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RESEARCH ARTICLE

Significance of serum protein electrophoresis in diagnosing multiple myeloma: A retrospective study at a tertiary care centre

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Multiple myeloma (MM) is a hematologic malignancy characterized by uncontrolled plasma cell proliferation in the bone marrow, initially asymptomatic, often causing symptoms like bone pain, anemia, renal dysfunction, and increased infection susceptibility. The study investigates the clinical significance of inconsistencies in albumin measurement methods in multiple myeloma patients, focusing on serum protein electrophoresis (SPEP) and the bromocresol green (BCG) assay. A comparative analysis was conducted to evaluate the differences between albumin levels measured by SPEP and BCG, exploring how these variations relate to disease severity and treatment decisions in MM patients. According to the results, SPEP albumin levels were significantly higher than BCG albumin levels in MM patients ($p < 0.001$). This difference is clinically significant, as lower BCG albumin readings could overestimate disease severity, potentially leading to misclassification and affecting treatment decisions. Accurate albumin measurement is crucial for proper staging and prognosis in multiple myeloma. In conclusion, this highlights the need to integrate SPEP and biochemical markers for more precise diagnosis and timely intervention. While SPEP is essential for diagnosing MM and monitoring M-protein (also known as monoclonal immunoglobulin or paraprotein), the BCG method remains useful for staging and prognosis. Standardizing laboratory protocols and exploring novel biomarkers could improve MM diagnosis, ensuring more accurate disease classification and better patient management. Further research is needed to assess the long-term impact of these discrepancies on treatment outcomes and survival rates.

1. INTRODUCTION

Multiple myeloma (MM) is a type of blood cancer characterized by the uncontrolled growth of plasma cells in the bone marrow. In the early stages, the disease may not show any symptoms. However, as it progresses, patients often experience symptoms such as bone pain, anemia, kidney problems, and a higher risk of infections (1,2). Despite extensive research, the etiology of multiple myeloma remains elusive. However, certain risk factors, including obesity, radiation exposure, and familial predisposition, have been identified.

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The pathogenesis of MM involves complex genetic abnormalities, including frequent alterations and translocations in promoter genes, particularly on chromosome 14, and mutations in oncogenes such as Neuroblastoma RAS Viral Oncogene Homolog (NRAS), Kirsten Rat Sarcoma Viral Oncogene Homolog (KRAS) and B-Raf Proto-Oncogene, Serine/Threonine Kinase (BRAF). These genetic changes contribute to malignant plasma cells' uncontrolled growth and survival (3).

Diagnosing multiple myeloma requires a multifaceted approach incorporating clinical, biochemical, and radiological assessments. A hallmark of MM is the presence of abnormal monoclonal antibodies, or paraproteins, produced by the malignant plasma cells, which can be detected in the serum and urine of affected individuals (3,4).

Serum protein electrophoresis (SPEP) is a pivotal laboratory technique in the diagnostic workup of multiple myeloma. SPEP separates serum proteins into distinct fractions based on their molecular weight and electric charge, facilitating the identification of monoclonal paraprotein. MM is diagnosed by detecting the M-spike, a narrow well-defined band on serum protein electrophoresis, that indicates the presence of monoclonal paraproteins in the serum (5). The normal electrophoretic pattern consists of a large albumin peak and five distinct globulin fractions: alpha (α)1, α2, beta (β) 1, β2, and gamma (γ) (6). In MM, the uncontrolled proliferation of monoclonal plasma cells leads to excessive production of a single immunoglobulin, resulting in a sharp M-spike, disrupting the normal balance of protein fractions. The M-spike is a crucial diagnostic feature in MM. Protein misfolding, aggregation, or degradation can cause abnormal migration patterns. SPEP separates serum proteins based on size, molecular weight, and electric charge, forming distinct bands. Albumin, the smallest and most negatively charged, migrates the fastest. α1 and α2 globulins (inflammation-related proteins) move slower, followed by β1 and β2 globulins (transport and immune proteins). Immunoglobulins (γ region) migrate slowly, where multiple myeloma's M-spike appears due to excessive monoclonal immunoglobulin production (5,6). The M-spike is predominantly observed in the gamma region, but can occasionally migrate to the beta or alpha regions depending on the physicochemical properties of the monoclonal immunoglobulin, such as molecular weight, glycosylation, charge, and conformational stability. The gamma region primarily consists of immunoglobulins, which are highly flexible and structurally heterogeneous due to their β-sheet-dominant fold. These immunoglobulins are structurally distinct from other globular proteins due to their high β-sheet content, flexible hinge regions, and post-translational modifications. The occasional migration of the M-spike to the beta or alpha regions can be explained by structural modifications, truncations, or paraprotein aggregation, which influence electrophoretic mobility (5). Accurately identifying and quantifying the M spike is crucial for diagnosing and monitoring the progression of multiple myeloma.

The study highlights the diagnostic challenges in MM due to discrepancies in albumin measurement between Serum Protein Electrophoresis and Bromocresol Green (BCG) methods. Serum albumin is crucial for disease severity assessment and staging MM. However, discrepancies between BCG assay and SPEP measurement methods raise accuracy concerns, as BCG may overestimate levels due to binding to non-albumin proteins, leading to potential misclassification and impacting treatment decisions (7). There is also a lack of standardization in albumin measurement, with BCG tending to overestimate albumin and SPEP providing a more direct electrophoretic measurement (7). The lack of a clear consensus on which method should be preferred in MM is a significant issue, causing an urgent need to evaluate the clinical impact of these differences. Misclassification of albumin can affect treatment intensity and patient outcomes, making it crucial to address this inconsistency to improve patient survival and quality of life (8). This study addresses these inconsistencies by comparing SPEP and BCG albumin measurements, evaluates their impact on MM prognosis, and emphasizes the need for standardized protocols. It also examines biochemical and hematological profiles of MM patients, explores M-protein occurrences outside the gamma globulin region, and analyzes variations in albumin estimation between the two methods.

2. MATERIALS AND METHODS

2.1. Study Design and Population

This retrospective study was conducted at a renowned tertiary health centre, Sri Ramachandra Medical College and Hospital, Chennai, India, involved 325 individuals with multiple myeloma. The study utilized a comprehensive dataset collected from a diverse patient population over three years (January 2020 to December 2023). Ethical approval was obtained from the Institutional Ethics Committee of Sri Ramachandra Institute of Higher Education and Research (Reference no: CSP/23/MAY/128/401). The objective was to investigate the role of serum protein electrophoresis (SPEP) in diagnosing multiple myeloma by examining various biochemical, hematological, and electrophoretic parameters.

2.2. Inclusion Criteria

The study included patients diagnosed with MM after SPEP screening, based on established criteria such as monoclonal paraprotein presence in serum or urine, bone marrow plasmacytosis, and evidence of end-organ damage such as bone lesions, anemia, renal impairment, or hypercalcemia.

2.3. Exclusion Criteria

This study meticulously considers and excludes cases that could affect the accuracy of albumin measurements in multiple myeloma. Patients with other hematological disorders like monoclonal gammopathy of undetermined significance (MGUS), macroglobulinemia, patients with severe liver or kidney disease, patients on albumin infusion therapy, Incomplete or missing laboratory data patients, patients with acute infections or inflammation are excluded to minimize confounding factors.

2.4. Data Collection

Data were meticulously extracted from our hospital's in-house electronic medical records software, focusing on various biochemical, hematological, and electrophoretic parameters. Key parameters: serum total protein; serum albumin (measured by both traditional methods and capillary electrophoresis) and non-key parameters: Patient demographics (age, gender); biochemical and hematological parameters (hemoglobin, blood urea nitrogen/BUN, creatinine, lactate dehydrogenase, calcium) were included.

2.5. Albumin Measurement

BCG albumin levels were measured using the Beckman Counter AU5800 analyzer, while SPEP albumin levels were assessed through serum protein electrophoresis method. Serum samples collected from patients were centrifuged at 3,000 rpm for 10 minutes at 4°C and stored at -80°C until further analysis. Serum protein electrophoresis was performed using the MINICAP FLEX-PIERCING system (Sebia, Georgia, USA), a fully automated capillary electrophoresis analyzer with primary tube piercing capability, allowing direct sampling from standard blood collection tubes. The analysis was conducted using the MINICAP Protein(E) 6 reagent kit (Sebia, Georgia, USA), comprising the separation buffer, conditioning solution, wash solution, system liquid, and necessary controls. The separation buffer provides the necessary alkaline pH (~9.9) for effective protein separation based on charge. The conditioning solution prepares and stabilizes the capillaries, ensuring consistency throughout the analysis. To prevent contamination between samples, the wash solution is used to rinse and clean the capillaries after each run. The system liquid helps maintain fluid flow within the capillary system, enabling efficient sample injection and movement. Proteins were separated in fused silica capillaries under alkaline conditions (pH ~9.9), based on their electrophoretic mobility and electroosmotic flow under high voltage. Migration was monitored by UV absorbance at 200 nm, and protein fractions were automatically quantified. The system resolved six major protein fractions: albumin, alpha1-, alpha2-, beta1-, beta2-, and gamma-globulins. Data acquisition and analysis were performed using PHORESIS software (Sebia, Georgia, USA), which generated densitometric profiles and quantified the percentage distribution of each protein fraction. Monoclonal proteins (M-spikes) were identified as sharp, narrow peaks on the electropherogram. The location and migratory pattern of these peaks were carefully evaluated. Electrophoretic profiles were further assessed for the incidence and distribution of monoclonal proteins (paraproteins), including those migrating outside the typical gamma-globulin region.

2.6. Statistical Analysis

Data was analyzed using SPSS version 20.0. Descriptive statistics, including mean, standard deviation, median, and interquartile range, were calculated for each parameter. Paired t-tests compared albumin concentrations obtained through traditional serum measurement and capillary electrophoresis. Statistical significance was set at $p<0.05$.

3. RESULTS AND DISCUSSION

The findings of this study underscore the pivotal role of SPEP in diagnosing MM and monitoring disease progression. Detecting monoclonal gammopathy through SPEP is crucial for accurate diagnosis and effective management of MM (9). The discrepancies in albumin levels between different measurement techniques underscore the importance of standardizing laboratory protocols. This standardization is a key step in ensuring diagnostic accuracy and consistency, providing reassurance to medical professionals and researchers. SPEP provides a reliable method for detecting and quantifying M proteins, which are essential markers in diagnosis and monitoring of MM.

3.1. Biochemical and Hematological Profiles of Study Participants

Descriptive statistical analysis was conducted for all biochemical and hematological parameters. Data following a normal distribution were expressed as the mean and standard deviation (SD), whereas median and interquartile range (IQR) were used for variables with non-normal distribution. These summaries provide an overview of the central tendency and variability within the multiple myeloma patient cohort, serving as the foundation for subsequent analytical assessments.

Table 1 summarizes the biochemical and hematological profiles of the study participants in our retrospective study on MM. This retrospective study included 325 patients diagnosed with multiple myeloma, consisting of 168 males (52%)

and 157 females (48%). The table provides the Mean, Standard Deviation, Median, and Interquartile Range for key parameters such as Age, Hemoglobin, blood urea nitrogen (BUN), Creatinine, Lactate dehydrogenase (LDH), Calcium, BCG Albumin, SPEP Albumin, and Total Protein, categorized by gender.

The study enrolled 325 MM patients, with a nearly equal gender distribution (52% males and 48% females). The mean age was higher for male patients (62 years) compared to female patients (57 years), a result that aligns with the established understanding that MM incidence increases with age and shows a slight male predominance.

Table 2 underscores the importance of age and gender in the distribution of biochemical parameters. Notably, albumin levels are higher in MM patients under 20 and over 80 years of age categories. The biochemical parameters such as hemoglobin, BUN, creatinine, LDH, calcium, BCG albumin, SPEP albumin, and total protein were measured. No significant gender differences were observed in these parameters, consistent with other studies reporting similar biochemical profiles across genders in MM patients.

Table 1. Biochemical and hematological characteristics of study participants

Characteristics	Total Population (n = 325)	Male (n = 168)	Female (n = 157)
Age Range (years)	60 (51-67)	62 (52-71)	57 (50-65)
*Hemoglobin (g/dL)	9.9 ± 2.222	9.9 ± 2.539	9.8 ± 1.825
*BUN (mmol/L)	17.80 ± 14.25	18.89 ± 13.05	16.60 ± 15.35
*Creatinine (mg/dL)	1.6 ± 1.526	1.6 ± 1.435	1.5 ± 1.620
*Lactate dehydrogenase (U/L)	177 ± 132.87	169 ± 92.12	185 ± 165.69
*Calcium (mg/dL)	9.29 ± 11.125	8.64 ± 1.197	9.98 ± 15.926
*BCG Albumin (g/dL)	3.02 ± 0.804	3.01 ± 0.791	3.03 ± 0.818
*SPEP Albumin (g/dL)	3.04 ± 0.802	3.04 ± 0.778	3.04 ± 0.828
*Total Protein (g/dL)	6.98 ± 1.832	7.07 ± 2.091	6.90 ± 1.534

Notes: * Mean ± standard deviation; BUN - blood urea nitrogen; BCG Albumin - Bromocresol green Albumin; SPEP Albumin - serum protein electrophoresis Albumin

The study's findings on the correlation between biochemical parameters and clinical outcomes provides valuable insights into the pathophysiology of MM. Elevated levels of BUN and creatinine were observed in the study population, indicating renal impairment. Renal dysfunction in MM is frequently attributed to monoclonal protein deposition in the kidneys and hypercalcemia-induced nephrocalcinosis (10). These renal complications are critical in the prognosis and management of MM, as they significantly impact patient outcomes and therapeutic strategies.

3.2. Prevalence of Anemia Subtypes in Multiple Myeloma Patients

To evaluate the hematological profile of multiple myeloma (MM) patients, a focused analysis was conducted on the prevalence and distribution of anemia subtypes. Anemia was classified in to subtypes, helping to identify common patterns associated with MM. This classification aids in understanding the underlying pathophysiology and its clinical implications.

The pie chart illustrating the distribution of anemia subtypes in the study population in Figure 1, indicates that most individuals with multiple myeloma (61%) have Normocytic Normochromic anemia, whereas 11% are not anaemic. Anemia is a prevalent complication in MM, primarily due to bone marrow infiltration by malignant plasma cells, which impairs erythropoiesis. In this study, 61% of patients had normocytic normochromic anemia, the most common type seen in MM patients. This finding is validated by the International Myeloma Working Group, a key authority in the field, which notes that normocytic normochromic anemia is a typical manifestation of MM. The presence of anemia in MM patients is a significant prognostic factor and often correlates with disease severity. The high prevalence of normocytic normochromic anemia among MM patients reflects the impact of bone marrow infiltration by malignant plasma cells, leading to reduced erythropoiesis (11).

3.3. M-Band Detection Across Different Regions

Capillary electrophoresis was employed to detect the presence and distribution of M bands in multiple myeloma patients. This method separates serum proteins into distinct regions—α1, α2, β1, β2, and γ—allowing precise localization of the monoclonal protein. The frequency of M band occurrence in each region was then calculated and is presented as a pie chart.

A pie chart presenting the percentage of M band detected at each region is shown in Figure 2. Among these patients, 66% had the M band in the gamma (γ) region, 8% in both the alpha (α)1 and α2 regions, and the lowest percentage in the beta (β)1 region.

The distribution of M proteins predominantly in the gamma region aligns with previous findings that highlight the tendency of monoclonal immunoglobulins to migrate to this region during electrophoresis (5,12). The introduction of capillary electrophoresis (CE) has revolutionized the detection and quantification of monoclonal immunoglobulins in serum and urine. This advancement has significantly improved the field, reducing the variation associated with different

dye-binding capacities in agarose gel electrophoresis (5,13). CE enhances the differentiation of the β region into β1 and β2 fractions, thus improving their separation. It offers better resolution compared to agarose gel electrophoresis by utilizing the principle of endosmosis and high voltage, which facilitates the separation of proteins into β1 and β2 fractions, primarily composed of transferrin, low-density lipoprotein, and complement proteins (C3, C4) (5,14).

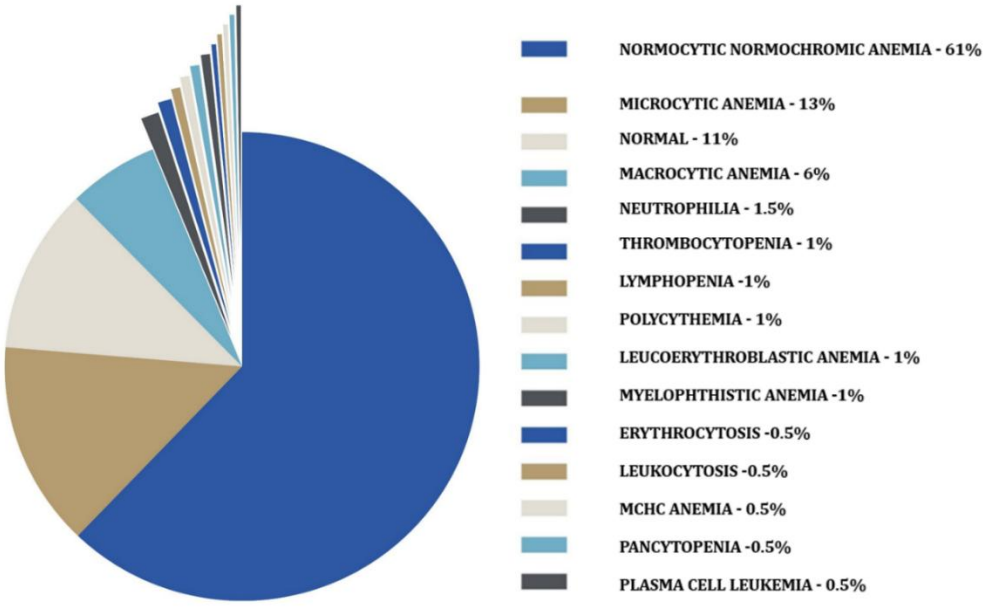

Figure 1. Pie chart representing the distribution of anemia subtypes in the study population

The α1 fraction, which mainly includes α1 antitrypsin and α1 acid glycoprotein (orosomucoid), shows increased conditions associated with an acute inflammatory response, such as trauma, inflammatory joint disease exacerbation, and burns (10). Similarly, the α2 fraction, which contains haptoglobin, ceruloplasmin, and α2 macroglobulin, often shows elevated levels in nephrotic syndrome due to the large size of α2 macroglobulin preventing its passage through the glomerular membrane (15). Additionally, α2 macroglobulin synthesis increases as a compensatory mechanism for the significantly decreased serum albumin levels in nephrotic syndrome.

Monoclonal proteins and physiologically present serum proteins in the β1 and β2 fractions may co-migrate, contributing to unusual elevations in these fractions. In iron deficiency anemia, a pseudo-monoclonal elevation in the beta fraction may occur due to increased serum transferrin levels, with a similar pattern observed in hemolyzed samples due to the co-migration of free hemoglobin (5,16). Due to falsely high fibrinogen levels, unusual elevations in the β2 fraction may also be seen in patients undergoing dialysis or anticoagulant therapy, such as heparin.

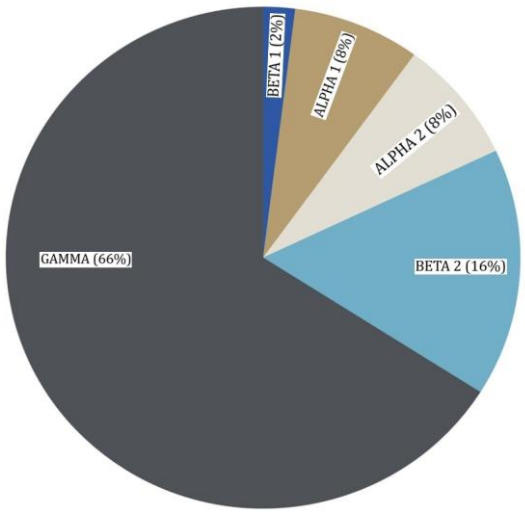

Figure 2. The pie chart illustrates the percentage distribution of M-band locations across various regions

Table 2. Distribution of biochemical parameters based on age and gender

AGE (years)	< 20			21- 40			41 - 60			61 – 80			> 80		
Population	**Total n=5**	**Male n=3**	**Female n=2**	**Total n=17**	**Male n=7**	**Female n=10**	**Total n=150**	**Male n=65**	**Female n=85**	**Total n=140**	**Male n=83**	**Female n=57**	**Total n=13**	**Male n=9**	**Female n=4**
Hemoglobin (g/dL)	11.8	15.5	8.1	10.6	11.7	9.6	10.1	10.1	10.1	9.5	9.4	9.6	9.7	10	9.3
BUN (mmol/L)	8.7	9	8	7.9	9	6.9	16.7	17.4	16	19.9	20.4	19.3	22.9	28.2	17.6
Creatinine (mg/dL)	0.9	0.9	0.9	0.75	0.95	0.56	1.55	1.59	1.52	1.60	1.53	1.68	2.12	2.94	1.30
LDH (U/L)	106	102	110	154	164	144	185	176	193	175	166	185	154	184	123
Calcium (mg/dL)	9.6	9.6	9.6	8.2	8.5	7.9	9.8	8.5	11.1	8.6	8.6	8.6	8.9	9.1	8.8
SPEP Albumin (g/dL)	4.08	4.35	3.80	3.40	3.43	3.38	3.07	3	3.13	2.88	2.94	2.82	3.31	3.48	3.13
BCG Albumin (g/dL)	4.02	4.25	3.80	3.44	3.46	3.42	3.04	2.98	3.10	2.86	2.90	2.81	3.33	3.46	3.20
Total protein (g/dL)	8.02	7.45	8.60	6.51	6.60	6.43	6.86	6.92	6.80	7.28	7.30	7.26	5.38	6.36	4.40

Notes: BUN – blood urea nitrogen; LDH – Lactate dehydrogenase; BCG Albumin - Bromocresol green Albumin; SPEP Albumin - serum protein electrophoresis Albumin

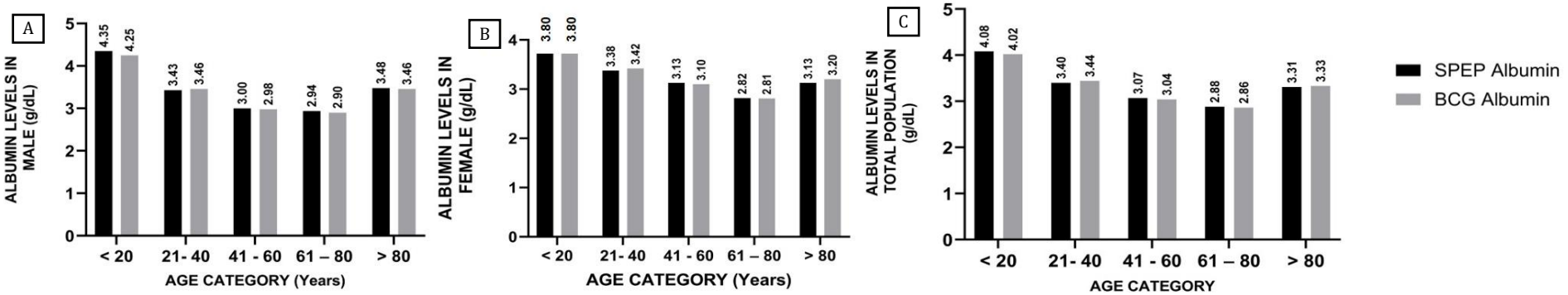

Figure 3. Column Graph representing Albumin levels. (A) Albumin levels in Male. (B) Albumin levels in Female. (C) Albumin levels in total population. X-axis: Age (years); Y-Axis: Albumin levels (g/dL); g/dL - grams per Deciliter

The gamma fraction is the most common region for monoclonal protein migration. However, extremely high serum CRP levels, uremia, rheumatoid factor, or degraded samples may also cause a pseudo-monoclonal increase in this fraction (17). Polyclonal IgA can result in β-γ bridging in the electrophoretogram, indicating a confluence of the β2 and gamma fractions. CE, combined with immunofixation (IS), plays a crucial role in identifying and characterizing even weak monoclonal immunoglobulin components in SPEP, instilling confidence in the diagnostic process and differentiating between pseudo-monoclonal proteins and paraproteins. Biochemical assays of serum proteins, along with free light chain assays and serum immunoglobulin levels, further confirm monoclonality CE and agarose gel electrophoresis are both 99% specific. However, CE has a sensitivity of 95% compared to 91% for gel electrophoresis (18).

Small monoclonal components do not always conform to typical patterns and may appear in fractions other than the gamma region, which can manifest as irregularities in the curves on electrophoretograms. The most common immunoglobulin associated with these irregularities is IgA, likely due to its tendency to polymerize. It can sometimes be challenging to determine whether such irregularities are caused by elevated levels of proteins normally present in that fraction or by monoclonal protein migration (5). This issue can be clarified using immunoelectrophoresis, a technique that uses antibodies to identify and separate proteins based on their charge and size, thereby helping to distinguish between normal and abnormal protein patterns.

3.4. Discrepancies in Albumin Measurement: SPEP vs. BCG in MM Patients

To evaluate the consistency and clinical relevance of albumin measurement methods in multiple myeloma patients, a comparative analysis was conducted between serum protein electrophoresis (SPEP) albumin and bromocresol green (BCG) albumin values. Albumin levels were compared across both genders, and a paired sample t-test was performed to assess statistical differences between the two methods.

Figure 3 displays Column graphs illustrating albumin levels in multiple myeloma patients across different age groups. Patients under 20 and over 80 exhibited higher albumin levels, whereas those in the 61-80 age group showed lower levels. Although male patients tended to have higher albumin levels than females, the difference was not statistically significant ($p > 0.05$).

Higher albumin levels were found in patients younger than 20 and older than 80, with lower levels in the 61-80 age group. This could be attributed to disease stage, comorbidities, and nutritional status differences across age groups. Although male patients had higher albumin levels than females, the difference was not statistically significant ($p>0.05$), indicating that gender does not substantially influence albumin levels in MM patients. The importance of measuring serum albumin in multiple myeloma patients has risen with the recent introduction of the International Staging System (ISS), which classifies prognosis based on albumin levels (19).

Figure 4 presents a Column graph comparing the average SPEP albumin and BCG albumin level. The graph highlights that SPEP albumin levels were consistently higher than BCG albumin levels in both Genders. A paired sample T-test comparing BCG Albumin and SPEP Albumin revealed a statistically significant difference, with a p-value of $p<0.001$. The study found significant differences between BCG albumin and SPEP albumin measurements, with higher SPEP albumin levels. This discrepancy highlights the need for standardized measurement techniques in clinical practice. Albumin is a critical marker for assessing the nutritional and inflammatory status of MM patients, and accurate measurement is essential for guiding treatment decisions. The significant p-value ($p<0.001$) from the paired sample t-test indicates a reliable difference between the two methods, advocating for consistent approaches in albumin estimation.

The significant difference between BCG and SPEP albumin levels further emphasizes the need for consistent measurement techniques in clinical practice (20). Despite these differences, both PEL and BCG assays performed similarly as predictors of patient survival. This may be because the impact of albumin on outcomes is most pronounced at the extreme ends of the albumin spectrum. In contrast, patients with intermediate albumin levels (around the 35 g/L threshold) have less influence on the prognostic value of the test. This finding supports the observation made by the ISS that albumin alone has limited prognostic value, and its effectiveness in prognosis is enhanced when combined with other variables, such as beta 2 microglobulin (21).

A 2024 study by Penickova et al. (22) compared bromocresol green (BCG) colorimetric, immunoturbidimetric, and capillary electrophoresis techniques revealed that BCG consistently reported higher plasma albumin levels, especially in patients with elevated markers of inflammation such as C-reactive protein and alpha-1/alpha-2 globulins. This overestimation by the BCG method in cases of inflammation and low albumin levels could lead to misguided treatment decisions.

Accurate albumin measurement is critical for staging multiple myeloma, assessing the nutritional and inflammatory status of MM patients and guiding therapeutic decisions (23). For most of the general population, M-spikes are either absent or present in very low concentrations. BCG and SPEP methods have shown good correlation with nephelometry for M-spikes ranging from 0 to 15 g/L. However, discrepancies between these assays can occur without an M spike, as BCG often overestimates albumin levels compared to PEL in standard samples. Therefore, it is recommended that measurements for the same patient be performed using the same assay, or the relationship between assays should be considered during interpretation.

Our study revealed that SPEP consistently measured higher albumin levels than the BCG assay in multiple myeloma patients, highlighting a notable discrepancy. This difference is clinically significant, as the BCG assay's underestimating albumin may lead to an overestimation of disease severity, potentially affecting staging and treatment decisions. Since albumin plays a crucial role in the ISS staging system, lower BCG values could misclassify patients into higher-risk categories, leading to unnecessarily aggressive treatment. In contrast, SPEP provides a more precise measurement by effectively distinguishing albumin from other serum proteins, reducing the risk of misclassification. These findings underscore the importance of using SPEP-based albumin assessment for MM staging to ensure accurate disease evaluation and appropriate treatment planning. Integrating SPEP-based albumin assessment into routine practice could improve staging and treatment decisions accuracy, ensuring patients receive optimal care based on their true disease status. Standardizing measurement techniques or adjusting for inter-assay differences could enhance staging accuracy and patient care.

3.5. Limitations and Future Scope

This study has limitations, including its retrospective design, which may introduce bias and a sample size that may not fully represent diverse populations. Variations in lab methods could also impact results. Additionally, the lack of long-term follow-up limits the assessment of clinical impact.

Future studies should explore the long-term impact of albumin measurement discrepancies on treatment outcomes and survival. A longitudinal follow-up could clarify their influence on disease progression and therapy response. Conducting prospective, multi-center studies with large diverse patient populations and novel biomarkers are needed to refine MM diagnosis and treatment. Integrating advanced genomic and proteomic technologies may further uncover disease mechanisms and new therapeutic targets.

4. CONCLUSIONS

This study comprehensively analyzes biochemical and electrophoretic profiles in MM patients, emphasizing the importance of integrating SPEP and biochemical markers for accurate diagnosis and timely interventions. Standardizing laboratory protocols and exploring novel biomarkers are essential for advancing MM diagnosis and treatment. SPEP plays a vital role in diagnosing multiple myeloma and tracking M-protein levels, while the BCG method adds value by offering essential albumin data crucial for staging and prognosis. These tests provide a well-rounded approach to understanding and managing the disease.

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