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Mathematical modeling of peritoneal dialysis

Peritoneal dialysis (PD) is a treatment option for patients with kidney failure that is available in most countries around the world. Its main goal is to remove waste metabolic product and excess water to the fluid infused into the peritoneal cavity that is finally drained out. The increasing usage of PD required special tools that would allow for the estimation of treatment efficiency. In particular, mathematical models allow for the quantitative description of bidirectional water and solute peritoneal transport.

Three types of mathematical models can be used for the modeling of the peritoneal transport: the classical membrane model, the three-pore model, and the distributed model. The first two models (typically applied in clinical and experimental research) use phenomenologically derived parameters that characterize peritoneal transport. However, their relative simplicity does not allow for the derivation of the information on the fundamental physiological processes that govern fluid and solute transport during peritoneal dialysis. Therefore, the distributed approach is used to provide detailed information on the peritoneal physiology and more realistic description of the complexity of the peritoneal anatomy and transport system. This approach is based on the local tissue and microcirculatory physiology and its parameters are derived from the local structure and properties of the tissue and microvasculature.

In order to describe bidirectional fluid and solute transport, the two-phase structure of the interstitium was taken into account, based on the previous experimental findings (Guyton et al, 1969). The two-phase system contains a water-rich, colloid-poor region (Fluid Phase, F), where fluid transport is driven by the hydrostatic pressure, and a colloid-rich, water-poor region (Colloid Phase, C). In general, Phase C corresponds to the matrix of macromolecules that makes up the interstitial ground substance. The system of nonlinear partial differential equation was solved numerically for the tissue layer of the muscle of 1 cm width with uniformly distributed capillary and lymphatic beds and an interstitial layer (0.015 cm) on the peritoneal surface free from cells and blood vessels using a distributed model. The model parameters were adjusted to provide a description of a typical single exchange with hypertonic glucose 3.86% solution. Diffusive and convective solute transport was analyzed on the example of plasma protein (albumin) and glucose (osmotic agent).

Numerical results of the developed model described the bidirectional water and protein transport in agreement with the data about flows and clearances from clinical studies. Computer simulation suggested that two-phase structure of the tissue allows for the separation of opposite fluid flows: fluid transport from the peritoneal cavity into the tissue (absorption) occurs mainly through the Fluid Phase, whereas the Colloid Phase is used for the water transport in the opposite direction (ultrafiltration). Moreover, the model predicted that glucose transport (mainly diffusive), occurs across both phases. In contrast, the peritoneal transport of albumin, which leaks by convection to the peritoneal cavity, occurs mainly through the Colloid Phase.