

MATHEMATICAL MODELLING OF HYDROLYSED SOLUTES TRANSPORT IN EXPERIMENTAL PERITONEAL DIALYSIS

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Abstract

Dipeptide-based peritoneal dialysis solutions may have potential advantages compared with the glucose or amino acid-based solutions. Dwell studies in rats were performed during 4 hours with dipeptide solutions containing 5 dipeptides (Gly-His, Ala-Tyr, Thr-Leu, Ser-Phe, Val-Lys), 8 or 16 mmol/l of each dipeptide (low or high dipeptide group). Dwell studies were also performed with a 1.1% amino acid solution (Nutrineal®). The model of dipeptide hydrolysis (hydrolysis rate K_H), diffusive (rate constant K_{BDD}) and convective transport as well as transport of constituent amino acids consists of mass balance equations, written for each dipeptide and amino acid. Peritoneal volume with the amino acid solution decreased much faster than that with the high and low dipeptide solutions. K_H for all dipeptides did not differ between the high and low dipeptide groups. In the low dipeptide group, K_H was 0.004 ± 0.004 ml/min (mean \pm SD) for Gly-His (the lowest) and 0.088 ± 0.048 ml/min for Thr-Leu (the highest) K_{BDD} was higher than K_H for all dipeptides, the average being 0.2 ± 0.05 ml/min.

Keywords: mathematical model, peritoneal dialysis, dipeptide, amino acid