

Abnormalities of Serum Protein Fractions in Hemodialysis Patients with Chronic Renal Failure at Ouagadougou, Burkina Faso

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Abstract

Introduction: The main objective of this study was to investigate abnormalities of serum protein fractions in hemodialysis patients with chronic renal failure (CRF) in Ouagadougou, Burkina Faso. **Methods:** This was a descriptive cross-sectional study of 48 hemodialysis patients with chronic renal failure (CRF) recruited at the Yalgado Ouedraogo Teaching Hospital (YO-TH), and 48 controls declared fit to donate blood by the Regional Blood Transfusion Center (RBTC) of Ouagadougou. Urea, creatinine, uric acid, and serum proteins were measured on the ARCHITECT C4000 equipment (ABOTT®), while the separating of the different protein fractions was performed on the Helena SAS 3 & 4 automated system. **Results:** A total of 96 individuals were included in the study. Protein levels were on average higher in controls (75.19 ± 6.56 g/L) than in hemodialysis patients (71.44 ± 12.33 g/L). Low blood albumin was significantly associated with the CRF hemodialysis groups compared to controls ($p < 0.000$). In terms of globin fractions, a significant increase in alpha-globulin 1, alpha-globulin 2 and gamma-globulin was present in the CRF hemodialysis group compared to controls ($p < 0.000$); while beta-globulin was on average lower in the CRF hemodialysis group compared to controls without significant difference ($p = 0.509$). Analysis of the electrophoretic profiles identified 57.17% polyclonal hypergammaglobulinaemia, 33.33% inflammatory profile, 10.42% undernutrition profile and 2.08% nephrotic syndrome in the CRF hemodialysis group. **Conclusion:** Serum protein electrophoresis is rapidly feasible and low cost. In hemodialysis CKD patients, it can be used to guide therapeutic management and predict morbidity and mortality related to variations in the various protein fractions.

Keywords

Protein Fractions, Albumin, Globulin, Hemodialysis

1. Introduction

Chronic kidney disease is a major and growing public health problem around the world. It is characterized by a decrease in renal function illustrated by a decrease in glomerular filtration rate (GFR) of less than 60 ml/min/1.73 m² or the presence of renal damage or both [1]. Faced with this disease, kidney replacement therapy is essential for the survival of the patient with end-stage chronic renal failure (CRF) [2]. However, hemodialysis is the most widely used treatment modality in the world, particularly in sub-Saharan Africa [3].

Chronic renal failure or even therapeutic management by hemodialysis can be responsible for several qualitative and quantitative protein abnormalities [4]. Indeed, during renal failure, the protein restriction necessary to limit the uremic syndrome, chronic inflammation, metabolic acidosis and peripheral insulin resistance can accelerate protein catabolism, while during hemodialysis infectious or toxic contaminations can cause dysproteinemia [5] [6].

The electrophoresis of serum proteins, which is a technique widely used in daily practice, makes it possible to orient the management of patients by observing the fractions of albumin, alpha 1 globulin, alpha 2 globulin, beta globulin and gamma globulin.

Studies specifically examining protein fraction abnormalities in CKD patients on hemodialysis are rare and focus on the albumin-globulin ratio to predict mortality [5] [7]. However, the description of major syndromes (nephrotic syndrome, inflammation, malnutrition, myeloma, etc.) by evaluating quantitative abnormalities of the 5 protein fractions can rapidly orient management by prescribing specialized examinations and thus contribute to reducing mortality in this population.

It is in this sense that we conducted the present study to evaluate the abnormalities of the five serum protein fractions of a group of CRF hemodialysis patients recruited from Yalgado Ouedraogo, Teaching Hospital (YO-TH) compared to a group control made up of people suitable for donating blood recruited at the Regional Blood Transfusion Center (RBTC) at Ouagadougou.

2. Materials and Methods

2.1. Type and Study Site

This was a descriptive cross-sectional study, the data collection of which was carried out over a period of two months from September 1 to October 31, 2020. The study population consisted of a group of controls recruited at RBTC and a group of CRF hemodialysis patients in the nephrology department of YO-TH.

CRF hemodialysis patients were included in the study following their consulta-

tion in the nephrology service and blood samples were taken the day after their dialysis session at the YO-TH biochemistry laboratory after a fast of at least 8 hours. The controls recruited are those declared suitable for donation following the interview prior to blood donation at the RBTC with a normal serum creatinine result.

The study population (hemodialysis CKD patients and controls) was only included after informed consent on the objectives of the study.

2.2. Collection of Blood Samples

All blood samples were taken in the collection room of the Biochemistry laboratory by a venipuncture at the elbow on a tube with a red cap in the morning between 7 a.m. and 9 a.m. in subjects fasting for at least 8 hours. The blood sample thus collected was immediately transported to the laboratory and centrifuged at 3500 rpm for 5 minutes. The resulting serum was aliquoted into a cryotube and stored in the freezer at 0°C for up to 7 days for assay.

The study variables concerned socio-demographic aspects such as age, sex, clinical aspects with the search for comorbidities (arterial hypertension, diabetes) and the date of the start of dialysis.

The biological variables we explored were uremia, creatinine, uric acid, protidemia and the electrophoretic profile of serum proteins. The analysis of the various serum electrophoretic profiles of hemodialysis CRF patients made it possible to look for polyclonal hypergammaglobulinemia (decrease in albumin and increase in gamma globulin fractions), inflammatory profiles (simultaneous increase in alpha1, alpha2 and gamma globulin fractions), undernutrition (simultaneous decrease in protidemia, albuminemia, alpha1, alpha2, beta and gamma globulin fractions) and nephrotic syndromes (decrease in albumin and increase in alpha2 globulins fractions).

2.3. Determination of Biochemical Parameters and Electrophoresis

All biochemical parameters (urea, creatinine, uric acid and protein) were assayed on the ARCHITECT Ci4000 (Abbott®) and electrophoretic profiles performed on the Helena SAS3 & SAS4 chain. Enzymatic methods allowed the determination of urea (urease/glutamate dehydrogenase) and uric acid (uricase). As for the serum creatinine and the protein level, they were assayed by modified Jaffe and biuret colorimetric methods. The separation of the different protein fractions on the Helena SAS3 & 4 machine was carried out by an electric field on an agarose gel in alkaline buffer (pH 8.5).

2.4. Data Analysis and Processing

The data were collected using Excel 2016 software. Statistical analyzes were performed using R software version 3.6.1. Means (*m*) and standard deviations (*SD*) were calculated for continuous variables such as age, urea, uric acid, creatinine, total protein, and proportions for binary variables (sex, hypertension, diabetes). The comparison of means was carried out using Student's *t* test. A probability

less than 0.05 was considered significant for all variables.

3. Results

3.1. Epidemiologic Data

In total, we included 96 subjects including 48 controls and 48 CRF hemodialysis patients for 1 to 6 years. The characteristics of the study population are presented in **Table 1**. The mean age of CRF hemodialysis patients was 44.77 ± 9.33 years and that of controls 35.42 ± 7.39 years. Clinically, all hemodialysis patients (100%) had arterial hypertension while 8.33% had associated diabetes. The control group had no comorbidities.

3.2. Biochemical Parameters of the Studied Population

Biochemical parameters of CRF hemodialysis patients compared to controls are presented in **Table 2**. Nitrogen profile of our study population showed elevated serum concentrations of uremia (16.04 ± 6.56 mmol/L), serum creatinine (1078.42 ± 363.73 μ mol/L), uric acid (371.44 ± 124.18 μ mol/L) on CRF hemodialysis compared to controls and this difference was statistically significant. In addition, glomerular filtration rate of CRF hemodialysis patients averaged 5.9 ± 2.56 ml/min/1.73 m².

Mean total protein levels were lower in the hemodialysis CRF group (71.44 ± 12.33 g/L) compared to the control group (75.19 ± 6.56 g/L). Analysis of the protein fractions of hemodialysed CRF showed a significant decrease in mean albumin concentrations (34.8 ± 7.09 g/L) in hemodialysed CRFs compared to controls (51.19 ± 4.83 g/L). In addition, a significant increase in alpha1 globulins (2.82 ± 1.31 g/L), alpha2 globulins (6.97 ± 2.8 g/L) and gamma globulins (20.28 ± 7.58 g/L) was observed in hemodialysis CRF compared to control. In addition, beta globulins were low in hemodialysis CRF (6.51 ± 1.93 g/L) compared to controls (6.75 ± 1.7 g/L).

3.3. Protein Fraction Abnormalities in Hemodialysis Patients

Frequency of abnormalities observed on each protein fraction of hemodialysed

Table 1. General characteristics of the study population.

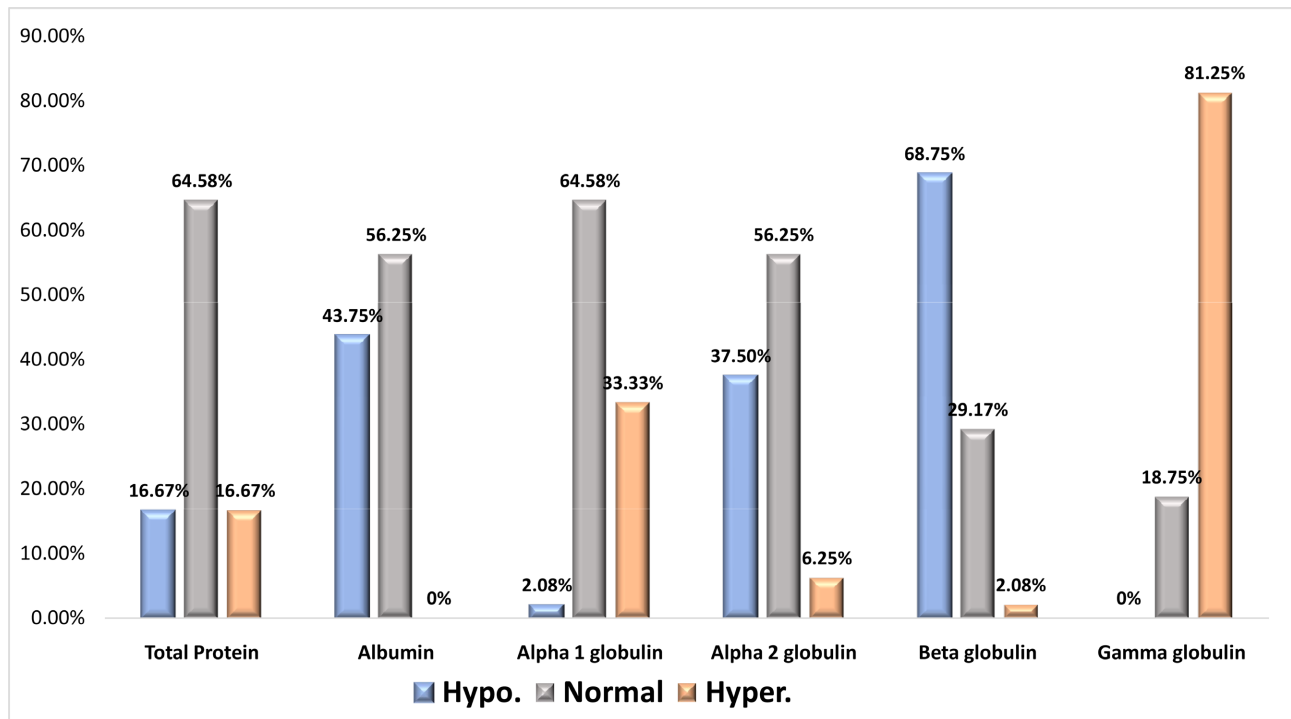
Characteristics		Controls (n = 48)	Hemodialysis (n = 48)	<i>p</i> -value
Ages (years). (m \pm SD)		35.42 \pm 7.39	44.77 \pm 9.33	<0.000*
Gender	Female n (%)	16(33.33)	23(47.92)	<0.000*
	Male n (%)	32(66.67)	25(52.08)	
High blood pressure n (%)		00(00)	48(100)	NA**
Diabetic n (%)		00(00)	04(8.33)	NA**
Mean duration of dialysis, (m \pm SD) (year)		2.96 \pm 1.32 ; Min = 1; Max = 6		

*Significant *p*-value, **Not Applicable.

Table 2. Nitrogen and protein profile of the general population.

Characteristics	Controls (N = 48)	Hemodialysis CRF N = 48)	p-value
Nitrogen profile			
Urea, m ± ET (mmol/L)	2.9 ± 1.17	16.04 ± 6.56	<0.000*
Creatinine, m ± ET (µmol/L)	75.1 ± 14.93	1078.42 ± 363.73	<0.000*
Uric acid, m ± ET (µmol/L)	323.38 ± 89.73	371.44 ± 124.18	0.032*
GFR** (m ± ET) (ml/min/1.73 m ²)	124.68 ± 23.74	5.9 ± 2.56	<0.000*
Protein profile			
Total protein, m ± ET (g/L)	75.19 ± 6.56	71.44 ± 12.33	0.065
Albumin, m ± ET (g/L)	51.19 ± 4.83	34.8 ± 7.09	<0.000*
Alpha 1 globulin, m ± ET (g/L)	1.8 ± 0.46	2.82 ± 1.31	<0.000*
Alpha 2 globulin, m ± ET (g/L)	4.97 ± 1.91	6.97 ± 2.8	<0.000*
Beta globulin, m ± ET (g/L)	6.75 ± 1.7	6.51 ± 1.93	0.509
Gamma globulin, m ± ET (g/L)	10.48 ± 2.03	20.28 ± 7.58	< 0.000*

*Significant p-value **GFR by MDRD: Glomerular filtration rate by Modified Renal Disease Diet (ml/min/1.73 m²).

**Figure 1.** Frequency of abnormalities of different protein fractions.

CRFs is presented in **Figure 1**. Indeed, the main abnormalities observed in this group were hypoalbuminemia (43.75%), hyperalpha1globulinemia (33.33%), hyperalpha2globulinemia (6.26%), hyperbeta globulinemia (2.08%) and hyper-

gamma globulinemia (81.25%).

3.4. Frequency of the Different Protein Electrophoretic Profiles

Different syndromes observed on serum protein electrophoresis are shown in **Figure 2**. Analysis of the protein electrophoresis profiles of dialysis patients showed 54.17% of patients with polyclonal gammaglobulinemia, 33.33% who had an inflammatory profile, 10.42% who had an undernutrition profile and 2.08% of patients who presented a nephrotic syndrome.

4. Discussion

In Burkina Faso, as in several countries in sub-Saharan Africa, the medical management of CRF is mainly linked to hemodialysis. Abnormalities in protein metabolism are often linked to the kidney disease itself and to dialysis. Thus, the main objective of this study was to study these qualitative and quantitative abnormalities of the protein fractions in patients with chronic renal failure undergoing hemodialysis by comparing them to controls (blood donor). Thus, despite the small size of the population of this study, one of the strengths is the analysis of the different protein fractions observed in CRF hemodialysis patients for an improvement in their management.

Biochemical profile of the study population

Nitrogen profile of the study population (hemodialysis CRF and controls) showed elevated levels of uremia, creatinine and uric acid in dialysis CRF compared to controls which had normal values; and these differences were statistically significant (**Table 2**). On the other hand, the mean GFR of CRF dialysis patients was 5.9 ± 2.56 ml/min/1.73 m². This trend has been found in almost all of the studies in patients with renal impairment and in accordance with the literature [2] [8] [9] [10].

In normal subjects, protidemia is kept in balance thanks to a pool of amino acids often provided by food and the degradation of certain proteins (proteolysis) [4]. In hemodialysis CRF patients, this balance is often disturbed not only by

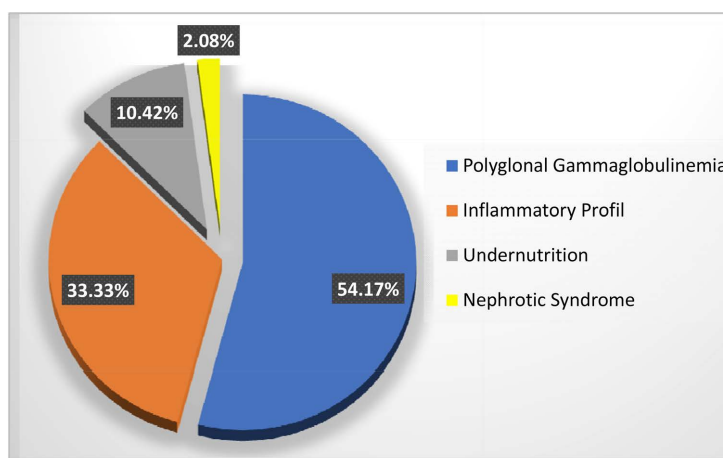


Figure 2. Distribution of protein electrophoretic profiles in hemodialysis CRF patients.

abnormalities linked to renal dysfunction (uremia, metabolic acidosis, insulin resistance, etc.), but also by hemodialysis [4].

Protidemias were on average higher in the controls compared to the CRF hemodialysis patients (Table 2). Hypoprotidemia was present in 16.67% of CKD hemodialysis patients (Figure 1). Hypoprotidemia in CRF hemodialysis patients is relatively well documented [11] [12] [13]. Indeed, it is multifactorial and could be linked to the protein-energy malnutrition from which nearly 6% to 8% of hemodialysis patients suffer, to the inflammation or to the accelerated catabolism of proteins during CRF [14] [15]. Hyperprotidemia was observed in 18.75% of patients on CKD hemodialysis. Hyperprotidemia present in our study was linked to associated hypergamma globulinemia.

Serum albumin was significantly lower in CRF hemodialysis patients (34.8 ± 7.09 g/L) compared to controls (Table 2). Lower levels are described in studies by Saizonou *et al.* (30.7 ± 8.3 g/L) [11] and Benazzouz *et al.* (29.5 ± 10.85 g/L) [12]. Hypoalbuminemia was present in 43.75% of patients on CRF hemodialysis. This hypoalbuminemia could be associated with several factors including a deficit in hepatic synthesis [16], albumin leakage through the membrane pores of some dialyzers [17], disorders of homeostasis of the internal environment linked to metabolic acidosis [4] [18] [19].

At the level of globin fractions, a significant increase in alpha 1 globulins (2.82 ± 1.31 g/L), alpha2 globulins (6.97 ± 2.8 g/L) and gamma globulinemia (20.28 ± 7.58 g/L) was present in CRF hemodialysis compared to controls (Table 2). These results are consistent with the data in the literature and have been described in several studies in CRF patients. [12] [13] [20]. Hyperalpha 1 globulin was present in 33.33% of CRF hemodialysis patients and could be explained by an increase in alpha1 glycoprotein acids (orosomucoids) associated with chronic inflammatory and degenerative conditions [21]. In addition, 5.25% of hemodialysis patients exhibited hyperalpha2 globulin which may be associated with an accumulation of alpha 2 microglobulins in certain tissues during amyloidosis observed in chronic dialysis patients [20]. Finally, hypergammaglobulinemia was present in 81.25% of hemodialysis patients and could be due to an increase in one or more immunoglobulins, requiring immunoglobulin typing, in relation either to infections (bacterial, viral, parasitic), hepatitis or lymphoproliferative patients [22].

Mean beta-globulin levels were low on CRF hemodialysis (6.51 ± 1.93 g/L) compared to controls (6.75 ± 1.7 g/L). Hypobeta globulinemia has been observed in 68.75% of hemodialysis patients and may be related to a decrease in transferrins, hemopexin, alpha and beta lipoproteins or complement. Hyperbeta globulinemia was present in 2.08% of hemodialysis patients and this could be explained by iron deficiency anemia characterized by the increase in transferrin which is a protein migrating to the level of the beta 1 globulin fraction on the electrophoresis of blood cells, serum proteins [13].

Protein electrophoretic profiles of hemodialysis CRF

Polyclonal gamma globulin profile was present in 54.17% of CRF hemodialy-

sis patients (**Figure 2**). Oualla *et al.* found 19% of polyclonal gammaglobulinemia associated with 10.52% of hepatopathies, 26.31% of infections, 10.52% of neoplastic pathologies in hemodialysis patients with CRF [13]. In fact, polyclonal gammopathies are often consistent with an overproduction of immunoglobulins by immune cells (lymphocytes, plasma cells) in the event of an infectious, inflammatory, autoimmune or malignant disease [22] [23].

Inflammatory profile concerned 33.33% of hemodialysis CRF patients. Oualla *et al.* found a frequency of 24%. A strong association between inflammation and uremia during kidney disease, particularly in patients with CRF hemodialysis, has been described in several studies [24] [25] [26] [27]. Thus, inflammation is characterized by an increase in reactive C proteins (CRP) and serum amyloid A protein (SAA) which are synthesized in the liver by being stimulated by interleukins 1,6,8 and TNF-alpha which the rates are increased in the CRF.

Undernutrition profile was present in 10.42% of CRF patients on hemodialysis. Various surveys and studies on dialysis malnutrition have estimated its prevalence between 18% and 75% depending on the studies or the judgment criteria used [28]. Ikizler *et al.* showed an increase in muscle proteolysis during the hemodialysis session [29]. In fact, hemodialysis is the cause of serum and protein muscle catabolism as well as a loss of protein reserves, thus predisposing patients to protein-caloric malnutrition.

Nephrotic syndrome was present in 2.08% of CKD hemodialysis patients. Nephrotic syndrome is characterized by a leakage of small molecules and an increase in hepatic synthesis of alpha 2 macroglobulins, LDL-c and haptoglobulins migrating to alpha 2 in order to limit the fall in oncotic pressure and the formation of edemas. Oualla *et al.* found 5% of CKD hemodialysis patients who presented with nephrotic syndrome and this was related to the efficacy of hemodialysis in controlling nephrotic syndrome [13].

5. Conclusion

Our study has shown that CRF hemodialysis patients are subject to several disturbances in protein metabolism. Indeed, by comparing the 5 protein fractions of the hemodialysis CRF patients with that of the controls, hypoalbuminemia, hyperalpha 1 globulinemia, hyperalpha 2 globulinemia and hypergamma globulinemia were the significant abnormalities observed in hemodialysis patients. The majority pathological profiles were linked to polyclonal gammaglobulinemias, inflammatory syndromes, undernutrition profiles and nephrotic syndromes. Thus, knowledge of these abnormalities linked to disturbances in protein metabolism in CRF hemodialysis patients not only guides therapeutic management but also makes it possible to prevent morbidity and mortality linked to the variation of certain proteins.

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Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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