Table 1. Episode characteristics according to catheter loss

	Loss (+) ($n = 47$)	Loss (–) ($n = 189$)	P-value
Mean first day cell count,/mm^3	4759.6 ± 3097.8	4769.3 ± 3106.5	0.985
Mean fifth day cell count,/mm^3	3621.3 ± 3144.1	1589.4 ± 2316.6	**<0.001**
Firth day cell count range			
0 to <300/mm^3	4 (8.5%)	80 (42.3%)	**<0.001**
≥300–1000/mm^3	9 (19.1%)	38 (20.1%)	1.000
≥1000/mm^3	34 (72.3%)	71 (37.6%)	**<0.001**
Culture			
Bacteria	28 (59.6%)	113 (59.8%)	0.856
Gram (+) bacteria	10 (21.3%)	83 (43.9%)	**0.002**
Gram (−) bacteria	15 (31.9%)	28 (14.8%)	**0.012**
Microorganism			
Pseudomonas spp	7 (14.9%)	3 (1.6%)	**0.001**
Fungi (Candida)	5 (10.6%)	0 (0%)	**<0.001**

followed by LC-MS. The cellular material was subjected to RNA sequencing. The Human Plasma Proteome database (peptideatlas.org/hupo/hppp) was used for referencing plasma proteins and estimating plasma concentration. A bioinformatic workflow conjoined information from the datasets to reveal novel insights into the 'PD effluentome,' especially clarifying the source of proteins found in PDE.
RESULTS: Combining two targeted metabolomics methods enabled detecting 207 unique metabolites in cell-free PDE. Metabolites not detected in our samples were included in the panel for *in vitro* studies of cellular systems. A mixed-effect ANOVA of all metabolites demonstrated dwell time-dependent concentration changes in 173 metabolites. Post-hoc testing revealed most metabolites to be changed between 1 and 16 h [ON] of fluid dwell (160), followed by 114 and 46 differently concentrated metabolites between 4 and 16 h and 1 and 4 h of dwell, respectively. We quantified 9797 transcripts in PD-effluent cells and 2729 solved proteins in PD effluent. A total of 342 proteins were filtered from plasma, while 800 proteins were attributable to local production. A quantitative analysis of the interaction proteome and cellular transcripts of roughly 1700 protein-transcript pairs showed clusters of proteins explained by overexpression in peritoneal cells compared to plasma concentrations.
CONCLUSION: Multi-omic profiling of PD effluent proved to be a valuable approach for revealing small molecule related changes during PD treatment. The exploitation of PD effluent information on multiple omics levels as identified by our bioinformatic approach has been shown to improve our understanding of the molecular processes in the peritoneal cavity and their role in development of complications for ultimately improving PD therapy. The combinatorial investigation of proteome and transcriptome of PD effluent represents a first step in identifying locally produced proteins for further validation as biomarkers of peritoneal health in peritoneal dialysis patients. Proteins of plasma origin could be tested for their value as diagnostic tools in monitoring treatment success and protein transport over the peritoneal barrier. Our work suggests feasibility of multi-omics approaches to investigate cell-derived biomarkers for their involvement in pathomechanisms relevant in PD.

MO702 ETIOLOGY AND THE IMPACT OF REFRACTORY PERITONITIS ON CLINICAL OUTCOMES OF PATIENTS ON PERITONEAL DIALYSIS—12 YEARS' SINGLE-CENTER EXPERIENCE FROM TURKEY

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BACKGROUND AND AIMS: The outcomes of refractory peritonitis in peritoneal dialysis (PD) patients have been reported to be inferior to those of solitary peritonitis. The current study aimed to examine the factors associated with treatment failure in PD patients experiencing refractory peritonitis.
METHOD: This single-center retrospective study included all episodes of refractory peritonitis in adult PD patients in Marmara University Hospital, Turkey, between 2009 and 2020. Patient characteristics, microbiological data, outcomes and factors associated with refractory peritonitis were analysed. The primary outcome was peritonitis-related catheter loss. Secondary outcomes were hospitalization and peritonitis-related death.
RESULTS: Overall, 236 episodes of refractory peritonitis occurring in 135 patients were included. Gram-positive, gram-negative and fungal infections accounted for 44.1%, 20.4% and 2.4% of all peritonitis episodes, respectively. Forty-seven patients (34.8%) needed catheter removal, 2 patients (1.5%) died due to peritonitis complications and 59 episodes (25%) needed hospitalization. Mean fifth day PD fluid cell count was significantly greater among patients who required PD catheter removal (3621.3 ± 3144.1 versus 1589.4 ± 2316.6 P < 0.001). Furthermore, patients with >1000/mm^3 cell count on the fifth day had higher rate of catheter removal (72.3% versus 37.6%, P < 0.001) as compared to patients with cell count under 300/mm^3. Treatment failure was more common in peritonitis episodes caused by gram (−) organisms (31.9% versus 14.8%, P:0.012). Pseudomonas and fungi-associated peritonitis were also significantly correlated with catheter loss (P:0.001 and P: <0.001) (Table 1). When peritonitis episodes with more and <1000 cells/mm^3 on the fifth day were compared, there were more episodes with gram (−) bacteria (29.7% versus 12.9%, P:0.003) and hospitalization (41.9% versus 11.4%, P: <0.001) in the group with more than 1000 cells/mm^3. In the multivariate analysis, factors associated with catheter loss were a cell count of >1000 on the fifth day and hospitalization, while presence of gram (+) bacteria related peritonitis was inversely correlated with catheter loss (Table 2).

Table 2. Factors correlated with catheter removal (multivariate analysis)

	Beta value	P-value	Exp (B) 95% CI
≥1000/mm^3 fifth day cell count	0.822	**0.044**	2.275 (1.022–5.062)
Hospitalization	1.337	**0.001**	3.809 (1.727–8.401)
Gram (+) bacteria	−0.864	**0.039**	0.421 (0.185–0.957)

CONCLUSION: Our study shows that the PD cell count on the fifth day of peritonitis can be used as a prognostic tool to determine the prognosis of refractory peritonitis episodes. Although we were unable to show the adverse prognostic effect of gram (−) bacteria related peritonitis, gram (+) bacteria related peritonitis was associated with better outcome. Prospective studies are needed to assess the risk factors for adverse outcomes of patients with refractory peritonitis, as the evidence in this area is sparse.

MO703 NONLINEAR ASSOCIATION OF FLUID OVERLOAD TO TECHNIQUE FAILURE IN PERITONEAL DIALYSIS? APPLICATION OF A CUBIC SPLINE MODEL

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BACKGROUND AND AIMS: Severe volume overload in peritoneal dialysis (PD) patients is associated with an elevated risk of technique failure [including death and transfer to hemodialysis (HD)] compared to moderate volume overload, euvolemia and volume depletion (Vrtovsnik et al., 2021 Clin Kidney J). Severe volume overload is often defined by a single cut-off value. However, such dichotomization of continuous variables in analytical models has shortcomings, especially when a nonlinear association is likely to be present.

The aim of the present analysis was to investigate whether the association of volume overload to technique failure was nonlinear in nature.
METHOD: The IPOD-PD study enrolled incident patients, on either continuous ambulatory PD or automated PD. Besides regular documentation of demographic, medical and laboratory data, body composition data from measurements employing the Body Composition Monitor (BCM, Fresenius Medical Care, Bad Homburg, Germany) were recorded.

In contrast to the previously published analysis (Vrtovsnik et al., 2021 Clin Kidney J), a competing risk analysis (kidney transplantation as competing risk) with cubic