THE EFFECT OF HEMODIAFILTRATION VS. HIGH FLUX DIALYSIS ON MIDDLE AND LARGE MOLECULES' REDUCTION AND ITS RELATION TO ALBUMIN LOSS USING BIG SURFACE AREA DIALYZER 2.6 M^2

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INTRODUCTION

- Uremic toxins are defined as molecules that accumulate in kidney impairment and have an adverse biologic effect. They can be broadly classified into three groups: small water-soluble molecule, middle molecule and protein-bound solutes **(Wolley et al., 2018)**
- Most of Hemodialysis techniques remove small water-soluble molecules. **(Wolley and Hutchison ., 2018)**
- Convective therapies and highly permeable membranes is known to remove medium – large sized molecular weight solutes giving higher dialysis adequacy but associated with higher transmembrane albumin loss than the previously routinely used low flux-HD. **(van Gelder et al., 2017)**

AIMS OF THE STUDY

Assessment of medium-sized molecules (free light chains, alpha-1 micro globulin, IL6 and procalcitonin) reduction in patients undergoing high flux dialysis versus HDF using high surface area dialyzer 2.6 $m^{2.}$

Assessment of cumulative albumin loss in patients undergoing high flux dialysis versus HDF and its correlation with convection volume.

PATIENTS AND METHODS

Type of Study: Crossover study.

Study Setting: Ain Shams University Hospitals hemodialysis units.

Sampling Method: Convenient sample.

Study Population: 25 ESRD patients on regular hemodialysis sessions

PATIENT'S SELECTION

Inclusion Criteria:

- Age 18-60 years.
- Prevalent HD patients on regular hemodialysis sessions for >6 months, 3 sessions/week of 4 hours duration.
- Patients with AV fistula.

Exclusion Criteria:

- Patients with hemodialysis catheters.
- Patients with active inflammation or infection.
- Decompensated heart failure.
- Liver Cell Failure (Child B, C)
- Patients with known malignancies.

DIALYSIS AND DIALYZER

Dialyzer:

- Biopure (BIOREMA) 260 H (effective surface area 2.6 m^2, super-flux polyethersulfone hollow fiber with steam sterilization, myoglobin SC 0.7)

Hemodialysis Modalities:

- Conventional hemodialysis
- Online Post- Hemodiafiltration

with washout period of 2 weeks using high flux dialyzers with max. surface area 2.0 m^2

- Pre/post dialysis levels of Free light chains , alpha-1-microglobulin, IL6 and procalcitonin were all done by ELISA technique, and were measured upon a single dialysis session.
- Dialysate Albumin (microalbumin mg/dl) was collected after half, 1st,2nd ,3rd hour and at the end of the dialysis session to estimate the cumulative albumin loss upon single session of high flux and HDF.

EQUATIONS

Reduction ratios for all solutes were measured using the following equation:

$$RR = \frac{Cpre - Cpost}{Cpre} \times 100\%$$

C_{pre} and C_{post} are serum concentrations of different solutes pre and post-treatment respectively.

κ/λ ratio was calculated for free light chains.

Correction of post dialysis levels for net UF with the following equation:

$$Fpost.c = \frac{Cpost}{\left(1 + \frac{\Delta BW}{0.2 \times BWpost}\right)}$$

C_{post} is solutes conc. after session, BW_{post} is the body weight after dialysis session.

EQUATIONS

Total albumin in dialysate (gm):

- $$Albumin\ \left(\frac{1}{2}, 1st\ hr\right) = \frac{Dialysate\ Alb.\left(\frac{mg}{dl}\right)}{100} \times \frac{\text{Dialysate flow}\left(\frac{\text{ml}}{\text{min}}\right) \times 30\ (\text{mins})}{1000}\ (gm)$$

- $$Albumin\ (2nd, 3rd, 4th\ hr) = \frac{Dialysate\ Alb.\left(\frac{mg}{dl}\right)}{100} \times \frac{\text{Dialysate flow}\left(\frac{\text{ml}}{\text{min}}\right) \times 60\ (\text{mins})}{1000}\ (gm)$$

Cumulative dialysate albumin (gm) :

Dialysate albumin after (30 mins+ 1st hr +2nd hr+3rd hr+4th hr)

RESULTS

COMPARISON BETWEEN PRE-DIALYSIS AND CORRECTED POST-DIALYSIS VALUES OF KAPPA AND LAMBDA IN HIGH FLUX HEMODIALYSIS

Parameter	Pre (n = 25)	Corrected Post (n = 25)	P value
	Mean ± SD		
Kappa (ng/ml)	250.60 ± 73.03	177.24 ± 54.83	P<0.001 *
Lambda (ng/ml)	267.80 ± 33.61	215.49 ± 26.60	P<0.001 *
Alph1 MG (mg/L)	47.90 ± 13.74	34.83 ± 10.76	P<0.001 *
IL-6 (ng/ml)	42.16 ± 13.59	28.36 ± 9.43	P<0.001 *
Procal (pg/ml)	146.40 ± 44.83	84.82 ± 25.15	P<0.001 *

SD: Standard deviation

*: Statistically significant at $p \leq 0.05$

COMPARISON BETWEEN PRE-DIALYSIS AND CORRECTED POST-DIALYSIS VALUES OF KAPPA AND LAMBDA IN HDF

Parameters	Pre (n = 25)	Corrected post (n = 25)	P value
	Mean ± SD		
Kappa (ng/ml)	249.0 ± 65.32	136.8 ± 40.07	<0.001*
Lambda (ng/ml)	275.8 ± 34.39	195.9 ± 19.24	<0.001*
Alph1 MG (mg/L)	55.68 ± 14.23	32.16 ± 8.94	<0.001*
IL-6 (ng/ml)	48.40 ± 13.61	26.43 ± 7.0	<0.001*
Procal (pg/ml)	206.8 ± 37.91	102.2 ± 22.27	<0.001*

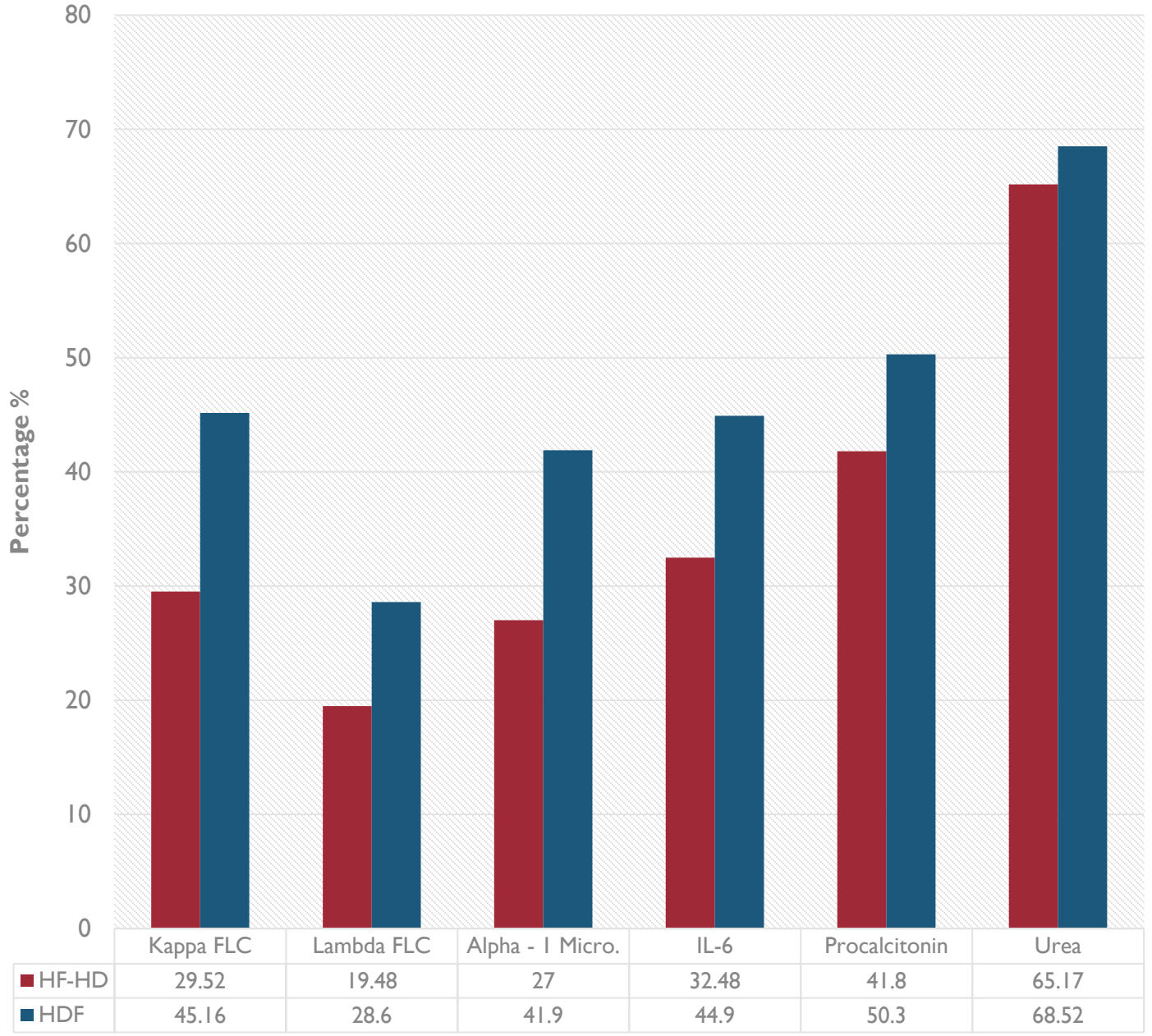
SD: Standard deviation

*: Statistically significant at $p \leq 0.05$

COMPARISON BETWEEN HD AND HDF ACCORDING TO RR% IN DIFFERENT PARAMETERS

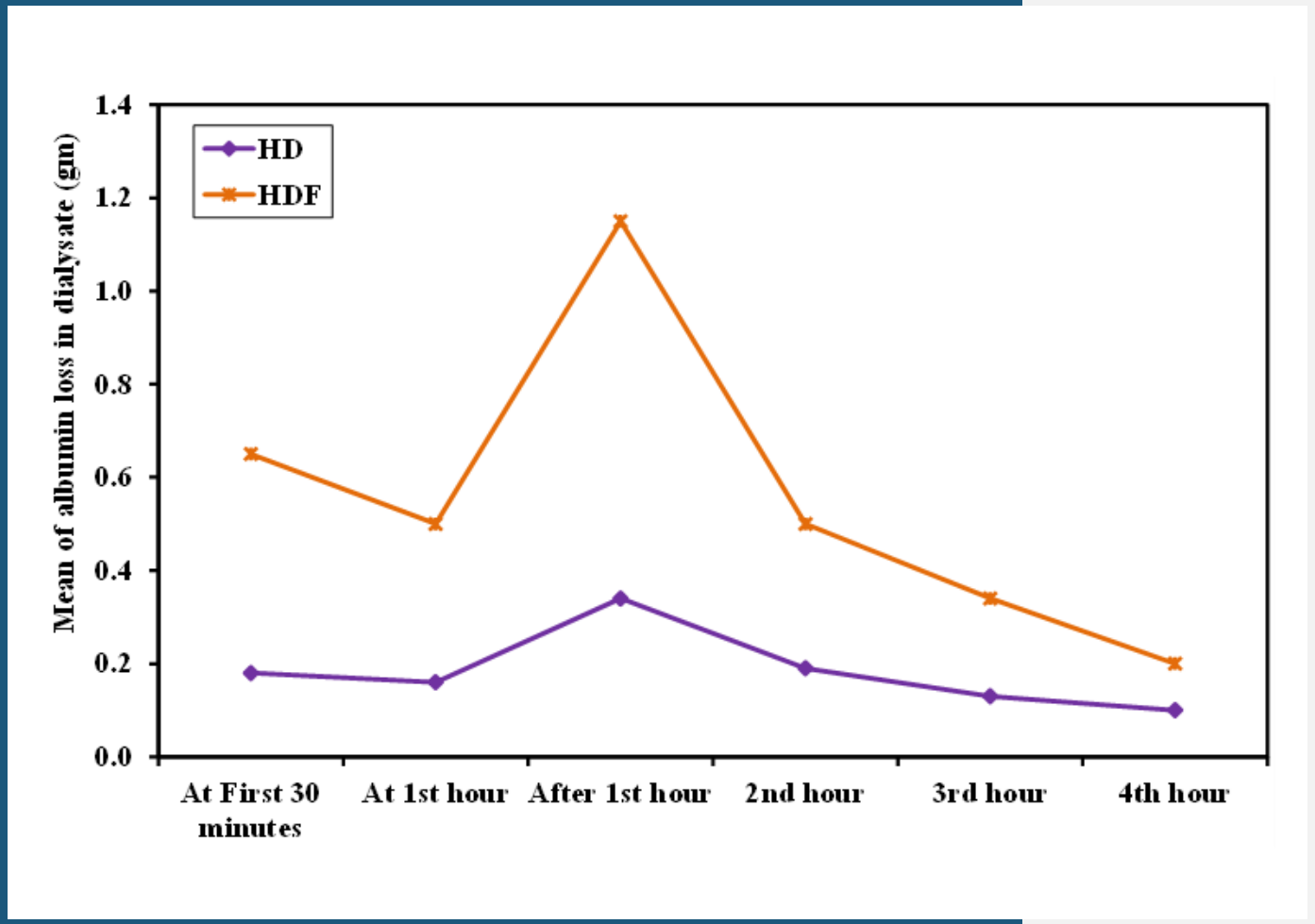
Molecule	Fold change
Kappa FLC	**1.56 ± 0.23**
Lambda FLC	**1.48 ± 0.26**
Alpha-1 micro globulin	**1.61 ± 0.38**
IL6	**1.42 ± 0.28**
Procalcitonin	**1.21 ± 0.14**
Urea	**1.05 ± 0.06**

HD Vs HDF as Regard RR% of Different Parameters



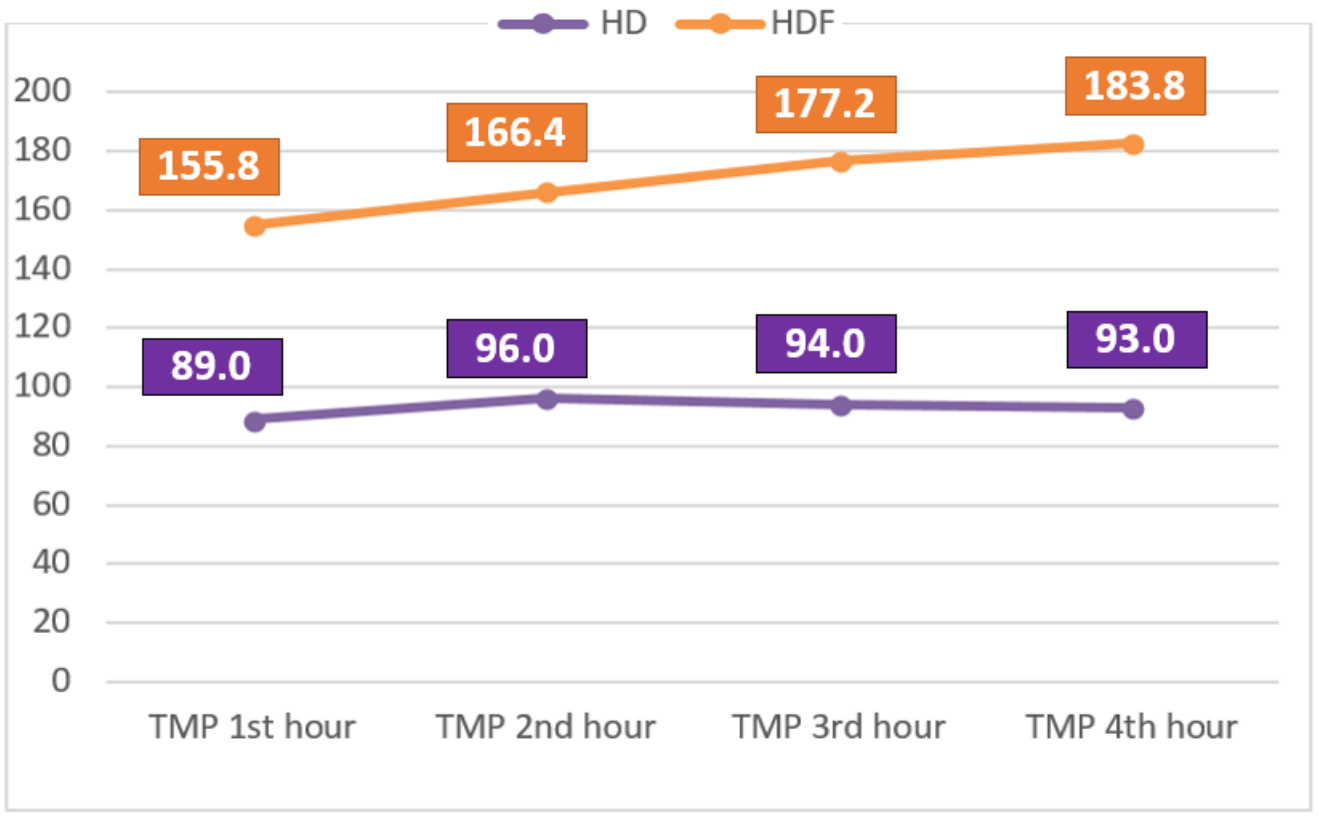
	Kappa FLC	Lambda FLC	Alpha - 1 Micro.	IL-6	Procalcitonin	Urea
HF-HD	29.52	19.48	27	32.48	41.8	65.17
HDF	45.16	28.6	41.9	44.9	50.3	68.52

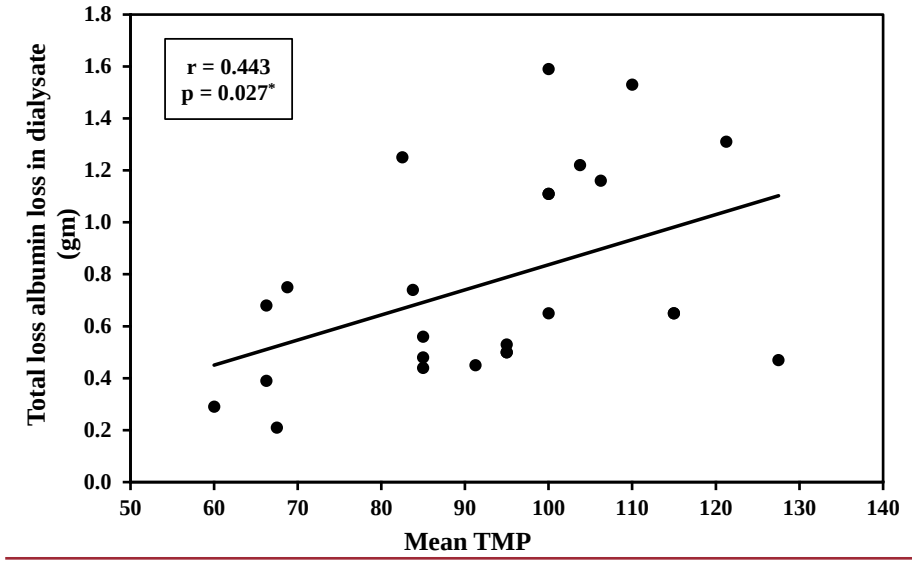
HD AND HDF ACCORDING TO ALBUMIN LOSS IN DIALYSATE



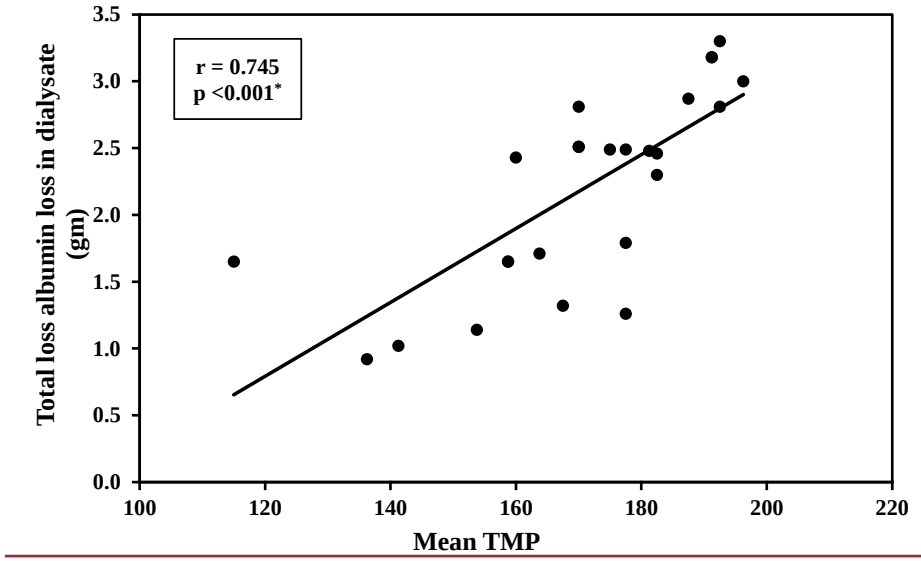
- Maximum albumin loss for patients on HDF was over the first hour with median 1.20 (0.77 – 1.3) with lower albumin loss in the next hours reaching median 0.17 (0.09– 0.24) in the fourth hour, on comparing it to albumin loss on high flux dialysis, there was significant reduction with $p<0.001$.
- There was statistical significance in total albumin loss in dialysate in patients on HDF dialysis with median 2.46 (1.7 – 2.8) compared to high flux dialysis with median 0.65 (0.48 – 1.1) with $p <0.001$.

HOURLY VARIATION IN TMP VALUES IN HIGH FLUX HD AND HDF





Total loss albumin loss in dialysate (gm) and mean TMP in HD (n = 25)



Total loss albumin loss in dialysate (gm) and mean TMP in HDF (n = 25)

CORRELATION BETWEEN TMP AND TOTAL ALBUMIN LOSS

CONCLUSION

BIOPURE 260H , High-flux dialyzer with effective surface area 2.6 m^2 ,is effective in medium-sized molecules' removal especially with online post-dilution hemodiafiltration with acceptable albumin loss.


thank you