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Dr. Apple responds:

To the Editor:

As lead author representing the IFCC C-SMCD coauthors, I acknowledge that our review on future biomarkers for detection of ischemia and risk stratification in acute coronary syndromes (ACS) was not meant to be all-inclusive. There was no intentional oversight of the inclusion of the biomarker “neopterin”, or any other biomarker, and we encourage investigators to submit manuscripts to Clinical Chemistry on biomarkers of potential utility in ACS, addressing both the clinical and assay evidence-based literature.

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<th>Recipient SNP allele</th>
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ego, CA). These were tested on 4 cases involving related living-donor kidney transplants, which we have previously examined for the presence of STR loci (4). For our current analysis, urinary DNA was extracted from 1 mL of recipient urine by commercial column technology (Roche) (9) and eluted in 50 μL of elution buffer, of which 3 μL was used for the subsequent PCR reaction. This amount corresponds to more than 3000 genome-equivalents of CF-DNA/mL of urine in these samples, which had collected within 24 h of transplantation (2, 4).

SNP loci were analyzed by the MassEXTEND MassARRAY® assay (Sequenom) (6, 7). Genotyping of the donor–recipient pairs, performed on 4 ng of genomic DNA, indicated that in only 16 instances was the donor SNP allele absent from the recipient genome (Table 1). The pertinent donor SNP allele was detected in each of these 16 instances with allelic differences (Table 1). Four representative traces are illustrated in the figure that accompanies the online version of this letter at http://www.clinchem.org/content/vol51/issue9/

Our data therefore suggest that the analysis of such SNP markers by MS may provide a new alternative for the detection of donor-derived CF-DNA. The accuracy of this approach will, however, have to be examined in a larger scale study and include samples taken at later postoperative stages, when the concentrations of urinary CF-DNA are lower than those examined in this study (2). In addition, it remains to be determined whether this MS approach will permit the reliable quantification of donor SNPs in urinary CF-DNA. As donor-derived CF-DNA has been found in the plasma of other organ transplantation recipients (10), this approach may be useful for the monitoring of transplant rejection in these patients as well.

References

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