COGAP

MetaCheck
Gene Diet

Your DNA
Your Diet

Information brochure

WE CARE FOR YOUR CHANGE

Why does everyone metabolize their food differently?

In the course of evolution, humans have adapted to different lifestyles and food conditions, and genetically adjusted their metabolism to it.

On the genetic level, there are small variants in the DNA, so-called polymorphisms, which differ between humans and which can affect the metabolism in its efficiency in the processing of macro-nutrients (carbohydrates, proteins and fats) as well as your calorie consumption during various sporting activities.

In this context, the term nutritional genetics (nutrigenetic) is also used. CoGAP has defined four genetic metabolism-types (Meta-Types).
These genetic variations ensure, among other things, that each person processes the consumed food differently. A conclusion you can relate to in your personal experience every time you encounter lean or stronger family members or friends.

The different Meta-Types

CoGAP distinguishes four Meta-Types: Alpha (α), Beta (β), Gamma (γ) and Delta (δ). In principle, each one of these Meta-Types processes the macronutrients in food differently.

α β γ δ

In addition, CoGAP assigns each Meta-Type one of the two exercise variants, namely E for „Endurance“ or S for „Speed“. According to CoGAP, these exercise variants can result in different calorie consumption rates depending on the type of activity.

Procedure

Consultation and taking of a sample (cheek swab)

Sending the sample to the lab

Analysis and delivery of the results

Follow-up consultation

The analysis result

- Simple and clear presentation for those seeking advice
- Individual nutrition and training recommendations considering personal goals and characteristics (gender, age, height and weight)
- Nutrition list
- Access to the CoGAP nutrition portal
- Access to web-based MetaCheck App
- 5 other important weight loss factors such as the yo-yo effect, muscle mass loss, hunger, satiety, and visceral adipose tissue

The advantages of the concept

For you as a consultant

- Image gain (modern, innovative)
- Patient commitment
- Innovative service
- Easy test management
- High acceptance (45%)[4]** for a personalised nutrition plan

For those seeking advice

- Individually adapted nutrition and exercise recommendations
- Long-term diet changes
- Weight-loss concept based on a single genetic test
- Easy cheek swab sample is enough
- Free access to the CoGAP nutrition portal

[4] Roosen J. et al., (2008); Consumer Demand for Personalized Nutrition and Functional Food; Int. J. Vitam. Nutr. Res., 78(6); S. 269-274.

Scientific basis

Within the framework of the CoGAP MetaCheck®, a complex calculation of genetic interactions is carried out, taking into account only those genes, whose effect is proven in line with the high criteria applied by our scientists.
Our labs analyse only those metabolic gene variants which, according to our research, cover different areas such as carbohydrate or fat metabolism and can be assigned to the individual Meta-Types.

Selection of the analysed metabolic genes

These include in particular metabolic genes of which we are convinced, that they

- are involved in the weight control system,
- that their effect on the body can be positively influenced by a change in nutrition or behaviour and
- differ significantly from person to person.

In addition to the genetic analysis, a comparison is made with scientific studies [6] that must meet the following quality criteria:

- Replicability of study results
- Sufficient number of study participants
- Significance (significance level)
- Validated study methods

Based on these criteria, the following genes were identified after careful valuation of the relevant studies and included in the CoGAP MetaCheck analysis.

[6] www.cogap.de/referenzen.pdf

The specific genes

The **ApoA2** gene encodes apolipoprotein II (apo-II), which is the second most common protein of HDL particles in the body. Changes in the gene lead to an above-average weight gain through absorption of fats.

The **FABP2** gene affects the resorption and oxidation of fats and can lead to insulin resistance. Changes in the gene cause firmer bonds to fatty acids, which greatly affect the absorption of fatty acids in the body. This causes increased absorption of fatty acids in the small intestine, so that extra weight gain is more likely when fatty foods are consumed.

The **FTO** gene is largely expressed in the hypothalamus and in the Langerhans islets of the pancreas. Overexpression of the gene leads to a regulation of energy intake, without being associated with a sense of satiety. Changes in the gene also have an effect on fat burning during repetitive movements. In the presence of such variants of the gene, higher calorie consumption can therefore be achieved through endurance sports.

The **ADRB2** gene encodes a receptor that plays an important role in the conversion of fat molecules into energy. Therefore, the ability to break down fat from fat cells depends heavily on this gene. Furthermore, in certain variants of this gene, endurance sports can be used to reduce weight more quickly and efficiently.

The **ADRB3** gene is mainly expressed in fatty tissue and is involved in the regulation of lipolysis and thermogenesis. Changes in the gene can cause deterioration of lipolysis and reduced fat burning during endurance sports.

The **PPARG** gene plays a central role in the processing of fat molecules. It also has a major effect on glucose insulin metabolism. Certain changes in this gene therefore promote weight gain when carbohydrates and fats are consumed.

The **IL-6** gene encodes a type of cytokine that performs various functions during inflammation and maturation of B-lymphocytes. Carriers of certain variants of the IL-6 gene are more likely to gain extra weight as a result of an inflammatory signal transduction during absorption of carbohydrates.

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