INCREASING THE CLEARANCE OF PROTEIN-BOUND SOLUTES BY INCREASING DIALYZER MASS TRANSFER AREA COEFFICIENT (K_oA) AND DIALYSATE FLOW (Q_d)

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Protein bound solutes (PBS) are poorly cleared by conventional hemodialysis (HD) because protein binding limits the 'free' solute concentration driving diffusion through the dialysis membrane. Kinetic modeling predicts that the clearance of PBS can be increased by raising K_oA and Q_d above conventional levels. We tested whether this can be accomplished in clinical practice. Five stable HD patients underwent an experimental dialysis treatment in which K_oA and Q_d were increased by the use of two dialyzers in series, each supplied with a Q_d of 800 ml/min by the use of two dialysis machines. Dialytic clearances were measured for urea and the PBS indican, p-cresol-sulfate (PCS) and kynurenic acid (KYNA). Clearances during the experimental treatment were compared to those during a standard treatment with a single dialyzer and one machine. Blood flow (Q_b) and duration of treatment were the same for both sessions. Results showed: (mean ± SD; *, $p < 0.05$ vs. standard; †, $p < 0.05$ vs. % increase in urea clearance)

	% Protein Bound	Standard Treatment Clearance (ml/min)	Experimental Treatment Clearance (ml/min)	% increase in clearance
Urea	0	256 ±18	318 ±21*	24 ±7
Indican	92 ±3	30 ±8	46 ±9*	58 ±30†
PCS	94 ±2	22 ±4	37 ±6*	70 ±19†
KYNA	90 ±2	42 ±4	71 ±5*	70 ±5†

Clearances of the PBS during standard treatment were predictably lower than urea clearance. Experimental treatment increased the clearances of all solutes. However, the increases in PBS clearances were much greater than the increase in urea clearance. These results indicate that the removal of protein-bound solutes in hemodialysis patients could be increased by raising K_oA and Q_d without any increase in treatment time.