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# A novel truncated protein of FUT1 with weak function was identified in one Chinese individual

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## CASE REPORT

The Bombay and para–Bombay phenotypes are characterized by lacking or expressing weak H antigens on the red blood cells (RBCs) or in their secretions[1]. The para–Bombay phenotype results from a silenced *FUT1* gene with an active *FUT2* gene to synthesize H type 1 (and therefore A or B antigens) in the secretions from tissue cells that may be adsorbed onto the RBCs from the plasma, or from a mutated FUT1gene resulting in great diminished enzyme activity to produce low amounts of H antigen[2,3]. A novel truncated protein of FUT1 created by bases deletion induced A para–Bombay phenotypein from one Chinese individual was confirmed and analyzed with molecular techniques.

A blood sample from a 64–year–old male patient was sent to our laboratory for the resolution and identification of an ABO discrepancy between the forward and reverse type. Standard serologic protocol was performed to characterize the RBCs´ phenotype. Genomic DNA was extracted and followed by sequence analysis of *ABO*, *FUT1* and *FUT2* genes. Exon 6 to Exon 7 and adjacent introns of the *ABO* gene were amplified and sequenced with TOPO cloning. The coding sequences of *FUT1* and *FUT2* were also cloned and analyzed.

The patient´s RBCs showed weak agglutination with monoclonal anti–A at 4°C and his serum reacted with A1 and B cells. H antigen was not detected on the RBCs using the anti–H. The PCR products of Exon 6 to Exon 7 and adjacent introns of the *ABO* gene were cloned and the DNA sequences were analyzed. There was no mutation in the sequence of Exon 6 to Exon 7 blasted with the reference sequence (GenBank accession no. NM_001329877). The ABO of serology and genotype for the individual were assigned as $Am^h$ and $O_1A$, respectively.

The whole *FUT1* gene was amplified and sequenced according to the method published previously[1]. The DNA sequences of *FUT1* was analyzed and one homozygotic mutation of TT deletion were identified at Position nt1602 and nt1603 compared with the reference sequence (GenBank accession no. NM_001329877). The TT deletion generating premature termination codon induced a truncation of *FUT1* at amino acid position aa294(reference sequence, GenBank accession no.NP_001316806.1) and resulted in greatly diminished enzymatic activity of a(1, 2)–fucosyltransferase I (***Fig. 1***). The complete coding sequence

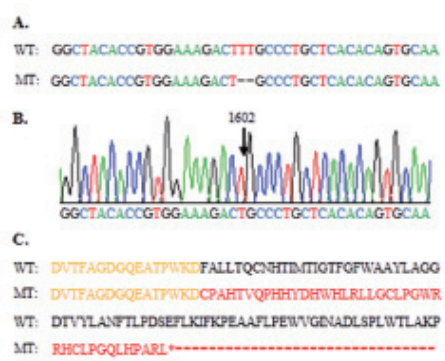


***Fig. 1.*** **Results of fractional gene and amino acids sequence of FUT1for the individual with para–Bombay phenotype.** (A). Partial sequencing of the novel deletion mutation (MT) compared with the sequence of wild type (WT). (B). The peaks of the cloning results of mutated FUT1 gene. The arrow indicated the position of deletion mutation. (C). The amino acids sequence of truncated FUT1 (MT) resulted from the frame–shifting mutation and translation termination. The asterisk indicated the translation termination.

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of this allele has been deposited in GenBank (accession no.KX852450). The FUT2 coding region was also executed with sequencing analysis. The results revealed (demonstrated) that one alleles 267G>A was identified compared with reference sequence (GenBank accession no. NM_001097638) but the mutation was nonsense with no alteration for the amino acid of Ser.

## DISCUSSION

It is fascinating to find that the homozygotes mutation of TT deletion different from single nucleotide polymorphism created frame–shifting mutation and generated premature termination codon neighboring the end of coding sequence. The mutated gene encoded one novel protein with truncated the primary structure of FUT1 triggering critically weakened function of catalysis. There are more para–Bombay phenotypes than Bombay in the Chinese population. Data indicated that the incidence of *FUT1* mutations was 1 per 8,000 in Taiwan, 1 per 15,620 in Hong Kong, and 1 per 8,539 in Fujian province located in mainland China[4]. To date, more than 43 silencing or weakening mutations of *FUT1* have been reported. This should add a new member to the Blood Group Antigen Gene Mutation Database.

### References

[1] Zanjani DS, Afzal Aghaee M, Badiei Z, et al. Molecular basis of Bombay phenotype in Mashhad, Iran: identification of a novel FUT1 deletion. *Vox Sang*, 2016, 111(1): 88–92

[2] Liang W, Xu H, Liu YY, et al. Molecular genetic analysis of para–Bombay phenotype in Chinese persons: a novel FUT1 allele is identified. *Transfusion*, 2015;55(6 Pt 2):1588.

[3] Xu X, Tao S, Ying Y, et al. A novel FUT1 allele was identified in a Chinese individual with para–Bombay phenotype. *Transfus Med*, 2011;21(6):385–93.

[4] Luo G, Wei L, Wang Z, et al. The summary of FUT1 and FUT2 genotyping analysis in Chinese para–Bombay individuals including additional nine probands from Guangzhou in China. *Transfusion*, 2013;53(12):3224–9.

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