Unraveling Genomic Architecture of The CYP3A Locus and ADME Genes Toward Personalized Tacrolimus Dosing

Methods
- GWAS using SNP array
- Targeted sequencing of ADME genes

Tacrolimus metabolizer
- Extensive metabolizer (*1/*1, ~5%)
- Intermediate metabolizer (*1/*3, ~35%)
- Poor metabolizer (*3/*3, ~60%)

Phase 1 enzyme
- CYP3A5
- CYP3A4

Conclusions
- CYP3A5 metabolizer phenotype is the most significant factor for inter-individual TAC variability.
- Stratification based on CYP3A5 metabolizer phenotype and rare variant profiling in ADME genes may further explain inter-individual TAC variability.

Yoon et al. Transplantation. 2021

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