



Monozygotic twins with NASH cirrhosis: cumulative effect of multiple single nucleotide polymorphisms?

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ABSTRACT

Multiple genetic and environmental factors interact to determine an individual's predisposition to non-alcoholic fatty liver disease and its phenotypic characteristics. Association studies have found a number of alleles associated with the development of non-alcoholic steatohepatitis. Our aim was to investigate whether multiple risk-associated alleles may be present in affected monozygotic twins, indicating underlying genetic predisposition to non-alcoholic steatohepatitis. We determined the genotype of 14 candidate gene polymorphisms (at 11 unlinked loci) in a set of monozygotic twins who presented with cirrhosis within 18 months of each other. Genotyping revealed multiple single nucleotide polymorphisms at 9 independent loci in genes *PNPLA3*, *APOC3*, *GCKR*, *TRIB1*, *LYPLAL1*, *PPP1R3B*, *COL13A1*, and *EFCAB4B*, previously implicated in contributing to non-alcoholic steatohepatitis pathogenesis. In conclusion, this case series illustrates the potential cumulative effect of multiple polymorphisms in the development and potential progression of a complex trait such as NASH cirrhosis.

Key words. PNPLA3. Genotype. NAFLD.

INTRODUCTION

Non-alcoholic fatty liver disease (NAFLD) has been considered highly heritable.¹ However, as with any complex trait, multiple genetic and environmental factors interact to determine an individual's predisposition to NAFLD and its phenotypic characteristics such as histological severity and disease progression. We describe identical twins presenting with cirrhosis secondary to non-alcoholic steatohepatitis (NASH) within 18 months of each other. A number of single nucleotide polymorphisms (SNPs) have been identified in candidate gene and genome-wide association studies (GWAS) as being associated with liver fat content, NAFLD/NASH.²⁻⁷ We deter-

mined the genotype of the twins at these loci with an aim to elucidate an underlying genetic predisposition to their liver disease.

MATERIAL AND METHODS

The study protocol conforms to the ethical guidelines of the 1975 Declaration of Helsinki as reflected in a priori approval by the East Midlands Research Ethics committee and both patients provided written informed consent for genetic testing and publication. Both cases had a negative liver screen (hepatitis A, B, C, and E serology, autoantibodies, serum copper, caeruloplasmin, ferritin and alpha1 antitrypsin levels), neither had

abused alcohol, though both had insulin resistance (IR) (Table 1).

Genotyping

Genomic DNA was prepared from whole blood using Flexigene DNA kit (Qiagen, Germany). Genotypes were determined by sequencing (Source Bioscience, UK) PCR products generated using the following primer pairs (Sigma-Aldrich, UK):

- **rs738409:** PNPLA3_1F, GAGCCAACAAACCTT-GGTCCTGTCTG and PNPLA3_1R, GCTGCCCG-GTAGCCTGGAAATAG (546bp).
- **rs6006460:** PNPLA3_2F, GTGTCTCTGGCTGT-GACGGCACC and PNPLA3_3R, TCACTACACAG-CAATGCGGAGGTA (454bp).
- **rs2854116 and rs2854117:** APOC3_1F, GAAGGT-GAACGAGAGAACATCAGTCTG and APOC3_1R, GCCTCGGGCCCATCTCAGCCTTCACACTG (513bp).
- **rs2385114:** TRIB_1F, ACAGACCTTGAGAG-GAAAAGGAATTGACC and TRIB_1R, GCTGGT-GCCCACACTGATACATGC (548bp).
- **rs7800894:** GCKR_1F, GAGACATAGTCTCACTCT-GTTGCCAGG and GCKR_1R, CCCAGCGTT-TAAATGTTAGGGCAATAGATGTAAACC (588bp).
- **rs1260326:** GCKR_2F, GGGTCTTAGGGTACCT-GCTCAGAGG and GCKR_2R, GGTAACCCAT-GACCTTGCCCAGC (546bp).
- **rs2228603:** NCAN_1F, GCCTCTGAATCAG-GCCCTCTCTCC and NCAN_1R, GGTGACAT-TCAGTGGGTGGGCTCC (520bp).
- **rs2645424:** FDFT_1F, CCTCTAAAAGAAGAG-GAAGGGCTTGG and FDFT_1R, GAGACAC-CACACTTAGCCTCACC (403bp).
- **rs1227756:** COL13A_1F, ACCATCCATGGCTCCT-CAGTGC and COL13A_1R, GGCGGAGAT-GGCAAGGAAGCTG (592bp).
- **rs887304:** EFCAB4B_1F, CCCATCAGTAAATTCTGTGAATGAATGCCCTACTCACC and EFCAB4B_1R, CTTGGTCCCCAGTGCAGT-GTTGGACCA (274bp).
- **rs4240624:** PPP1R3B_2F, CCAGGCTGGTCTC-GATCCCCTTGG and PPP1R3B_2R, ACCAACGGAGTGCCAGTACACG (525bp).
- **rs58542926:** TM6SF2_F1 CAGGCATGAGCCACCG-CACC and TM6SF2_R2 ACAGATGTCCAGCAG-GGTTC (330bp).
- **rs12137855:** LYPLAL_1F, TAAAAGTTACAT-GCCCTCCTTATAGG and LYPLAL_1R, GCCCATG TAG TTGTTACAGACACTGG (430bp).

Phusion polymerase and HF buffer (New England Biolabs, UK) was used to amplify each region from the genomic DNA templates and products were gel purified (Machery Nagel, Germany).

RESULTS

Case 1

A 69 year old Caucasian male was referred to the haematologists in July 2010 with thrombocytopenia (platelet count of $53 \times 10^9/L$). Bone marrow examination was suggestive of consumptive thrombocytopenia with normal cytogenetics. A subsequent liver ultrasound indicated cirrhosis and he was referred to Hepatology services in November 2010. He drank about 14 units of alcohol/week, and had mild hypertension, there being no significant family or drug history. On examination besides palmar erythema there were no other stigmata of chronic liver disease. His BMI was 27.2 with a waist hip ratio of 0.97, though there had been a 14 kg unintentional weight loss over the last six months. Initial laboratory tests are shown in table 1. A liver screen was negative and liver ultrasound suggested cirrhosis with a splenomegaly of 14.7 cm. A percutaneous liver biopsy performed on 23rd March 2011 confirmed cirrhosis with patchy steatosis involving 15% of the hepatocytes. He did have a variceal bleed in March 2011 requiring banding and

Table 1. Laboratory data at presentation in the two cases.

Test	Case 1	Case 2
Haemoglobin (12.5-18 gms/dL)	12.4	16.5
White cell count ($4-11 \times 10^9$)	14.7	5.1
Platelets ($150-450 \times 10^9$)	123	41
Liver tests		
Bilirubin (0-21 $\mu\text{mol/l}$)	21	32
AST (0-40 iu/l)	48	43
ALT (0-41 iu/l)	48	63
ALP (40-129 iu/l)	63	120
GGT (10-71 iu/l)	226	204
Albumin (35-52 gm/l)	36	43
INR (0.8-1.4)	1.4	1.2
AFP (<5.8 ku/l)	3.2	NA
MELD score	10	12
Child Pugh score	5	6
Fasting blood glucose (3.2-11 mmol/l)	6.3	4.2
Fasting Insulin (pmol/l)	530	454
HOMA-IR	21.4	12.2
HbA1C (20-42 mmol/mol)	34	33
Lipids		
Cholesterol (2.8-5 mmol/l)	2.4	2.5
HDL cholesterol (> 1 mmol/l)	1.1	1.4
Cholesterol/HDL ratio	2.2	1.8
LDL cholesterol	NA	0.8
Triglyceride (0.8-1.7 mmol/l)	NA	1.1

developed grade 2 hepatic encephalopathy that has responded to medical therapy. More recently he has been diagnosed with hepatocellular cancer (HCC).

Case 2

A 71 year old Caucasian man presented to our institute in November 2012 with hematemesis and melena. He had drunk alcohol (<16 units/week) for about 10 years aged 40-50 years. Of note his identical twin brother had been diagnosed with cirrhosis in 2010 (as above). There was no significant past medical history and he was on no medication. On examination he had liver palms, multiple spider angiomas, a firm 3 cm hepatomegaly and moderate ascites. His BMI was 28.4, though he had had an unintentional 7 kg weight loss in the last four months. Initial laboratory tests are shown in table 1. An urgent gastroscopy revealed grade two oesophageal varices (with stigmata of recent bleeding) that were banded. A liver screen (see methods) was negative and transient elastography (TE) (Echosens 502 Touch) confirmed cirrhosis (liver stiffness measurement (LSM) 15.9 kPa) with controlled attenuation parameter (CAP) of 266 dB/m. A triple phase CT scan of the liver revealed a 6 cm HCC in segment 3. He was referred to the regional tertiary centre where he underwent successful transarterial chemoembolization (TACE).

Patient genotypes

The genotyping results are listed in table 2 along with the effect alleles and the expected frequencies for these genotypes. This analysis revealed that both patients were heterozygotes for: *PNPLA3* rs738409 (Ile148Met); *APOC3* rs2854116; *APOC3* rs2854117 (which is closely linked to rs2854116); *GCKR* rs7800894, and *EFCAB4B* rs887304 indicating that they had a single 'risk' allele at 4 independent genetic loci. We also found heterozygosity for a functional *GCKR* variant (Pro446Leu) rs1260326, which has been shown to be closely linked to rs7800894.⁸ The twins were homozygotes for the 'risk' allele at: *PNPLA3* rs6006460 (encoding Ser453); *TRIB1* rs2385114; *LYPLAL1* rs12137855; *PPP1R3B* rs4240624 and *COL13A1* rs1227756. The 'risk' allele was absent for *FDFT1* rs2645424, *NCAN* rs2228603 (encoding Pro92) and the linked *TM6SF2* rs58542926 (encoding Glu167). The probability of having this allele combination at the 11 separate loci (when only one of closely linked polymorphisms is included) implicated in disease development, by chance would be 0.00036 assuming Hardy-Weinberg equilibria based on the population minor allele frequencies listed in the Ensembl database.

The sequences obtained for both patients were identical for all the polymorphisms tested and for SNPs in the flanking regions sequenced (totalling 5232 bp and containing an additional 64 SNP sites).

DISCUSSION

We describe two cases (monozygotic twins) who presented with cirrhosis within 18 months of each other. In the first case, percutaneous liver biopsy revealed cirrhosis with background hepatic steatosis. In the second case TE suggested cirrhosis (15.9 kPa) with a CAP of 266 dB/m (indicative of hepatic steatosis).⁹ Therefore, in view of negative liver screen, absence of other risk factors (alcohol), and presence of IR and elevated BMI, both most likely had NASH related cirrhosis. The clinical course was also similar with development of variceal bleeding and HCC.

An earlier report of monozygotic twins with NASH cirrhosis with a similar clinical course¹⁰ did not involve genetic analysis. Our targeted approach, genotyping candidate genetic markers revealed the presence of effect alleles at 11 of the 14 polymorphic sites studied in these two patients (Table 2). Each of the SNPs investigated in these twins has previously been shown to have an association with indicators of NASH or NAFLD such as hepatic fat content, steatosis and or inflammation,²⁻⁷ though none has been directly linked to BMI or IR. These findings are suggestive of a likely cumulative effect of multiple SNPs contributing to the genetic susceptibility that led to the development and progression of NASH. However, we acknowledge that our method could easily have overlooked other polymorphism/s or novel mutations more directly responsible for the cirrhotic phenotype. Additionally, since the cases were monozygotic twins, their gene profiles were similar- had they been dizygotic, the finding would be more significant.

The *PNPLA3* rs738409 polymorphism has been identified as a risk factor for both susceptibility to NAFLD as well as its progression in a number of cohorts.^{3,4,5,6,11} The encoded lipase mediates lipid hydrolysis in hepatocytes and adipocytes and the G allele (I148M substitution) is associated with increased hepatic fat content³ and steatosis.¹² Additionally, carriage of each copy of the G allele confers an additive 2.3 fold risk for HCC.^{13,14} Both twins were heterozygous for rs738409 and developed HCC. The twins were also homozygous for the rs6006460 SNP in this gene.

The twins were heterozygous for SNPs in apolipoprotein-encoding *APOC3* at positions -482 and -455, which are in strong linkage disequilibrium with each other. These variant alleles increasing *APOC3* expression have been found to be associated with coronary artery disease, hypertriglyceridaemia, metabolic syndrome¹⁵ and with NAFLD in Indian males² in earlier but not in subsequent studies.³⁻⁷

Table 2. SNP details and genotype of twins.

Gene	SNP	Change	Effect Allele*	Patient's genotype	Genotype Frequency**
PNPLA3, Patatin-like phospholipase domain-containing protein 3	rs738409	C > G Ile148Met	<u>G</u>	<u>CG</u>	0.40
PNPLA3, Patatin-like phospholipase domain-containing protein 3	rs6006460	G > T Ser453Ile	<u>G</u>	<u>GG</u>	0.94
APOC3, Apolipoprotein C-III	rs2854116	C > T -455 5'UTR	<u>I</u>	<u>CI</u>	0.50
APOC3, Apolipoprotein C-III	rs2854117 (linked to rs2854116)	T > C -482 5'UTR	<u>C</u>	<u>TC</u>	0.50
GCKR, Glucokinase regulatory protein	rs7800894	T > C intron	<u>I</u>	<u>IC</u>	0.48
GCKR, Glucokinase regulatory protein	rs1260326 (linked to rs7800894)	T > C Pro446Leu	<u>I</u>	<u>IC</u>	0.47
TM6SF2, transmembrane 6 superfamily member 2	rs58542926	C > T Glu167Lys	<u>I</u>	<u>CC</u>	0.88
NCAN, Neurocan	rs2228603 (linked to rs58542926)	C > T Pro92Ser	<u>I</u>	<u>CC</u>	0.90
TRIB1, Tribblespseudokinase 1	rs2385114	C > T intron	<u>I</u>	<u>II</u>	0.38
LYPLAL1, Lysophospholipase-like 1	rs12137855	C > T 3'UTR	<u>C</u>	<u>CC</u>	0.71
PPP1R3B, Protein phosphatase 1 regulatory subunit 3b	rs4240624	G > A intron	<u>A</u>	<u>AA</u>	0.81
FDFT1, Farnesyl-diphosphate-farnesyltransferase 1	rs2645424	A > G intron	<u>A</u>	<u>GG</u>	0.22
COL13A1, Collagen type XIII alpha 1	rs1227756	G > A intron	<u>G</u>	<u>GG</u>	0.37
EFCAB4B, EF-hand calcium binding domain 4B	rs887304	T > C 3'UTR	<u>I</u>	<u>CI</u>	0.26

* The allele previously associated with relevant phenotypic effect. ** Based on the Hardy-Weinberg equation using allele frequency from Ensembl database. The probability of an individual having this genotype combination at these 12 effect loci (frequencies shown in bold italics) would be 0.00036.

A number of recent association studies have reported an association between the GCKR rs7800894 intronic polymorphism and the histological features of NAFLD including hepatic steatosis (odds ratio = 1.45),⁵ steatohepatitis and fibrosis.^{6,11,12} Carriage of the minor T allele, associated with decreased insulin release, elevated triglycerides and development of fatty liver,¹⁶ and the linked rs1260326 risk allele, were present in the twins in our study (heterozygotes).

Both patients were homozygous for the TRIB1 rs2385114 polymorphism identified through GWAS studies to be associated with elevated ALT, steatosis, steatohepatitis and fibrosis in NAFLD.⁶ This risk allele was significantly associated with elevated serum triglycerides and cholesterol levels in a GWAS screening for

coronary artery disease risk factors.¹⁶ Two further polymorphisms, rs1227756 and rs887304, identified by GWAS as associated with lobular inflammation in NAFLD patients,⁴ were present in both patients (Table 2); they were homozygous for the effect allele of COL13A1 (encoding collagen type XIII α 1), and heterozygous for rs887304 in EFCAB4B which encodes a calcium-sensor involved in immune cell activation. Two loci within PPP1R3B (involved in lowering plasma lipids¹⁴) were associated with NAFLD in GWAS analyses: rs4240626⁵ and rs11777327.⁶ However, the risk alleles have not been established.^{5,11} A recent study described an association between ultrasonographically assessed hepatic steatosis¹² with the rs4240624 A allele which was present in the twins (homozygotes).

The *FDFT1* (involved in cholesterol biosynthesis) rs2645424 effect allele was not present in our patients. Initial reports of an association of this SNP with histological NAFLD activity score⁴ were not replicated.

The NCAN Pro92Ser variant had been identified as a NAFLD risk factor in two GWAS studies^{5,6} and the gene product, neurocan, suggested to have a role in regulating cell adhesion and lipoprotein metabolism. In candidate gene studies, the risk allele was associated with steatosis, inflammation and fibrosis in an American cohort¹⁷ but not in obese Asian children with NAFLD.¹¹ Recently, NCAN expression in liver cells was demonstrated and the variant allele, in addition to *PNPLA3* rs738409, was associated with the development of HCC (OR=2.29) in patients with alcohol related liver disease.¹⁸ The second variant in this chromosomal region, rs58542926 in *TM6SF2* was also recently found to be associated with elevated hepatic triglyceride and serum ALT⁷ and suggested to influence fibrosis progression in NAFLD.¹⁹

A twin study (included both concordant and discordant twins), showed that the *ADRB2* gene had pleiotropic effects on plasma levels of gammaglutamyltransferase (GGT) and triglycerides, indicating shared genetic codetermination with traits of metabolic syndrome.²⁰ In a more recent twin study, a panel of 10 miRNAs differentiated the twin with NAFLD from the one without.²¹ MicroRNAs may have an influence beyond genetics, though our twins were concordant and not discordant as in Zarrinpar, *et al.*'s study.²¹

CONCLUSION

In conclusion, we describe for the first time, monozygotic twins with NASH related cirrhosis who on genotyping demonstrated heterozygosity for six SNPs (in four gene loci) and homozygosity for five risk-associated alleles in genes that could potentially have been linked to the pathogenesis and progression of NASH. This case series provides further credence to the genetic predisposition to NASH and is suggestive of how the cumulative effect of a number of genes may add up to define a complex trait, i.e. NASH.

ABBREVIATIONS

- **ALT:** alanine transaminase.
- **BMI:** body mass index.
- **CAP:** controlled attenuation parameter.
- **GGT:** gammaglutamyltransferase.
- **GWAS:** genome-wide association studies.
- **HCC:** hepatocellular carcinoma.
- **IR:** insulin resistance.
- **LSM:** liver stiffness measurement.

- **miRNA:** micro RNA.
- **NAFLD:** non-alcoholic fatty liver disease.
- **NASH:** non-alcoholic steatohepatitis.
- **PCR:** polymerase chain reaction.
- **SNP:** single nucleotide polymorphisms.
- **TACE:** transarterial chemoembolization.

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CONFLICT OF INTEREST

None.

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REFERENCES

1. Schwimmer JB, Celedon MA, Lavine JE, Salem, R, Campbell, N, Schork NJ, Shiehmoreza M, et al. Heritability of nonalcoholic fatty liver disease. *Gastroenterology* 2009; 136: 1585-92.
2. Petersen KF, Dufour S, Hariri A, Nelson-Williams C, Foo JN, Zhang XM, Dziura J, et al. Apolipoprotein C3 gene variants in nonalcoholic fatty liver disease. *N Engl J Med* 2010; 362: 1082-9.
3. Romeo SJ, Kozlitina C, Xing A, Pertsemlidis D, Cox LA, Pennacchio E, Boerwinkle E, et al. Genetic variation in *PNPLA3* confers susceptibility to nonalcoholic fatty liver disease. *Nature Genetics* 2008; 40: 1461-5.
4. Chalasani NX, Guo R, Loomba MO, Goodarzi T, Haritunians S, Kwon J, Cui J, et al. Genome-wide association study identifies variants associated with histologic features of nonalcoholic Fatty liver disease. *Gastroenterol* 2010; 139: 1567-76.
5. Speliotes EK, Yerges-Armstrong LM, Wu J, Hernaez R, Kim LJ, Palmer CD, Gudnason V. Genome-wide association analysis identifies variants associated with nonalcoholic fatty liver disease that have distinct effects on metabolic traits. *PLoS Genetics* 2011; 7: e1001324.
6. Anstee QM, Darlay R, Leathart J, Liu YL, Tordjman J, Clement K, Aithal G, et al. A candidate gene approach to validation of genetic modifier associations using a large cohort with histologically characterised non-alcoholic fatty liver disease. *J Hepatol* 2013; 58: S46.
7. Kozlitina J, Smagris E, Stender S, Nordestgaard BG, Zhou HH, Tybjaerg-Hansen A, Vogt TF, et al. Exome-wide association study identifies a *TM6SF2* variant that confers susceptibility to nonalcoholic fatty liver disease. *Nat Genet* 2014; 46: 352-6.
8. Beer, NL, Tribble ND, McCulloch LJ, Roos C P, Johnson R, Orho-Melander M, Gloyn AL. The P446L variant in GCKR as-

sociated with fasting plasma glucose and triglyceride levels exerts its effect through increased glucokinase activity in liver. *Hum Mol Genet* 2009; 18: 4081-8.

9. Sasso M, Tengher-Barna I, Ziol M, Miette V, Fournier C, Sandrin L, Poupon R, et al. Novel controlled attenuation parameter for noninvasive assessment of steatosis using Fibroscan®: validation in chronic hepatitis C. *J Viral Hepatitis* 2012; 19: 244-53.
10. Faris AE, Scully L. An identical clinical course in monozygotic twins with non-alcoholic steatohepatitis- a case report supporting a genetic component to the pathogenesis of this disease. *CCDW* 2007; Abstract 238.
11. Lin YC, Chang PF, Chang MH, Ni YH. Genetic variants in GCKR and PNPLA3 confer susceptibility to nonalcoholic fatty liver disease in obese individuals. *Am J Clin Nutr* 2014;99:869-74.
12. Hernaez R, McLean J, Lazo M, Brancati FL, Hirschhorn JN, Borecki IB, Harris TB, et al. Association between variants in or near PNPLA3, GCKR, and PPP1R3B with ultrasound-defined steatosis based on data from the third national health and nutrition examination survey. *Clin Gastroenterol Hepatol* 2013; 11: 1183-1190.
13. Liu YL, Patman GL, Leathart JB, Piguet AC, Burt AD, Dufour JF, Day CP, et al. Carriage of the PNPLA3 rs738409 C>G polymorphism confers an increased risk of non-alcoholic fatty liver disease associated hepatocellular carcinoma. *J Hepatol* 2014; 61(1): 75-81.
14. Trepo E, Nahon P, Bontempi G, Valenti L, Falleti E, Nischalke HD, Hamza S, et al. Association between the PNPLA3 (rs738409 C>G) variant and hepatocellular carcinoma: Evidence from a meta-analysis of individual participant data. *Hepatol* 2014; 59: 2170-7.
15. Miller M, Rhyne J, Chen H, Beach V, Ericson R, Luthra K, Dwivedi M, et al. APOC3 Promoter Polymorphisms C-482T and T-455C Are Associated with the Metabolic Syndrome. *Archives of Medical Research* 2007; 38: 444-51.
16. Teslovich TM, Musunuru K, Smith AV, Edmondson AC, Stylianou IM, Koseki M, Pirruccello JP, et al. Biological, clinical and population relevance of 95 loci for blood lipids. *Nature* 2010; 5: 707-13.
17. Gorden A, Yang R, Yerges-Armstrong LM, Ryan KA, Spiliotes E, Borecki IB, Harris TB, et al. Genetic variation at NCAN locus is associated with inflammation and fibrosis in non-alcoholic fatty liver disease in morbid obesity. *Hum Hered* 2013; 75: 34-43.
18. Nischalke HD, Lutz P, Kramer B, Sohne J, Muller T, Rosenthal J, Fischer J, et al. A common polymorphism in the NCAN gene is associated with hepatocellular carcinoma in alcoholic liver disease. *J Hepatol* 2014; 61: 1073-9.
19. Liu YL, Reeves HL, Burt AD, Tiniakos D, McPherson S, Leathart JB, Allison ME, et al. TM6SF2 rs58542926 influences hepatic fibrosis progression in patients with non-alcoholic fatty liver disease. *Nat Commun* 2014; 5: 4309.
20. Loomba R, Rao F, Zhang L, Khandrika S, Ziegler MG, Brenner DA, O'Connor DT. Genetic covariance between gamma-glutamyl transpeptidase and fatty liver risk factors: role of beta 2-adrenergic receptor genetic variation in twins. *Gastroenterol* 2010; 139: 836-45
21. Zarrinpar A, Gupta S, Maurya MR, Subramaniam S, Loomba R. Serum microRNAs explain discordance of non-alcoholic fatty liver disease in monozygotic and dizygotic twins: a prospective study. *Gut* 2015. doi 10.1136/gutjnl-2015-309456

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