frontiers | Frontiers in Immunology

TYPE Correction
PUBLISHED 23 August 2024
DOI 10.3389/fimmu.2024.1476204

OPEN ACCESS

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RECEIVED 05 August 2024
ACCEPTED 08 August 2024
PUBLISHED 23 August 2024

CITATION
Rydberg V, Aradottir SS, Kristoffersson A-C, Svitacheva N and Karpman D (2024) Corrigendum: Genetic investigation of Nordic patients with complement-mediated kidney diseases.
Front. Immunol. 15:1476204.
doi: 10.3389/fimmu.2024.1476204

Corrigendum: Genetic investigation of Nordic patients with complement-mediated kidney diseases

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KEYWORDS

complement, atypical hemolytic uremic syndrome, C3 glomerulopathy, membranoproliferative glomerulonephritis, genes

A Corrigendum on

Genetic investigation of Nordic patients with complement-mediated kidney diseases

By Rydberg V, Aradottir SS, Kristoffersson A-C, Svitacheva N and Karpman D (2023). *Front. Immunol.* 14:1254759. doi: 10.3389/fimmu.2023.1254759

In the published article, there was an error in Table 3 as published. Under the heading C3, rowc.4030-4C>G was under the ACMG classification stated as "P" when it should be "LB". Under the heading CFHR2, row R141S, "c.423G>A" should have been written as "c.423G>T". And finally, under the heading CLU, row K444Q, "c.1339A>C" should be corrected to "c.1330A>C". The corrected Table 3 and its caption appear below.

In the published article, there was an error in Supplementary Table 1. The C3 level of patient 314 was given as "normal" when it should have been written as "low". The corrected Supplementary Material File has now been published.

The authors apologize for these errors and state that they do not change the scientific conclusions of the article in any way. The original article has been updated.

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10.3389/fimmu.2024.1476204

TABLE 3 Variants in C3G patients included in this study.

Variant or deletion	Nucleotide shift	Type of variant	dbSNP	Domain	Minor Allele frequency	Functional studies	ACMG classification	Reference
CFH								
D693N [a]	c.2077G>A	Missense	rs148403790	SCR12	0.0001592		Conflicting	(48)
Q950H	c.2850G>T	Missense	rs149474608	SCR16	0.003911	NPE	LP	(45, 51)
N1050Y[b]	c.3148A>T	Missense	rs35274867	SCR18	0.01469	NPE	LB	(45, 54)
S1209T	c.3625T>A	Missense	rs561146868	SCR20	0.00000398	–	LB	(48)
C3								
K155Q	c.463A>C	Missense	rs147859257	MG2	0.002705	GoF	LP	(58, 59)
V326M[c]	c.976G>A	Missense	rs375264020	MG3	0.00004779	–	VUS	This study
Q1061H	c.3183A>T	Missense	rs373054812	TED	0.00007704	–	VUS	This study
E1516A	c.4547A>C	Missense	rs1019532370	C345C	0.00001193	–	VUS	This study
W1631*	c.4893G>A	Stop	NA	C345C	–	LoF	P	(61)
	c.4030-4C>G	Splice acceptor site	NA	Between CUB and MG8	–	–	LB	(55)
CFI								
	c.1534+5G>T	Intronic splice	rs114013791	Intron 12	0.00866	–	–	(33)
G328R	c.981G>A	Missense	rs144164794	Linker 2	–	LoF	LP	(55, 65)
CD46								
A353V[a,b]	c.1013C>T	Missense	rs35366573	TM	0.01541	LoF, NFE	Conflicting	(33, 73)
C5								
P233L	c.698C>T	Missense	rs531284110	MG3	0.0000252	–	VUS	(81)
L354M	c.1060C>A	Missense	rs34552775	MG4	0.0055	–	B	(82)
G385R	c.1153G>C	Missense	–	MG4	Unknown	–	–	This study
CFHR1								
Deletion		Deletion			–	–	LB	(76)
Exon 6 duplication		Duplication				–	LB	This study. Other duplications reported in (83)
CFHR2								
R141S	c.423G>T	Missense	rs142929868	SCR2	0.002947	–	–	This study
CFHR3								
Deletion		Deletion			–	–	–	(76)
CFHR4								
Y43F[d]	c.128A>T	Missense	rs202234955	SCR1	0.001747	–	LB	This study
	c.799+3A>C	Intronic splice	Rs196876631	–	0.001286	–	LB	(82)
CFHR5								
E163Kfs*10	c.485_486dup	Frameshift (insertion)	rs565457964	SCR3	0.006750	NPE	–	(77)

(Continued)

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TABLE 3 Continued

Variant or deletion	Nucleotide shift	Type of variant	dbSNP	Domain	Minor Allele frequency	Functional studies	ACMG classification	Reference
CFHR5								
E226Dfs*7	c.678del	Deletion	rs1438537910	SCR4	0.000007964	–	P	This study
Y279N	c.835T>A	Missense	rs143240067	SCR5	0.0001274	–	Conflicting	(78)
R356H[b]	c.1067G>A	Missense	rs35662416	SCR6	0.01633	NPE	LB	(77, 84)
CFP								
D299N	c.895G>A	Missense	rs61737993	TSP t1 5	0.001472	–	B	(85)
CLU								
K444Q	c.1330A>C	Missense	rs2612311022	β-chain	0.0001026	-	-	This study
PLG								
R89K	c.266G>A	Missense	rs143079629	PAN	0.006191	–	B	(48)
R261H	c.782G>A	Missense	rs4252187	Kringle 2	0.002501	–	Conflicting	(80)

a, Mentioned in the complement database (www.complement-db.org) with reference to (4). b, Minor allele frequency > 1% but this variant was previously associated with aHUS. c, Previously reported in the ClinVar database in association with age-related macular degeneration and aHUS. d, Previously reported in the ClinVar database in association with aHUS. CFH, Complement factor H; C3, Complement C3; CFB, Complement factor B; CFI, Complement factor I; CD46, CD46/Membrane cofactor protein; C5, Complement C5; CFHR1-5, Complement factor H related 1-5; CFP, Complement factor properdin; PLG, Plasminogen. Domains, SCR, Short consensus repeats; MG1-8, Macroglobulin domain 1-8; TED, Thiol ester-containing domain; C345C, C345C/NTR domain; CUB: C1r/C1s, Urchin embryonic growth factor, Bone morphogenetic protein 1; TM, Transmembrane protein; TSP t1, Thrombospondin type-1 1-5; PAN, Plasminogen-Apple-Nematode; NPE, No phenotypic effect; GoF, Gain of function; LOF, Loss of function (including low plasma concentration); VUS, Variant of unknown significance; LP, Likely pathogenic; LB, Likely benign; P, Pathogenic.