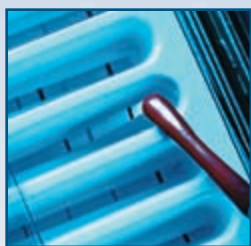


GenoType[®] HH

Based on DNA•STRIP[®] Technology



- simple
- safe
- fast
- easy to combine
- can be automated



CC-labelling
Quality management
certified to ISO 9001



Hereditary Hemochromatosis

Hereditary hemochromatosis (HH), with a prevalence of between 1:200 and 1:400 for homozygous carriers, is the most common genetic metabolic disease in Northern Europe. This inherited autosomal recessive disease is characterised by chronic excess iron absorption and deposition in various organs. This consequently leads to irreversible tissue damage, particularly in the liver and pancreas. The symptoms, in addition to liver cirrhosis, are cardiomyopathy, arthropathy and hypogonadism. Due to the combination of hyperpigmentation of the skin and functional impairment of the pancreas, it is also referred to as "bronze diabetes".

Following the identification of the hemochromatosis HFE gene by Feder et al. (1996), the mutation C282Y has been identified as the most common cause in HH patients (> 80% are homozygous). In addition it was possible to show an increased risk of developing HH where compound heterozygosity C282Y/H63D was present. The findings are similar for the heterozygous development of S65C and C282Y (in trans). A strong phenotypical characteristic can also be found in the presence of E168X in combination with C282Y or in the homozygous E168X genotype.

Clinical symptoms generally do not present themselves until after organ damage has been established. Early diagnosis is difficult due to the unspecific clinical symptoms. Cycle-related fluctuations in women can therefore also make iron-based laboratory diagnosis more difficult. If treatment is initiated early enough, no reduction in life expectancy is anticipated, whereas the prognosis if the disease is left untreated is not favourable. Therefore great importance is attached to early identification of indicators, since simple treatments are available using regular phlebotomy and diet. Thus irreversible damage to the affected organs, which might in some circumstances result in lifelong dialysis and transplants, can be avoided.

The **GenoType® HH** test kit identifies the 4 most significant HFE gene mutations (C282Y, H63D, S65C, E168X) safely, quickly and reliably in a single procedure. Due to the simple combination of **GenoType® HH** with all the parameters of the **GenoType®** series, it can easily be integrated into the routine diagnostics of any laboratory.

For technical information, please see the brochure "**DNA-STRIP® Technology**". Further literature is available direct from HAIN LIFESCIENCE.

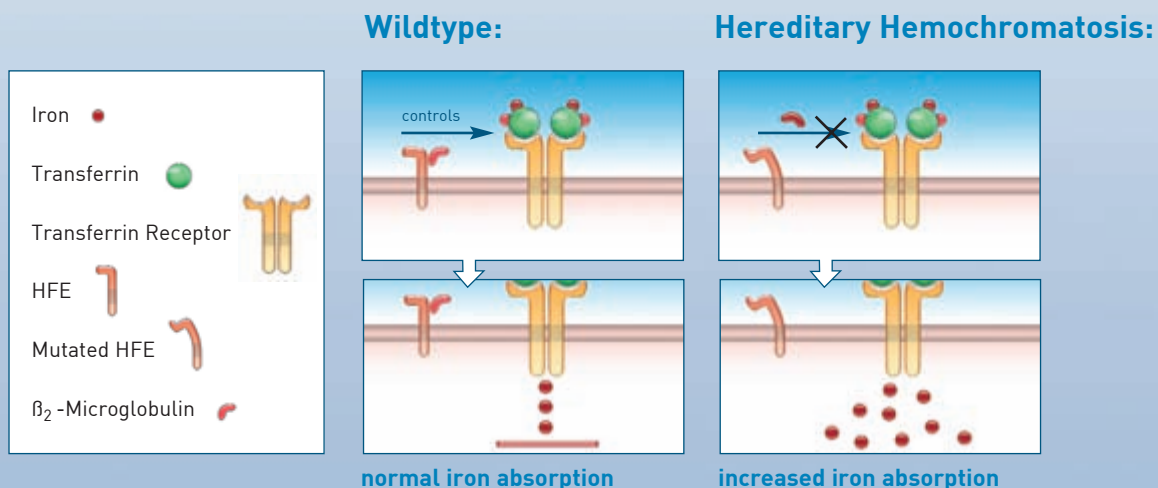
Key words

Mutations in the HFE gene are associated with a disturbed cellular iron metabolism. The most significant mutations and their prevalence in the standard population and in HH patients are shown below.

Mutation	Total Population	HH Patients
C282Y heterozygote	4-9 %	1 %
C282Y homozygote	0,2 %	80-90 %
H63D heterozygote	17 %	n.k.
H63D homozygote	3 %	n.k.
C282D/H63D Compound-heterozygote	2 %	4-5 %
S65C heterozygote	1 %	n.k.
S65C homozygote	n.k.	n.k.
E168X heterozygote	1 %	n.k.
E168X homozygote	n.k.	n.k.

Indications for GenoType® HH testkit

- Patients with HH
- Patients with early HH symptoms
- Identification of carriers in affected families
- Differential diagnosis in chronic viral hepatitis or alcohol-induced liver damage
- Distinguishing primary and secondary HH



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