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Comparison of two automated immunoassay methods for C-Peptide measurement: Alinity® versus Cobas e411®

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ABSTRACT

Introduction: C-peptide measurement is an essential tool in the assessment of endogenous insulin secretion and in the management of diabetes. However, differences in analytical methods between platforms may impact result comparability. This study aims to evaluate the agreement between two commonly used automated immunoassays for C-peptide quantification: Alinity® (Abbott) and Cobas e411® (Roche Diagnostics).

Material and Methods: A total of 100 serum samples were randomly selected from routine C-peptide tests. Internal quality controls were performed daily on both analyzers, prior to each C-peptide assay run, on the same day. Statistical analyses were carried out using MedCalc® software (version 23.1.7).

Results: The two methods showed good correlation ($r^2 = 0.9907$). Bland-Altman analysis revealed a mean bias of −6.61% between the two analyzers, indicating that Alinity® tends to provide slightly lower values compared to Cobas e411®. The Passing-Bablok regression equation obtained was: y (Alinity®) = −0.154 + 0.989 × x (Cobas e411®).

Discussion and Conclusion: Although both methods demonstrated strong correlation and satisfactory linearity across the entire concentration range, the observed systematic difference may have clinical implications, particularly in patient monitoring or interpretation of C-peptide–derived indices. These findings highlight the importance of standardization and harmonization of assay methods to ensure optimal comparability between analytical platforms.

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Abbreviations

CHU, Centre Hospitalier Universitaire ; CMIA, Chemiluminescent Microparticle Immunoassay; ECLIA, Electrochemiluminescent Immunoassay; IRR, International Reference Reagent; ng/mL, nanogram per milliliter; P, Cusum test for linearity; R^2 / r^2, correlation coefficient ; CRM, Certified Reference Material

Introduction

C-peptide is a bioactive endogenous peptide secreted by pancreatic beta cells. It is formed during the cleavage of proinsulin, producing both active insulin and C-peptide, which are subsequently secreted in equimolar amounts into the bloodstream. Due to its longer half-life, C-peptide reaches higher plasma concentrations than insulin (1). C-peptide plays a crucial role beyond insulin biosynthesis by acting on several organs, including the kidneys, heart, neurons, vascular endothelium, and microcirculation. It helps mitigate dysfunction and early damage caused by type 1 diabetes, such as glomerular hyperfiltration, endothelial inflammation, and neuronal demyelination. By binding to its specific receptor, it activates signaling pathways involving G proteins and calcium, thereby promoting the production of endothelial nitric oxide synthase, Na^+/K^+-ATPase, and transcription factors that regulate apoptosis, inflammation, and cellular defense mechanisms (1,2).

The measurement of C-peptide, in conjunction with insulin, glucose, and glycated hemoglobin levels, represents a promising approach for the early diagnosis of diabetes. Furthermore, recent advances regarding its biological properties-particularly its potential as a hormone -pave the way for its use as a therapeutic option for diabetic neuropathy and nephropathy (3). Concurrently, the fasting C-peptide/glucose ratio has emerged as a critical biomarker for distinguishing between insulin deficiency and excess profiles, thereby facilitating more personalized therapeutic management according to diabetes subphenotypes (4).

The aim of our study is to compare two C-peptide assay methods using two different analyzers: the Alinity® system (Abbott), based on chemiluminescent microparticle immunoassay (CMIA) technology, and the Cobas e411® (Roche Diagnostics), which uses electrochemiluminescent immunoassay (ECLIA).

Materials and Methods

This comparative study was conducted in the biochemistry laboratory of the Mohammed VI University Hospital Center (CHU) in Oujda over a one-month period, from February 1 to March 1, 2025. The study sample consisted of a Moroccan population, including both outpatients and inpatients at CHU Mohammed VI in Oujda.

In total, 100 blood samples were collected in dry tubes without separating gel from venous blood, following quality criteria for sample collection. Hemolyzed, inadequate tubes, or samples collected more than one hour before processing were excluded. The samples were then centrifuged for 10 minutes at 1500 revolutions per minute. The serum was collected by pipetting and aliquoted into two tubes simultaneously, then analyzed directly using two analyzers: the Alinity® system and the Cobas e411®.

Corrective actions were taken for abnormal quality control values on each analyzer on the same day and prior to any C-peptide analysis in our samples. A new calibrator and control kit, provided by the manufacturers, was used for each analyzer. Calibration of the C-peptide parameter was successfully performed. Quality control for the parameter was conducted, and the results obtained for each level and each analyzer are as follows: for Alinity®, the target value for level 1 is 0.78 ng/mL and for level 2 is 5.19 ng/mL; for Cobas e411®, the target value for level 1 is 1.11 ng/mL and for level 2 is 4.41 ng/mL. C-peptide assay results were expressed in ng/mL. Finally, the data obtained were analyzed using the statistical software MedCalc® version 23.1.7. The characteristics of the two assay methods are presented in Table 1.

Table 1 . Comparison of the characteristics of the two C-peptide assay methods. (IRR: International Reference Reagent; WHO: World Health Organization)

Characteristic	Abbott Method	Roche Method
Principle	CMIA	ECLIA
Reagent stability once opened and loaded	30 days	8 weeks
Sample type	Serum	Serum
Calibrator traceability	WHO IRR 84/510	WHO IRR 84/510
Limit of Quantification/Detection (ng/mL)	0.03	0.010
Measuring range (ng/mL)	0.03 to 30	0.010 to 40.0
Reference value (ng/mL)	0.78 to 5.19	1.11 to 4.41
Intra-assay precision (%)	1.93%	3.18%
Total precision (%)	2.1%	3.2%
Assay time (minutes)	30	18

Results

A total of 100 serum samples were analyzed to compare two immunoassay methods for C-peptide measurement. The concentrations measured ranged from 0.01 to 19.65 ng/mL for Alinity® and from 0.012 to 20.98 ng/mL for Cobas e411®. Both methods demonstrated good agreement, with a concordance correlation coefficient of $r^2 = 0.9907$ (Table 2).

The Bland-Altman plot analysis (Figure 1) revealed a mean bias of -0.18 ng/mL (-6.61%) between Alinity® and Cobas e411®, indicating that the Alinity® system yields slightly lower values. The 95% limits of agreement (-0.92 to +0.56) encompassed the majority of differences, and the homogeneous distribution of data points around the mean suggests no significant proportional bias.Regarding Passing-Bablok regression (Figure 2 and Table 3), the equation obtained was: y (Alinity®) = −0.154 + 0.989 × x (Cobas e411®), with a slope of 0.9890 (95% CI: 0.9446 to 1.0448) and an intercept of -0.1538 (95% CI: -0.2853 to -0.08821). The Cusum test for linearity (P = 0.85) indicated no significant deviation, confirming that the relationship between Alinity® and Cobas e411® follows a valid linear model. Finally, Deming regression yielded a slope B = 0.9923 (95% CI: 0.9038 to 1.0808) and an intercept of -0.1606 (95% CI: -0.3741 to 0.05286)

Table 2 . Coefficient of variation and correlation results between Alinity® and Cobas e411®.

Parameter	Value
Y Variable	Alinity®
X Variable	Cobas e411®
Sample size	100
Overall mean	2.7209
Coefficient of variation (%)[a]	31.8856
95% Confidence interval	26.8624 to 37.1076
Correlation coefficient (r)	0.9907
Significance level	P < 0.0001
95% Confidence interval for r	0.9861 to 0.9937

Table 3. Results of Passing-Bablok and Deming regression analysis.

Parameter	Passing-Bablok	Deming
Systematic differences		
Intercept (A)	-0.1538	-0.1606
95% Confidence Interval	-0.2853 to -0.08821	-0.3741 to 0.05286
Proportional differences		
Slope (B)	0.9890	0.9923
95% Confidence Interval	0.9446 to 1.0448	0.9038 to 1.0808
Linearity validity		
Cusum test for linearity (P)	0.85	No significant deviation from linearity

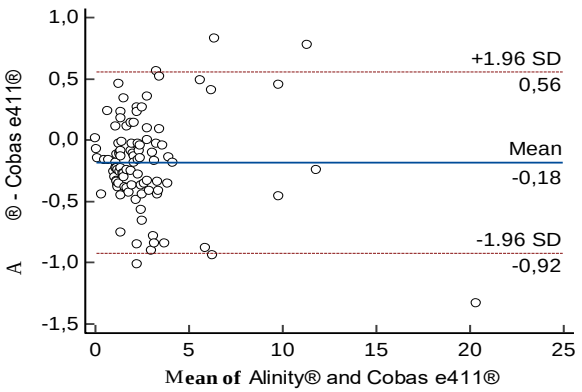

Figure 1. Bland-Altman plot showing the difference between Alinity® and Cobas e411® in C-peptide measurement.

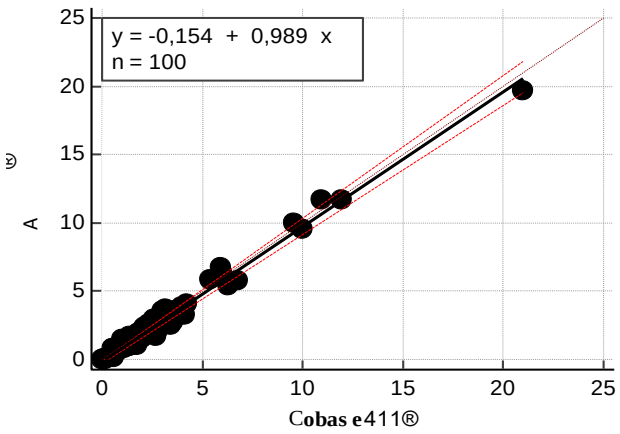

Figure 2. Linear regression between Alinity® and Cobas e411®.

Discussion

C-peptide is considered a reliable marker of endogenous insulin secretion in diabetic patients. Beyond its diagnostic usefulness, it is involved in the prevention of certain chronic complications of type 1 diabetes, contributes to the diagnosis of insulinoma, and currently has therapeutic potential (1,2). In recent years, C-peptide measurement has become increasingly common, highlighting the importance of further scientific research into assessing its accuracy and comparability between laboratories worldwide.

Several studies have reported method comparisons for C-peptide measurement, conducted in reference laboratories or multicenter settings, under highly standardized analytical conditions and with large sample sizes. However, the results of these comparisons are not always directly comparable.

Unlike multicenter studies or those conducted in reference laboratories, our study was carried out in a routine hospital laboratory using two widely deployed automated immunoassay platforms at a tertiary university hospital in Morocco. Although the sample size is modest, it reflects routine laboratory activity and encompasses a clinically relevant range of C-peptide concentrations, thereby providing a more accurate representation of everyday clinical practice.

Our results demonstrate a strong linear correlation between the Alinity® and Cobas e411® systems C-peptide immunoassays (r^2 = 0.9907), indicating high analytical concordance. Bland-Altman analysis showed that 94% of measurements fell within the predefined limits of agreement (-0.92 to 0.56 ng/mL), with a mean bias of -0.18 ng/mL (-6.61%), suggesting that the Alinity® tends to slightly underestimate C-peptide concentrations compared with the Cobas e411®. Although this bias is below generally accepted analytical error limits and unlikely to affect clinical decisions in most situations, it may be relevant during longitudinal patient monitoring or for values near clinical decision thresholds, highlighting the importance of consistent use of the same analytical platform.

At higher C-peptide concentrations (>10 ng/mL), a few values exceeded the limits of agreement, suggesting increased variability, which may be partly explained by methodological differences, including assay technology (CMIA vs. ECLIA), reagent stability, and analytical sensitivity (lower limit of quantification for Cobas e411® at 0.010 ng/mL vs. 0.03 ng/mL for Alinity®). Regression analyses further confirmed a slight constant systematic bias, as shown by the Deming regression equation (Alinity® = −0.1606 + 0.9923 × Cobas e411®) and the negative intercept (-0.1538), while the slope close to unity (0.9890-0.9923) indicated minimal proportional bias and overall good agreement between the two methods.

These findings are consistent with previously published studies comparing C-peptide assays. Hörber et al. (5), reported that Cobas e411® provides C-peptide concentrations approximately 16.3% higher than those obtained with Alinity®, despite a good linear correlation ($r^2 > 0.97$). Similarly, a recent study conducted in China by Zhou et al., (6) involving 94 laboratories and several analytical platforms (Abbott, Roche, and Siemens), reported overall satisfactory analytical performance but highlighted persistent inter-system differences, underlining the ongoing challenges of assay harmonization.

The slight variability between methods observed in our study can also be explained by the current limitations of C-peptide assay calibration. Indeed, C-peptide immunoassays are currently calibrated using an old international reference standard (IRR 84/510), which is now depleted and has been replaced by a new WHO standard (13/146) (7). However, calibration strategies based on purified standards have not ensured optimal inter-method comparability. Recent studies suggests that the use of commutable materials, such as plasma or serum samples representative of the biological matrix, could improve harmonization (8). In this context, a new Japanese reference material (CRM 6901-b), developed from human serum, appears promising for enhancing inter-method accuracy. Nevertheless, the coexistence of different standardization approaches and regulatory differences between countries continues to complicate recalibration efforts (9).

Based on these findings, several practical recommendations can be proposed to reduce the impact of analytical variability on clinical management: verification of reagents accuracy and specificity, establishment of local reference intervals adapted to the population and analytical method used, consideration of sample type (serum versus plasma), systematic communication with clinicians in case of method changes, maintenance of continuous dialogue between biologists and clinicians, and regular participation in external quality assessment programs.

Our study has certain limitations. First, its single-center design, due to the availability of C-peptide testing in only one tertiary hospital in our city, may limit the generalizability of the results. Second, the relatively small sample size (100 samples), due to the cost of assay kits, is also a limitation. Future multicenter studies, including a larger number of samples and additional analytical systems, would be useful to further evaluate the comparability between methods and support larger-scale harmonization efforts.

In order to establish an accreditation procedure for the analyses performed in our laboratory, our study fits into a relevant continuity by adding to the other comparison studies already carried out within the biochemistry laboratory of the Mohammed VI University Hospital in Oujda (10–12). In accordance with the requirements of NF EN ISO 15189 and NF EN ISO/IEC 17025 standards concerning the quality management system, the central laboratory of the Mohammed VI University Hospital in Oujda is continuing the implementation of quality processes, including method verification procedures according to application area A, as well as validation of the methods necessary for qualifying most routine tests, including C-peptide assays (13).

Conclusion

Improving laboratory performance in selecting appropriate measurement systems for C-peptide requires the implementation of a harmonization and standardization process. This would help optimize the therapeutic management of diabetic patients, refine diabetes classification, and enhance the comparability of research studies.

Declarations

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None.

Conflicts of interest

The authors declare that they have no conflicts of interest in relation to this article.

Authors' contributions

KJ was responsible for writing the original manuscript, data collection and processing, biological analysis of samples, as well as the study methodology and conceptualization. DM, HS, and MC contributed to the critical review and revision of the manuscript, results visualization, validation, and supervision.

Ethics approval

The study was conducted in accordance with the Declaration of Helsinki

References

1. Shpakov AO, Granstrem AO. C-peptide structure, functions and molecular mechanisms of action. Tsitologiia. 2013 Jan 1;55(1):16–27.

2. Ao S. New achievements in the study of the mechanisms and targets of action of proinsulin c-peptide. Tsitologiia. 2015 Oct 1;57(6):405-14.

3. On P, If U. Molecular mechanisms of action and physiological effects of the proinsulin C-peptide (a systematic review). Biomeditsinskaia Khimiia. 2020 May 1;66(3).

4. Fritsche A, Heni M, Peter A, Gallwitz B, Kellerer M, Birkenfeld AL, et al. Considering Insulin Secretory Capacity as Measured by a Fasting C-Peptide/Glucose Ratio in Selecting Glucose-Lowering Medications. Exp Clin Endocrinol Diabetes. 2020 Sep 18;130:200–4.

5. Hörber S, Orth M, Fritsche A, Peter A. Comparability of C-Peptide Measurements – Current Status and Clinical Relevance. Exp Clin Endocrinol Diabetes. 2023 Jan 11;131(3):173–8.

6. Zhou W, Deng Y, Zhao H, Zhang C. Current Status of Serum Insulin and C-Peptide Measurement in Clinical Laboratories: Experience from 94 Laboratories in China. Ann Lab Med. 2022 Jul 1;42(4):428–37.

7. Moore M, Dougall T, Ferguson J, Rigsby P, Burns C. Preparation, calibration and evaluation of the First International Standard for human C-peptide. Clin Chem Lab Med. 2017 Jul 26;55(8):1224–33.

8. Wiedmeyer HM, Polonsky KS, Myers GL, Little RR, Greenbaum CJ, Goldstein DE, et al. International comparison of C-peptide measurements. Clin Chem. 2007 Apr 1;53(4):784–7.

9. Kinumi T, Goto M, Eyama S, Kato M, Kasama T, Takatsu A. Development of SI-traceable C-peptide certified reference material NMIJ CRM 6901-a using isotope-dilution mass spectrometry-based amino acid analyses. Anal Bioanal Chem. 2012 Jul 1;404(1):13–21.

10. Bensalah M, Bouayadi O, Rahmani N, Lyagoubi A, Lamrabat S, Choukri M. Comparative study of the serum measurement of PTH on Roche Cobas e411® versus the Abbott Architect ci8200®. Ann Biol Clin (Paris). 2018 Jan 1;76(1):61–7.

11. Lamrabat S, Lyagoubi A, Bouayadi O, Elmalki J, Elkouche K, Bensalah M, et al. Comparison between Roche Integra 400 plus and Abbott Architect ci8200 in Alanine aminotransferase assay. Pract Lab Med. 2019 May 1;15:e00121.

12. Sebbar E houcine, Choukri M. Comparison between two automated immunoassay methods for total 25-hydroxyvitamin D: Architect ci8200 ® versus Cobas e411®. Mater Today Proc. 2023 Jan 1;72:3484–6.

13. Lorec-Pénet AM, Saunier V, Lombard E, Arfi C, Portugal H. Du GBEA à l'accréditation dans un laboratoire de biochimie de CHU : application à une structure multi-sites. Rev Francoph Lab. 2010 Feb 1;2010(419):33–44.

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