased risk of lung, larynx and bladder cancers, as well as skin basal carcinomas.

GST enzyme activities are induced in part by the products of cruciferous and allium vegetables. These should be increased significantly in the diet to increase activity of other GST enzymes to compensate for decreased activity. Daily intake is recommended. When dietary intake is inadequate a high quality supplement containing DIM may be required.

Detoxification continued

Phase II Detoxification continued

NQ01 609 C>T

NADP(H:) quinone oxidoreductase 1 (NQO1) often referred to as Quinone Reductase is primarily involved in the detoxification of potentially mutagenic and carcinogenic quinones derived from tobacco smoke, diet and oestrogen metabolism. NQO1 also protects cells from oxidative stress by maintaining the antioxidant forms of ubiquinone and vitamin E.

YOUR RESULT: TC

The variant is a C-to-T transition resulting in a proline to serine amino acid substitution at codon 187 in the protein. The variant T allele results in reduced enzymatic activity. Compared with the wild type CC genotype, the heterozygote variant (TC) has a three-fold decrease in enzyme activity. Individuals with the TC genotype show an increased risk for developing certain cancers including breast, colorectal and gastrointestinal cancers especially when there is exposure to cigarette smoke. The polymorphism has also been linked to benzene toxicity.

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Risks and Limitations

DNAlysis Biotechnology has a laboratory with standard and effective procedures in place for handling samples and effective protocols in place to protect against technical and operational problems. However as with all laboratories, laboratory error can occur; examples include, but are not limited to, sample or DNA mislabelling or contamination, failure to obtain an interpretable report, or other operational laboratory errors. Occasionally due to circumstances beyond DNAlysis Biotechnology's control it may not be possible to obtain SNP specific results.