A NEW METHOD INCLUDING THE QUANTIFICATION OF CIRCULATING MIRNAS ALLOWS THE EFFICIENT IDENTIFICATION OF NASH PATIENTS AT RISK WHO SHOULD BE TREATED

BACKGROUND

The efficient management of the NASH patient population thus requires new non-invasive diagnostic tools. NASH diagnosis necessitates an invasive procedure, the liver biopsy, that can only be performed by an experienced person.

NASH is a silent, asymptomatic disease, affecting a large number of patients from the general population. Diagnosing NASH is crucial to prevent the development of liver complications and to detect patients at risk of liver outcomes from the general population of NASH patients.

AIM

A NEW METHOD INCLUDING THE QUANTIFICATION OF CIRCULATING MIRNAS ALLOWS THE EFFICIENT IDENTIFICATION OF NASH PATIENTS AT RISK WHO SHOULD BE TREATED

METHODS

Data and plasma samples from the 275 healthy control patients and 500 NASH patients included in the GOLDEN study were used for this study. All patients were of normal weight, with a wide spectrum of NASH severity, and the same ethnic origin.

The NASH diagnosis was based on the presence of at least 3 of the following features: a steatosis grade of 3 or more, a fibrosis stage of 2 or 3, and a clinical score of 4 or more. In addition, a fibrosis score of 4 or more establishes a diagnosis of cirrhosis and hepatocellular carcinoma.

The following variables were considered for the definition of NASH patients: BMI, waist circumference, fasting glucose, fasting insulin, fasting triglycerides, HDL-cholesterol, alanine transaminase, aspartate transaminase, alkaline phosphatase, gamma-glutamyl transferase, total bilirubin, total cholesterol, LDL-cholesterol, A2M, miR-200a, miR-34a, and P3PN.

RESULTS OVERVIEW

The variables identified with the Bootstrap algorithm are the same as those identified with the Median algorithm. The results provide also the proof of the added value of miRNAs as diagnostic markers in NASH. The variables identified with the Bootstrap algorithm are predictive of NASH stages and severity.

CONCLUSION

The two biostatistical approaches, allowing the identification of the patients that should be treated, were most similar to the objective of the study since the same markers were identified by the two methods.

The variables identified with the Bootstrap algorithm were the same as those identified with the Median algorithm. The observation strengthens the clinical relevance and confidence of these results.

Additionally, a comparative study demonstrates that these 2 algorithms are more powerful than existing screening systems to identify the patient that should be treated.

The results provide also the proof of the added value of miRNAs as diagnostic markers in NASH.

This work is still ongoing, and the 2 algorithms will be improved through the implementation of new methods and parameters.

All the algorithms will be validated using independent cohorts.

REFERENCES


All the algorithms will be validated using independent cohorts.

A2M + miR-200a + miR-34a + HbA1c + P3PN

AUC = 0.82

ELF

Bootstrap algorithm

AUC = 0.69

AUC = 0.56

REFERENCES