Recent experience of ABO blood discrepancies with aids of ABO genotyping

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【**Background**】 ABO genotyping is essential for the resolution of ABO discrepancy and for the determination of ABO subgroups. Most clinical samples, including suspected inherited subgroups and acquired variant phenotypes, can be determined by PCR-sequencing of exons 6 and 7 in the *ABO* gene. Here, we described the recent cases of ABO discrepancy with helping of ABO genotyping.

【**Methods**】 We conducted a retrospective investigation of serological and genotypical data requested for ABO discrepancy to the blood bank at Chonnam National University Hospital and Chonnam National University Hwasun Hospital between August 2013 and December 2014. ABO genotyping was performed with PCR-direct sequencing of exons 6 and 7 in the *ABO* gene; the standard serologic tests were also performed.

【**Results**】 The causes of discrepancy were categorized as follows: extra serum reactivity was the most common cause with 10 cases (37%), and weak/missing red cell reactivity (9/27, 33%), mixed field red cell activity (5/27, 19%), and weak/missing serum reactivity (3/27, 11%) are following (Table 1). Aids of ABO genotyping, 59% (16/27) of ABO discrepancies could be resolved and *cis-AB* allele was the most common allele (7/16, 44%) which were demonstrated as a cause of ABO discrepancy by ABO genotyping (Table 2). A half of cases (8/16) requested for ABO genotyping was the case with *in vitro* fertilization – embryo transfer (IVF-ET) twin. Above them, 2 of 8 cases with IVF-ET twin were the blood chimera showing phenotype of $A_{int}B_3$.

【**Conclusion**】 We ensure that ABO genotyping using PCR-direct sequencing is useful for the resolution of ABO discrepancies and for the investigation of ABO subgroups. ABO genotyping will be also helpful for the evaluation of IVF-ET twin arising as a cause of ABO discrepancy recently.

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