

Comparison of Protein-bound Uremic Toxins Indoxyl Sulfate and Indole Acetic Acid Reduction Ratios in Blood and Spent Dialysate during Haemodialysis with Different Modalities

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Spent dialysate analysis as a possibility to monitor uremic toxins' removal during haemodialysis is of growing interest. In this study we evaluated reduction ratio (RR) estimations of protein-bound uremic toxins indoxyl sulfate (IS) and indole acetic acid (IAA) from serum and spent dialysate of 22 chronic haemodialysis patients by four different dialysis protocols:

- standard HDF ($Q_b=300.8 \pm 12.7$ mL/min, $Q_d=470.8 \pm 105.4$ mL/min, dialyzer area 2.0 ± 0.2 m²)
- low flux HD ($Q_b=200$ mL/min, $Q_d=300$ mL/min, dialyzer area 1.5 m²)
- medium flow HDF ($Q_b=299.7 \pm 1.0$ mL/min, $Q_d=799.8 \pm 0.9$ mL/min, dialyzer area 2.2 m²)
- high flow HDF ($Q_b=364.2 \pm 27.1$ mL/min, $Q_d=800.0 \pm 0.0$ mL/min, dialyzer area 2.2 m²)

Blood and dialysate samples were collected at the beginning and at the end of each dialysis session and concentrations of IS and IAA were determined with high-performance liquid chromatography. RR-s of unbound IS and IAA in blood and dialysate were calculated and the differences between the two methods were compared via a paired t-test assuming unequal variances, p-value of <0.05 was considered significant. The comparison of the RR-s calculated from the blood and dialysate samples for IS and IAA is presented in figure 1.

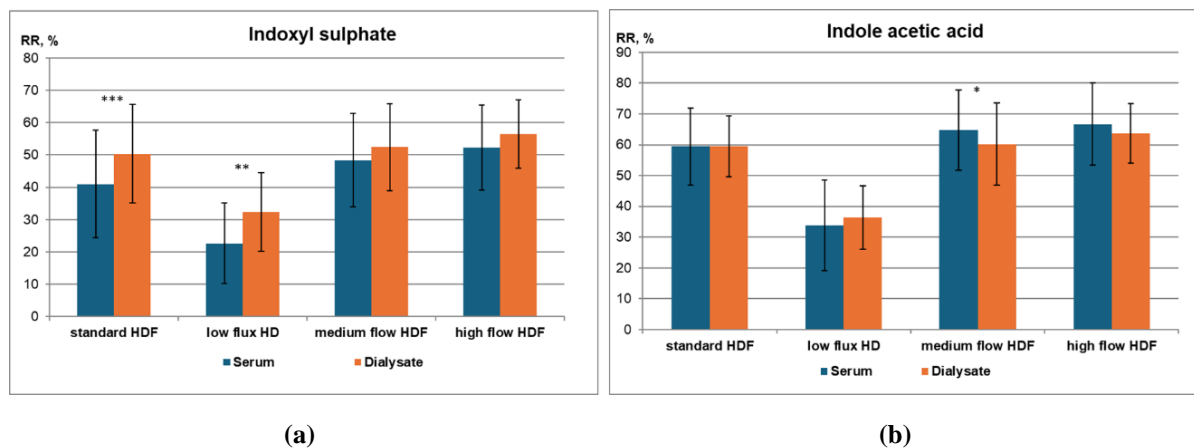


Figure 1. Comparison of reduction ratios (RR) of free indoxyl sulfate (a) and free indole acetic acid (b) in serum and dialysate by different dialysis protocols. The statistical differences are marked as *** $p < 0.001$; ** $p < 0.01$; * $p < 0.05$ serum vs spent dialysate.

This study shows that most of the RR estimations between blood and spent dialysate were comparable for IAA and less for IS. Blood *versus* dialysate RR for IAA was statistically different in medium flow HDF, whereas for IS the statistical difference was seen in standard HDF and HD. The discrepancy between the two solutes could be explained by differences in affinity to albumin or rebound effect. Additionally, the overall lowest RR-s were seen in low flux HD, suggesting that this modality may be insufficient for clearing certain protein-bound uremic toxins, compared to HDF.