

# ASSOCIATION OF NON-ALCOHOLIC FATTY LIVER DISEASE AND HYPERCHOLESTEROLEMIA WITH MUTATIONS ON GENES *LEP*, *UGT1A1*, *ATP7B*

**Agnese Zarina<sup>1</sup>, Linda Piekuse<sup>1</sup>, Zane Steinberga<sup>1</sup>, Madara Kreile<sup>1</sup>, Astrida Krumina<sup>3</sup>, Jazeps Keiss<sup>2</sup>, Valentina Sondore<sup>2</sup>**

<sup>1</sup> Riga Stradiņš University Scientific Laboratory of Molecular Genetics, Latvia

<sup>2</sup> Infectology Centre of Latvia, Riga, Latvia

<sup>3</sup> Latvian Biomedical Research and Study Centre, Riga, Latvia

## BACKGROUND

It is likely that leptin (Lep), a polypeptide hormone, has been implicated in pathogenesis of non-alcoholic fatty liver disease (NAFLD).

Wilson's disease (WD) is a severe disorder of copper misbalance, caused by mutations in the gene *ATP7B* and is accompanied by accumulation of copper in tissues, especially in the liver, that can manifest as liver pathology (including NAFLD). Gilbert syndrome could be involved in lipid metabolism.

## AIM

To determine whether the below mentioned polymorphisms and mutations are associated with dyslipidemia in patients with steatohepatitis (non-alcoholic fatty liver disease).

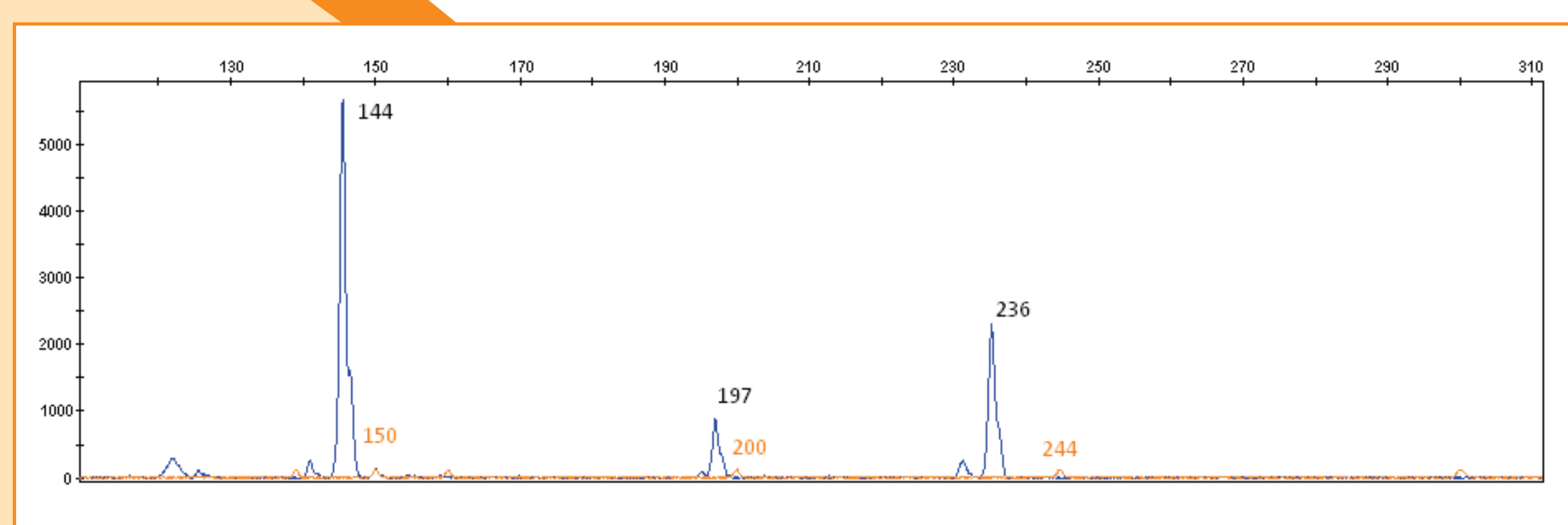
## OBJECTS

- \* The study population included 18 patients who had been screened for hypercholesterolemia (total cholesterol >5mmol/l) and 9 patients with steatohepatitis.
- \* In the control population there were 55 individuals.

## MATERIAL AND METHODS

The research material was DNA isolated from leukocytes. Mutation H1069Q testing was performed by PCR Bi-PASA method, (TA)<sub>n</sub> – fluorescent PCR and sequencing, 3'untranslatable region tetranucleotide (TTTC)<sub>n</sub> polymorphism – PCR, agarose gel electrophoresis (detecting short and long allele), fluorescent PCR – detecting precise length of allele. (Fig.1.)

Fig.1. Fluorescent PCR for detection *UGT1A1* (TA) polymorphism and *LEP* tetranucleotide polymorphism using sequencing. Recorded an individual with *UGT1A1* genotype (TA)7/(TA)7 and leptine short/long allele (TTTC)144/(TTTC)236



## RESULTS

(TA)7 allele frequency in the affected individuals 0.5303 (p=0.47, OR 0.85, CI95% 0.46 – 1.58), leptine long allele frequency – 0.39 (p=0.12, OR 0.63, CI 95% 0.35-1.14). H1069Q allele frequency 0.01 was not found in the control group. After the linear regression analysis there was not found any significant association (p>0.05) with any biochemical marker. Analysis of the precise length of tetranucleotide repeats did not reveal any statistically significant difference (Fig.2.)

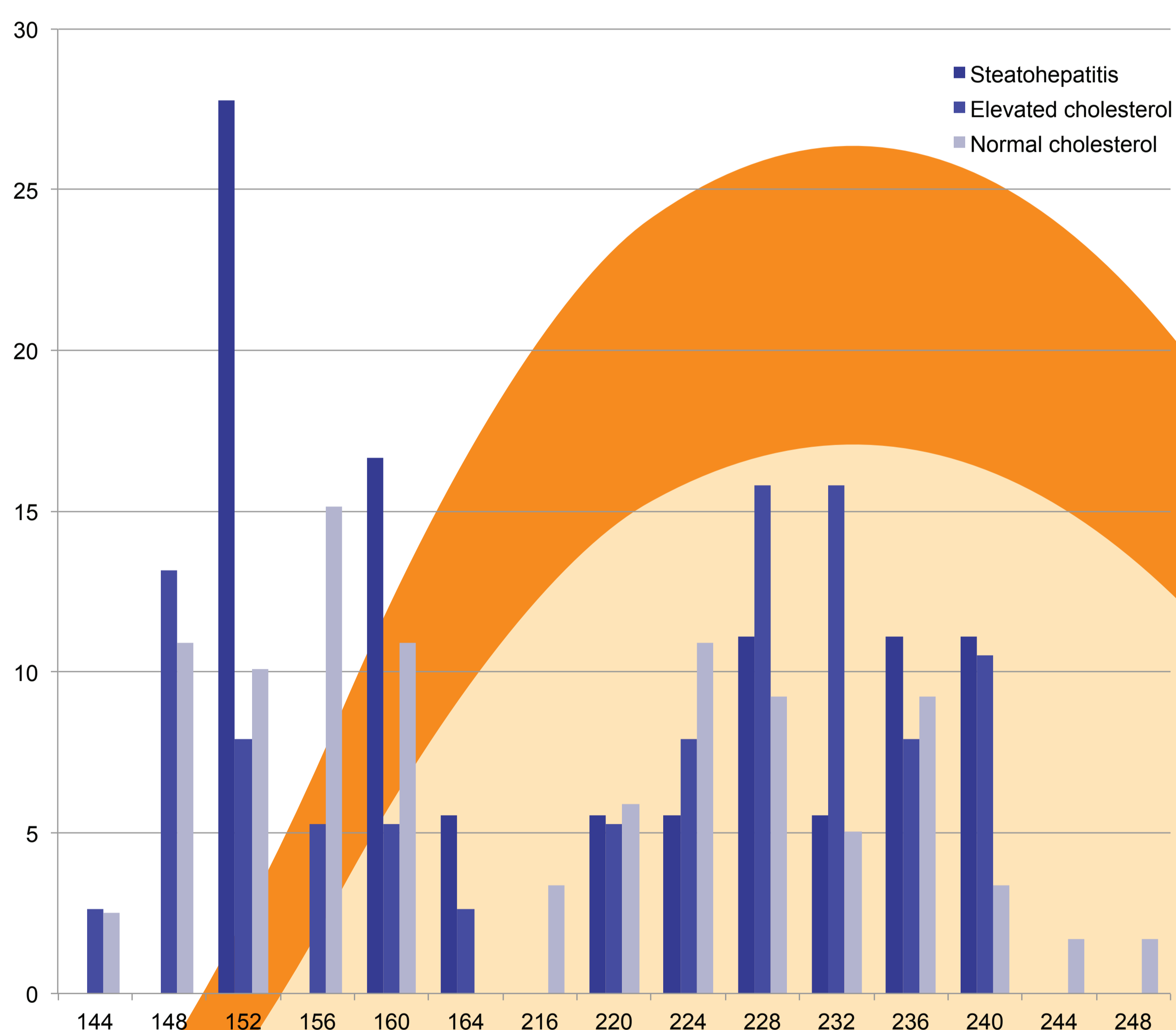


Fig.2. Leptine tetranucleotide repeat alleles in all analyzed groups

## CONCLUSIONS

(TA)6 allele, leptine tetranucleotide repeat short allele, and H1069Q allele could be promoting changes in cholesterol level leading to steatohepatitis. In order to prove the interaction, the study has to be continued.