Corrigendum

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Corrigendum to "Ferroportin disease: A systematic meta-analysis of clinical and molecular findings" J. Hepatol. 2010 Nov;53(5):941–949

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In the above named article there were three errors:

1. In the section on "How to differentiate between SLC40A1 mutations and polymorphisms", a reference was left out of the following paragraph. The paragraph and reference are now listed below.

   Ferroportin disease is genetically heterogeneous with 36 different SLC40A1 mutations reported [8–10,12,26–29,38–41,45–68,78] as summarized in Table 3. In addition, nine ferroportin gene polymorphisms were reported, three of which were associated with increased serum ferritin in various populations (Table 4) [29,34]. The allele frequencies of 29 disease-associated ferroportin mutations had been determined in matched populations and was found to be <1:100. It remains unclear whether L233V and D270P, each of which have been identified in single patients with iron overload, are disease-causing mutations or represent benign sequence variants [43,65].

   [78] Wallace DF, Clark RM, Harley HA, Subramaniam VN. Autosomal dominant iron overload due to a novel mutation of ferroportin1 associated with parenchymal iron loading and cirrhosis. J Hepatol 2004;40:710–3.

2. In Tables 3 and 4 there were some errors. The tables are now reproduced correctly on the following pages.

   The authors apologise for these errors.

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Table 3. Molecular genetics of *SLC40A1* mutations. The frequency of mutations highlighted with * in the control population can be inferred from studies, in which control populations have been screened for the presence of another mutation, which affect the same residue.

		EXON	SIFT score	PolyPhen					
mutation (protein)	mutation (cDNA)		predicted consequence on protein function	predicted consequence on protein function	PolyPhen score	Number of patients reported	Biochemical phenotype	Frequency in control population	Reference
	c.-59-45del	1				1		<1:50	[42]
	c.-188A>G	1				1		<1:50	[47]
Y64N	c.190T>C	3	affected	probably	2.736	8	non-classical	<1:100	[26]
V72F	c.214G>T	3	affected	possibly	1.706	5	non-classical	<1:50	[38]
A77D	c.230C>A	3	tolerated	possibly	1.992	24	variable	<1:100	[34, 44, 48, 49, 50, 51 52]
G80V	c.239G>T	3	affected	probably	2.499	2	classical	<1:50	[62]
G80S	c.238G>A	3	affected	possibly	1.824	6	variable	n/a	[48, 52]
R88G	c.262A>G	3	affected	probably	2.429	1		<1:50	[42]
R88T	c.263G>C	3	affected	probably	2.204	7	variable	<1:60	[40]
N144H	c.430A>C	5	tolerated	possibly	1.736	20	variable	<1:200	[39, 53, 54]
N144D	c.430A>G	5	tolerated	possibly	1.676	2		n/a (<1:100)*	[78]
N144T	c.431A>C	5	tolerated	possibly	1.751	1		n/a (<1:100)*	[55]
I152F	c.758A>T	5	affected	possibly	1.799	2		n/a	[43]
D157G	c.470A>G	5	affected	probably	2.189	1		<1 :80	[56]
D157N	c.469G>A	5	affected	possibly	1.739	3	classical	<1:50	[38]
V162del	c.484_486del3	5				27	classical (>95%)	<1:100	[44, 45, 46, 52, 57, 58, 59, 60, 61]
N174I	c.521A>T	6	affected	probably	2.738	3	variable	n/a	[48, 52]
R178G	c.532C>A	6	affected	probably	2.429	3	variable	n/a	[46]
I180T	c.539T>C	6	affected	probably	2.204	1		<1:60	[40]
D181V	c.846A>T	6	affected	probably	2.639	4	classical	<1:50	[62]
Q182H	c.546G>T	6	tolerated	probably	2.026	1	classical	<1:80	[56]
R178Q	c.533G>A	6	tolerated	possibly	1.824	1		<1:50	[42]
N185D	c.553A>G	6	tolerated	possibly	1.838	15	variable	<1:50	[63]
L233P	c.698T>C	6	affected	probably	2.243	1		n/a	[43]
G267D	c.1104G>A	7	tolerated	possibly	1.722	1		<1:50	[62]
D270V	c.808A>T	7	tolerated	probably	2.099	1		n/a	[65]
G323V	c.968G>T	7	affected	probably	2.499	1		<1:80	[56]
C326S	c.977G>C	7	tolerated	possibly	1.877	7	non-classical	n/a (<1:100)*	[11, 25]
C326Y	c.977G>A	7	tolerated	probably	3.237	4	non-classical	<1:300 in Thai <1:100 in Vietnamese	[8, 10]
S338R	c.1014T>G	7	affected	possibly	1.602	1		<1:94	[9]
splice site**	c.1402G>A	8				1		n/a	[66]
R489S	c.1467A>C	8	affected	probably	2.204	2	variable	n/a (<1:100)*	[67]
R489K	c.1466G>A	8	affected	possibly	1.529	6	classical	<1:100	[68]
G490D	c.1468G>A	8	affected	probably	2.049	3	variable	<1:100	[41]
G490S	c.1468G>A	8	affected	possibly	1.754	2	variable	<1:100	[42]
Y501C	c.1502A>G	88	tolerated	possibly	1.830	7	non-classical	<1:200	[12]

** predicted G468S

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Table 4. *SLC40A1* non-synonymous single nucleotide polymorphisms. SNPs, which have been associated with high serum iron parameters, are highlighted in bold and italics.

			SIFT score		PolyPhen			
polymorphism (protein)	base substitution (cDNA)	EXON	predicted consequence on protein function	catfile score	predicted consequence on protein function	PolyPhen score	Frequency in control population	Reference
Q248H	**c.744G>T**	***6***	**tolerated**	**0.10**	**benign**	**0.123**	Heterozygozity 11.6%**	**[27, 28, 29]**
F324S	c.971T>C	7	affected	0.01	probably	2.507	n/a**	ENSEMBL
G339D	**c.1016G>A**	***7***	**tolerated**	**0.62**	**possibly**	**1.648**	0.5% in African American	**[34]**
L384M	***c.1149T>A***	***7***	**affected**	**0.01**	**benign**	**1.118**	1.5% Allelic frequency in African American 10% Italian blood donors with high ferritin	**[29, 34]**
L384V	**c.1149T>G**	***7***	**tolerated**	**0.08**	**benign**	**1.343**	1.5% Allelic frequency in African Americans 5% in Italian blood donors with high ferritin	**[29, 34]**
F405S	c.1214T>C	7	tolerated	0.31	benign	0.982	n/a**	ENSEMBL[3]
M432V	c.1294A>G	7	tolerated	0.5	benign	0.76	Heterozygozity 0.4%**	NCBI [2]
P443L	c.1328C>T	7	tolerated	0.67	possibly	1.758	Heterozygozity 4.4%**	NCBI [2]
R561G	**c.1681A>G**	***7***	**tolerated**	**0.28**	**benign**	**0.015**	Heterozygozity 2.8% **	NCBI [2] [35]

** predicted G468S
[2] as reported in the NCBI SNP database (http://www.ncbi.nlm.nih.gov/projects/SNP/snp_ref.cgi?chooseRs=coding&go=Go&locusId=30061)
[3] http://www.ensembl.org/Homo_sapiens/Variation/Summary?v=ENSSNP12180430;vdb=variation