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Erratum
X-linked agammaglobulinemia: investigation of clinical and laboratory findings, novel gene mutations and prevention of infective complications in long-term follow-up. Am J Clin Exp Immunol. 2021; 10(1): 37-43

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The article drew attention of two BTK researchers (D. Philips and M. Vihinen), they wanted explanations for the mutations of 5 patients. We sent them the corrected data from our clinical genetics fellows. And they accepted. The errors were due to these patients' interpretations being made years ago, and it was unfortunately not rechecked before submission.

Fifteen of twenty patients have been genetically examined by our colleagues in Medical Genetics Department in Ege University and they are all correctly written. The wrongly spelled and typed five patients were all examined and reported in other hospitals and labs between 2007-2014, not in our university.

Patient 1: In the manuscript it was written as C663C. This patient was analyzed in 2007 in a private genetic laboratory and the result was reported as C633C. We corrected the report as c.1899C>T (p.Cys633Cys).

Patient 3: In the manuscript it was written as Arg5256/g. The mutation should be written as c.1573C>G (p.Arg525Gly). (It has been wrongly typed in the paper).

Patient 5: In the manuscript it was written as complete deletion of exon 5.

This patient has been examined in a private genetic lab in 2014 (their report is attached). It was also examined in our Medical Genetics Department. In order to detect the exact breakpoint regions of the deletion, array system should be used. Patient's DNA sample was analyzed by Next generation sequencing system that cannot detect the breakpoints of the deletion. That region couldn't be amplified for sequencing which was considered to be deletion of exon 5.

Patient 16: In the manuscript it was written as c.656aa. It should be corrected as c.493T>G (p.Cys165Gly). This patient and the patient number 10 are siblings and have the same mutation.

Patient 17: In the manuscript it was written as 3UTR+119A>C. It is a mutation in the 3'UTR region of the BTK gene. It is corrected as c.*119A>C according to nomenclature.

We do apologize for these errors and report the corrected data in **Table 2** in the article prepered as erratum.

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Table 2. Novel and known mutations in *BTK* gene (NM_000061.3) of our XLA patients

Patient No	Mutation	Type of Mutation
1	Hemizygous c.1899C>T (p.Cys633Cys) mutation	Missense mutation (known)
2	Hemizygous c.226G>T (p.Glu76*) mutation	Missense mutation (novel)
3	Hemizygous c.1573C>G (p.Arg525Gly) mutation	Missense mutation (known)
4	Hemizygous c.1289A>G (p.Lys430Arg) mutation	Missense mutation (known)
5	Hemizygous exon 5 deletion mutation	Deletion mutation (known)
6	Hemizygous c.36G>C (p.Lys12Asn) mutation	Missense mutation (novel)
7	Hemizygous c.1563C>A (p.Asp521Glu) mutation	Missense mutation (novel)
8	Hemizygous c.1835A>C (p.Gln612Pro) mutation	Missense mutation (known)
9	Hemizygous c.1684C>T (p.Arg562Trp) mutation	Missense mutation (known)
10	Hemizygous c.493T>G (p.Cys165Gly) mutation	Missense mutation (novel)
11	Hemizygous c.83G>A (p.Arg28His) mutation	Missense mutation (known)
12	Hemizygous c.83G>A (p.Arg28His) mutation	Missense mutation (known)
13	Hemizygous c.1573C>G (p.Arg525Gly) mutation	Missense mutation (known)
14	Hemizygous c.337G>A (p.Val113Ile) mutation	Missense mutation (novel)
15	Hemizygous c.763C>T (p.Arg255*) mutation	Stop codon mutation (known)
16	Hemizygous c.493T>G (p.Cys165Gly) mutation	Missense mutation (novel)
17	Hemizygous c.1980+119A>C (c.*119A>C) mutation	Missense mutation (novel)
18	Hemizygous c.36G>C (p.Lys12Asn) mutation	Missense mutation (novel)
19	Hemizygous c.1383T>G (p.Tyr461*) mutation	Stop codon mutation (novel)
20	Hemizygous c.226G>T (p.Glu76*) mutation	Missense mutation (novel)