

Review

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Advancements and challenges in high-sensitivity cardiac troponin assays: diagnostic, pathophysiological, and clinical perspectives

On behalf of the Italian Study Group on Cardiac Biomarkers

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Abstract: Although significant progress has been made in recent years, some important questions remain regarding the analytical performance, pathophysiological interpretation and clinical use of cardiac troponin I (cTnI) and T (cTnT) measurements. Several recent studies have shown that a progressive and continuous increase in circulating levels of cTnI and cTnT below the cut-off value (i.e. the 99th percentile upper reference limit) may play a relevant role in cardiovascular risk assessment both in the general population and in patients with cardiovascular or extra-cardiac disease. International guidelines recommend the use of standardized clinical algorithms based on temporal changes in circulating cTnI and cTnT levels measured by high-sensitivity (hs) methods to detect myocardial injury progressing to acute myocardial infarction. Some recent studies have shown that some point-of-care assays for cTnI with hs performance ensure a faster diagnostic turnaround time and thus significantly reduce the length of stay of patients admitted to emergency departments with chest pain. However, several confounding factors need to be considered in this setting.

A novel approach may be the combined assessment of laboratory methods (including hs-cTn assay) and other clinical data, possibly using machine learning methods. In the present document of the Italian Study Group on Cardiac Biomarkers, the authors aimed to discuss these new trends regarding the analytical, pathophysiological and clinical issues related to the measurement of cardiac troponins using hs-cTnI and hs-cTnT methods.

Keywords: cardiac troponins; high-sensitivity methods; myocardial infarction; myocardial injury; point-of-care testing (POCT) methods; cardiovascular risk

Introduction

We have come a long way since September 2000, when the Joint European Society of Cardiology/American College of Cardiology Committee consensus document on the redefinition of myocardial infarction recommended for the first time that cardiac troponin I (cTnI) and T (cTnT) should be considered the preferred biomarkers for the differential diagnosis of acute coronary syndrome (ACS) [1]. Currently, all guidelines recommend that the clinical cut-off value for the diagnosis of acute myocardial infarction (AMI) should be set at the 99th percentile of the cTn distribution in a reference population (i.e. 99th percentile upper reference limit - URL) and that the analytical imprecision of cTn assays at this value (coefficient of variation, CV) should be $\leq 10\%$ [2–5]. Furthermore, these recommendations require that cTn assays measure the distribution of the biomarker (including the 99th percentile URL) in a reference population with reasonable accuracy [1–3]. However, almost 15 years passed before manufacturers commercialized the first cTn immunoassays with analytical performance that met these quality specifications [2, 5, 6].

In May 2018, the expert opinion of the Academy of American Association of Clinical Chemistry (AACC) and the Task Force of the International Federation of Clinical

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Chemistry (IFCC) [2] stated that two criteria are needed to define high-sensitivity methods for cardiac troponin I (hs-cTnI) and T (hs-cTnT) assays: 1) the measurement error of the hs-cTn concentration, corresponding to the 99th percentile URL value, should be $\leq 10\%$; 2) measurable hs-cTn concentrations should be achievable at or above the assay's limit of detection (LoD) in $\geq 50\%$ of healthy individuals of both sexes [2].

In August 2018, the Fourth Universal Definition of Myocardial Infarction [3] stated that: "The detection of an elevated cTn value above the 99th percentile URL is defined as myocardial injury". The myocardial injury is considered acute if there is a rise and/or fall in cTn values [3]. Myocardial injury can occur in several cardiac and systemic pathologies [3]. Moreover, the definition of AMI requires the preliminary detection of acute myocardial injury by means of hs-cTn assay in the setting of clinical evidence of acute myocardial ischaemia [3].

Several confounding factors must be considered when evaluating a patient presenting with chest pain to the Emergency Department (ED). Standardized clinical algorithms based on temporal changes in circulating hs-cTn levels should be used to detect myocardial injury progressing to AMI [2]. In August 2020, the European Society of Cardiology (ESC) guidelines suggested that clinical algorithms based on temporal changes of even less than 3 h may be used to diagnose ACS in patients presenting without persistent ST-segment elevation using hs-cTn methods [4].

Although significant progress has been made in recent years, some important questions remain regarding the analytical performance, pathophysiological interpretations and clinical use of hs-cTnI and hs-cTnT assays [5–8]. Some key issues relate to the analytical performance and clinical interpretation of hs-cTnI and hs-cTnT levels, in particular the implementation of new laboratory tests for hs-cTn assay in clinical practice according to the principles of precision medicine and near-patient testing methods [7–11]. In this respect, the methodology of immunoassay methods has been implemented in the last 5 years to establish some point-of-care testing (POCT) methods with analytical performances similar to those of hs-cTnI and hs-cTnT immunometric assays of analytical platforms usually used in clinical laboratories [9–21]. In particular, some POCT hs-cTnI methods have recently been commercialized and their analytical performance and clinical relevance have been validated in independent cohorts [12–14, 16–20].

From a pathophysiological perspective, the cardiomyocyte can undergo either reversible or irreversible damage, e.g. due to a brief occlusion of a coronary artery or intense physical activity [22–28]. Several recent studies have shown that reversible cardiomyocyte damage is characterized by the release into the circulation of a limited amount of

cytoplasm or some blebs containing degraded sarcomeric proteins with a lower molecular weight (MW) but a higher plasma turnover rate compared to the intact sarcomeric proteins cTnI (MW=23.5 kDa) and cTnT (MW=33.5 kDa) [21–31]. Recent studies have shown that some forms of troponins I and T with reduced MW and faster plasma clearance than sarcomere-bound troponins are often measured after intense and prolonged physical exercise (e.g. marathon or cycling race) [26, 27, 29–31]. In addition, degraded forms of cTnI and cTnT can be measured in patients with end-stage renal disease [32, 33]. Unfortunately, the immunometric methods for hs-cTnI and hs-cTnT cannot directly measure and identify the circulating forms of the biomarker with lower rather than higher MW [30, 31]. Therefore, currently available hs-cTnI and hs-cTnT assays cannot differentiate between reversible and irreversible myocardial damage by a single biomarker measurement [21, 30, 31]. From a clinical point of view, some recent studies have suggested that a progressive and continuous increase in circulating levels of hs-cTnI and hs-cTnT, both in the general population and in patients with cardiovascular or extra-cardiac disease, may play a relevant role in cardiovascular risk assessment, even when the biomarker levels are still below the 99th percentile URL value [34–41]. Furthermore, a novel approach may be the use of machine learning methods to develop an algorithm for the early diagnosis of AMI in patients presenting to the emergency department, taking into account the results of laboratory methods (including hs-cTn assay) as well as other clinical data [42–44]. This review article aims to discuss these new trends in analytical, pathophysiological and clinical issues related to the measurement of cardiac troponins using hs-cTnI and hs-cTnT methods.

Analytical and methodological issues

In the last 10 years, the use of hs-cTnI and hs-cTnT has allowed the time to diagnosis of AMI to be reduced from 6–12 h to less than 3 h in most patients [4, 5, 9–11, 45, 46]. In particular, the ESC 2020 guidelines recommend the fastest clinical algorithms with blood sampling on admission and after 1 or 2 h (0–1 h or 0–2 h) for the diagnosis of non-ST-segment elevation myocardial infarction (NSTEMI) [4]. This recommendation is based on large multicentre studies reporting that these algorithms (especially the 0–1 h algorithm) allow a diagnosis to be made in the shortest possible time, in particular to rule out AMI, thus reducing the time spent in the emergency department [4, 19, 47–53]. However, faster algorithms can only be effectively implemented in

hospitals where the ED works in close collaboration with the clinical laboratory, allowing a turnaround time (TAT) of <60 min, including the time from when the sample arrives at the laboratory to when the testing is completed and the laboratory prepares and releases the results [10–12, 41, 46].

Recently, several expert documents and guidelines have suggested that POCT methods for cTnI and cTnT with high analytical sensitivity may represent a fundamental advance because these methods could further reduce the TAT of cTnI and cTnT measurement in patients with NSTEMI [9–11, 15, 54, 55]. Furthermore, these hs-cTn POCT methods may allow the diagnosis of NSTEMI at home, in the outpatient clinic or even in the ambulance, as these assays do not require sample centrifugation or other preanalytical sample processing [9–11, 15–17, 54–57]. Since 2019, some experimental studies have evaluated the analytical performance of some POCT methods for cTnI assay to test whether these methods meet the requirements for high-sensitivity assays [12–14, 57–61]. The analytical sensitivity data (i.e. limit of detection, LoD, and limit of quantitation, LoQ) and 99th percentile URL values of some POCT cTnI methods reported in these independent studies [12, 14, 57–59] are summarized in Table 1. In addition, the IFCC Committee on Clinical Applications of Cardiac Biomarkers (IFCC C-CB) regularly updates a specific and detailed document reporting the analytical characteristics and performance of all commercially available hs-cTnI and hs-cTnT methods (including POCT assays) according to the technical reports provided by the manufacturers [62]. In addition, several studies have compared the diagnostic

accuracy of the POCT hs-cTnI assay with traditional hs-cTnI and hs-cTnT methods in patients with suspected NSTEMI-ACS [12–14, 54–66].

In January 2002, the IFCC C-CB published a document containing an in-depth analysis of the analytical characteristics and clinical relevance of these new POCT methods for cardiac troponins. In particular, the IFCC C-CB document provides several specific requirements for high-sensitivity imprecision criteria concerning the evaluation of several analytical parameters, including: sensitivity values (i.e., LoB, LoD, LoQ), two specific high-sensitivity criteria, linearity, imprecision, analytical specificity, examination of high-dose hook effect, comparison of sample matrix, assessment of hematocrit dependence, and comparison between methods [11]. A very common aphorism among experts in laboratory medicine is that “good, fast and cheap” laboratory testing is a mission impossible [15]. For example, a cheap test may not be cost-effective (or vice versa). However, accurate, rapid and cost-effective laboratory methods are exactly what are needed to detect acute ischaemic myocardial injury in patients presenting to the emergency department with chest pain [9–11, 15–17, 21, 67]. However, from an analytical point of view, some POCT methods are known to be more susceptible to interference from haemolysis, lipemia or sample contamination than hs-cTnI and hs-cTnT methods using automated platforms, which are more difficult to control outside a clinical laboratory [9–11]. In addition, environmental factors such as temperature fluctuations can also affect the performance of POC devices, particularly in

Table 1: Recent studies reporting an independent validation of analytic sensitivity and calculation of 99th percentile upper reference limit (URL) values of point-of-care (POC) methods for cTnI assay methods.

Immunometric system	Instrument	LoD, ng/L	LoQ 10 %, ng/L	99th percentile URL, ng/L	References
PATHFAST POC hs-cTnI	PATHFAST™ instrument	2.9	11.0	W:21.1 (13.4–25.3) ^b n=236 M:27.0 (18.5–27.7) ^b n=238 Overall: 24.2 (17.6–27.4) ^b	Sorensen NA et al. (2019) [12]
KM SPFS POC hs-cTnI method	KM SPFS POC desktop analyzer	0.54	3.9	W:10.7 (n=300) M:20.6 (n=300) Overall:12.2 ng/L (9.2–39.2) ^b	Braga F et al. (2020) [57]
Siemens POC atellica® VTLi hs-cTnI	Atellica® VTLi patient-side immunoassay analyzer	1.2	6.7	W:18.0 (9.0–78.0) ^b n=330 M:27.0 (21.0–37.0) ^b n=363	Apple FS et al. (2021) [14]
Super flex POCT hs-cTnI	SuperFlex platform	1.8	12.0	W:24.0 (n=312) M:27.0 (n=308) Overall: 25.6 (22.0–33.3) ^a	Zhang R et al. (2021) [58]
Siemens POC atellica® VTLi hs-cTnI	Atellica® VTLi patient-side immunoassay analyzer	1.24	2.1	F:18 (9–78) ^a (n=330) M: 27 (21–37) ^a (n=363) Overall: 23(20–32) ^a	Christenson RH et al. (2022) [59]

LoD, limit of detection; LoQ 10 % CV, limit of quantitation 10 % CV; W, women; M, men; overall, M+W; n, number of enrolled individuals; ^a 90 % confidence interval; ^b 95 % confidence interval.

environments without consistent climate control, potentially affecting the reliability of results. Other factors that may lead to false elevations or inaccurate results include: location of the device, allocation of collection and testing, responsibility for (non-laboratory) staff, maintenance of the device, initial and recurrent training, quality control, proficiency assessment, capture of discrepant results, troubleshooting and inventory management [11].

Although hs-cTn POCT methods significantly reduce turnaround time by providing results at the patient's bedside, they still require blood to be drawn. A possible new perspective is the development of wearable devices capable of estimating circulating cTn levels through the skin (so-called "on vivo" testing) [68, 69]. The development of wearable devices with similar analytical performance to the hs-cTn assay is a very complex task. Infrared spectroscopy is an inherently sensitive mode of detection due to its ability to interact with the material at the molecular level and has the advantage of requiring minimal or no sample preparation [67]. The same group of researchers discussed the ability of non-invasive transdermal monitoring of cTnI to provide estimates of cTn blood concentration in a first article [68], while a second article reported the clinical results obtained using the non-invasive transdermal device supported by a deep learning model [69]. In particular, the authors found a significant correlation between optically derived data obtained with the non-invasive transdermal instrument and blood-based immunoassay measurements ($r=0.777$, $p<0.001$, $n=52$ biologically independent samples) with an area under the curve (AUC) value of 0.895 (sensitivity 96 %, specificity 60 %) for predicting a clinically meaningful threshold for defining elevated circulating cTnI levels [68]. The main limitation of this study is the relatively small sample size ($n=52$) [68]. Sengupta et al. [69] tested the feasibility of a wrist-worn transdermal infrared spectrophotometric sensor (transdermal-ISS) and the performance of a machine learning algorithm to identify elevated hs-cTnI in 238 patients with ACS from 5 different hospitals. A deep learning model derived from the transdermal-ISS was trained and externally validated using hs-cTnI and echocardiography and angiography. The transdermal I-SS model predicted elevated hs-cTnI levels with an AUC of 0.90 [95 % CI: 0.84–0.94; sensitivity 86 %, specificity 82 %] for the internal cohorts and 0.92 (95 % CI, 0.80–0.98; sensitivity 94 %, specificity 64 %) for the validation cohorts. In addition, the model predictions were associated with regional wall motion abnormalities [odds ratio (OR), 3.37; CI, 1.02–11.15; $p=0.046$] and significant coronary stenosis (OR, 4.69; CI, 1.27–17.26; $p=0.019$).

The results of these two studies [68, 69] should be considered very preliminary due to the relatively small sample size. However, these studies represent an important first step in the long process of developing some portable devices capable of accurately measuring circulating levels of

cardiac troponins [15, 17, 67]. The incorporation of machine learning (ML) and artificial intelligence (AI) capabilities into POCT could lead to compact and portable, even more miniaturized and accurate devices for hs-cTnI and/or hs-cTnT measurements.

Take-home messages

- In the last 10 years, the time to diagnosis of AMI in patients presenting to the ED with suspected ACS has been reduced from 6–12 h to less than 3 h [4, 5, 9–11, 45, 46].
- Several expert documents and guidelines have suggested that the development of POCT methods for hs-cTnI and hs-cTnT may represent a fundamental advance, as these methods could further reduce the turnaround time for cTnI and cTnT measurement in patients with NSTEMI [9–11, 15, 54, 55].
- The IFCC C-CB has published a document outlining the analytical characteristics and clinical relevance required for POCT hs-cTn methods [59].
- A very recent study reported some results on portable devices based on infrared spectroscopic detection of circulating cardiac troponin levels through the skin in hospitalized patients with ACS [69].

Pathophysiological issues

Despite dramatic improvements in assay sensitivity over the past 25 years, Kavsak et al. [70] recently reported that approximately 1/3 of devices measuring hs-cTnT do not meet the precision target at the female URL value recommended by international guidelines. Furthermore, the specific recommendation to evaluate the 99th percentile URL values of hs-cTnI and hs-cTnT methods using a reference population of >400 healthy men and women is not followed even by some studies specifically designed to evaluate the analytical performance of POCT cTnI methods (Table 1) [12, 14, 57, 58]. These data confirm that the evaluation of cut-off values (i.e. the 99th percentile URL) of hs-cTnI and hs-cTnT assays remains an open question [4–6, 11–15, 21, 45, 46, 70–73]. There are at least four main points to consider when evaluating the 99th percentile URL values of cardiac troponins in a reference population: 1) the distribution of circulating levels of hs-cTnI and hs-cTnT is highly right-skewed in healthy men and women; 2) men have significantly higher biomarker levels than women of the same age; 3) biomarker concentrations increase progressively after 55 years of age in both sexes; 4) there is no global consensus on defining health or 'normality'

in a reference population [70–75]. Collectively, these factors make the evaluation of 99th percentile URL values very challenging.

As an example, the sex-specific distributions of circulating hs-cTnI levels measured by the ARCHITECT hs-cTnI method (Abbott Laboratories, Abbott Park, IL, USA) in an Italian reference population are shown in Figure 1A for women and in Figure 1B for men. These data were obtained in a healthy Italian reference population (mean age 51 years; range 18–86 years; number of women: 648; number of men: 665) [72, 73]. In particular, considering that the LoD value of the ARCHITECT hs-cTnI method is 1.3 ng/L [72, 73, 76], more than 50 % of the healthy women enrolled in this reference population have a hs-cTnI value higher than the LoD value (Figure 1A). Although the 99th percentile values of the Italian reference population were evaluated according to all recommendations of international guidelines [2, 5, 45, 46], the sex-specific calculated 99th URL values show very large 95 % confidence intervals (CI), especially for women. In fact, the difference (i.e. 14.1 ng/L) between the high (i.e. 22.6 ng/L) and low (i.e. 8.5 ng/L) value of the 95 % CI is larger than the calculated 99th percentile value for the healthy female population (i.e. 12.4 ng/L) (Figure 1A). However, there were only two women (Figure 1A) and two men (Figure 1B) showing hs-cTnI values above the sex specific 99th URL values (i.e., clearly indicated in the Figure as outliers with an arrow). These 2 women (respectively with age of 39 and 41 years) and men (respectively with age of 22 and 48 years) should be considered true outliers because they had an age < 50 years. To summarize, 99th URL values for hs-cTnI and

hs-cTnT show a large variability in the reference population (i.e., including only healthy individuals), because it depends not only on the analytical performances of hs-cTnI or hs-cTnT methods, but also on age, sex and body mass of the reference population [41, 77]. Circulating hs-cTn levels of healthy adult subjects represent a reliable index of the physiological cardiomyocyte renewal, which is defined as the ability to replace loss of cardiomyocytes by new ones, as demonstrated by several experimental and clinical studies [23–25, 41, 77–79]. On average, the biological variation of cardiac troponins is similar in healthy subjects [80–85] and patients with cardiac or non-cardiac diseases [86–91]. Overall, the results of these studies [80–91] have demonstrated that both cardiac troponins have an average intra-individual biological variability of about 10 % CV as well as an individuality index of 0.3 [41, 77]. In particular, the individuality index value of cardiac troponins is comparable to that of creatinine, which is considered a reliable biomarker of skeletal muscle turnover [92]. Considering the peculiar biological and physiological characteristics of cardiac troponins, it is not surprising that the evaluation of circulating biomarker levels between two (or more) samples over a given time interval can provide more accurate pathophysiological and clinical information than the comparison of a concentration value measured in only one sample with the 99th percentile URL value of hs-cTnI and hs-cTnT, which is characterized by a high degree of statistical uncertainty because this cut-off value is calculated from a large reference population [41, 71–73, 77].

The commonly recommended statistical approach to assess the variation of a biomarker measured by the same method in two samples is to calculate the reference change

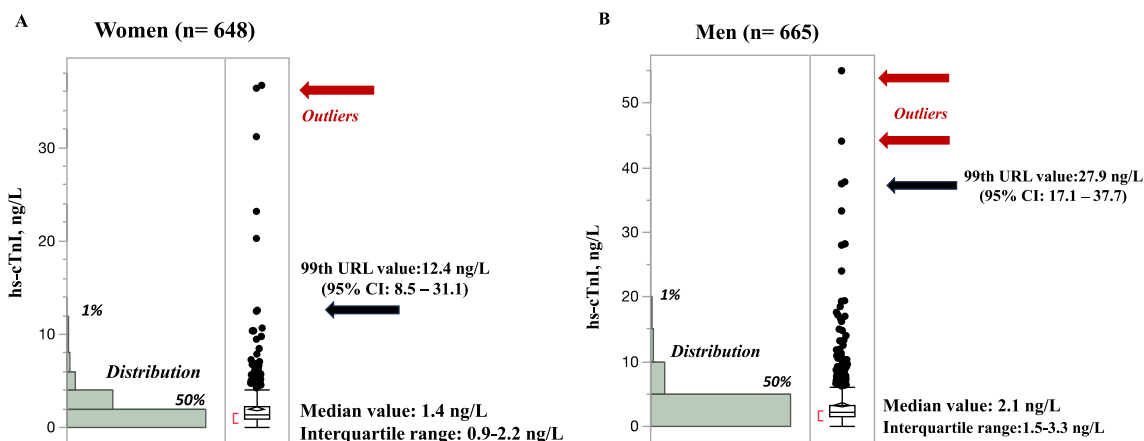


Figure 1: Sex distribution of hs-cTnI circulating levels, measured in an Italian reference population. The circulating hs-cTnI levels were measured in an Italian reference healthy population (mean age: 51.4 years; range from 18 to 86 years; number of healthy men: 665, number of healthy women: 648, using the ARCHITECT hs-cTnI method in the clinical laboratory of the Fondazione G. Monasterio, CNR and Regione Toscana CNR (Pisa, Italy), as previously reported in detail [72, 73]. The distribution of circulating levels and the 99th percentile URL values of the ARCHITECT hs-cTnI method (Abbott laboratories, Abbott Park, IL, USA) were calculated using the JMP-17 statistical software (SAS, statistical discovery LLC, 920 SAS camp drive cary, NC 27513) according to the harrell-davis distribution-free (non-parametric) quantile estimator [71, 72], as suggested by the International guidelines [2, 10, 11]. (A) Distribution of hs-cTnI circulating levels, measured in an Italian reference healthy population of healthy women. (B) Distribution of hs-cTnI circulating levels, measured in an Italian reference healthy population of healthy men.

value (RCV) using the following mathematical formula (1) [92, 93]:

$$RCV = 2^{\frac{1}{2}} \times Z \times [(CVA)^2 + (CVi)^2]^{\frac{1}{2}} \quad (1)$$

Where

- CVA indicates the analytical variability of the method (i.e., the analytical imprecision expressed as a coefficient of variation, CV%);
- CVi is the intra-individual variability of the subject (expressed as %);
- Z is the Zeta score for a bidirectional probability of 95 %, equal to 1.96;
- The value $2^{\frac{1}{2}}$ (i.e., square root of 2, approximately: 1.41142) must be used when the RCV is calculated using two consecutive samples collected from the same subject.

Considering the formula (1), the RCV related to the measurement with hs-cTnI and hs-cTnT methods of two consecutive samples from the same subject should be equal to 39 % if both CVA and CVi are equal to 10 % [41, 72, 73, 77]. In turn, CVA and CVi are considered equal to 10 % because international guidelines specifically require that all hs-cTnI and hs-cTnT methods should measure the 99th percentile URL value with an analytical error ≤ 10 % CV (2), and the intra-individual variability is ≤ 10 % in both healthy subjects [80–85] and patients with cardiac or non-cardiac disease [86–91].

The analytical error of a typical immunometric method, expressed as CV% values, shows a curvilinear relationship with the measured biomarker concentration [6, 15, 73]. As an example, the results shown in Figure 2A report the imprecision profile of the five most popular hs-TnI and hs-cTnT methods used by clinical laboratories in European and North American countries. The analytical error is very high for concentrations < 3 ng/L, but decreases rapidly to a plateau value corresponding to approximately $CV \leq 5$ % for all measured hs-cTnI and hs-TnT values near and above the 99th percentile URL (i.e., hs-cTnI values ≥ 10 ng/L). In addition, Figure 2 calculates the curvilinear fit, using a reciprocal function, between the data related to the imprecision profile of the five hs-TnI and hs-cTnT methods. In other words, the reciprocal function reported in Figure 2A could be considered as the “mean” imprecision profile among the five hs-cTnI and hs-TnT methods. Overall, the data presented in Figure 2A and B suggest that: 1) the imprecision profiles of the 5 hs-cTnI and cTnT methods are very similar, especially for biomarker values ≥ 10 ng/L; 2) the analytical error of 10 CV % of these methods corresponds on average to a hs-cTn concentration of 6.3 ng/L. However, it is important to note that the differences in CV at low concentrations between the

hs-cTnI and hs-cTnT methods, are relevant for the diagnosis of NSTEMI using rapid rule-out algorithms in patients presenting to the emergency department [4, 45, 46].

From a clinical point of view, several experimental studies have confirmed that biomarker variations measured by hs-cTnI and hs-cTnT methods are clinically relevant when the RCV is greater than 30 % [94–97]. This practical approach can be considered as a general rule of thumb that applies without exception to all hs-cTnI and hs-cTnT methods, as well as to any clinical condition where an increase and/or decrease in biomarker concentrations should be verified for the diagnosis of myocardial injury [3, 41].

Take-home messages

- The 99th percentile URL values for hs-cTnI and hs-cTnT show a large variability in the reference population (i.e. including only healthy adult individuals) because it depends not only on the analytical performance of the hs-cTnI or hs-cTnT method, but also on the age, sex and body mass characteristics of the reference population [41, 71, 77].
- The hs-cTnI and hs-cTnT methods have different measured concentration values and reference limits, but the RCV values are similar for the biomarker values measured around the 99th percentile URL [41, 72, 73, 77].
- Several experimental studies have shown that biomarker variations measured by hs-cTnI and hs-cTnT methods are clinically relevant when the RCV is ≥ 30 % [94–97].

Clinical interpretation of temporal hs-cTnI and hs-cTnT variations

The Study Group on Cardiac Biomarkers of the Italian Societies of Laboratory Medicine has recently discussed the importance of evaluating hs-cTnI and hs-cTnT variations for a) the differential diagnosis of ACS in patients admitted to the emergency department [41, 98]; b) the prediction of cardiovascular risk in patients undergoing major cardiac or non-cardiac surgery [99], or c) asymptomatic subjects from the general population or athletes [31, 39, 41]; d) the assessment of cardiotoxicity caused by the administration of some chemotherapeutic drugs [100]; e) the assessment of cardiovascular risk in pregnancy [101].

For the diagnosis of ACS, both the 2020 [4] and the most recent 2023 [102] ESC guidelines recommend the most rapid algorithms (0–1 h or 0–2 h). The assessment of biomarker

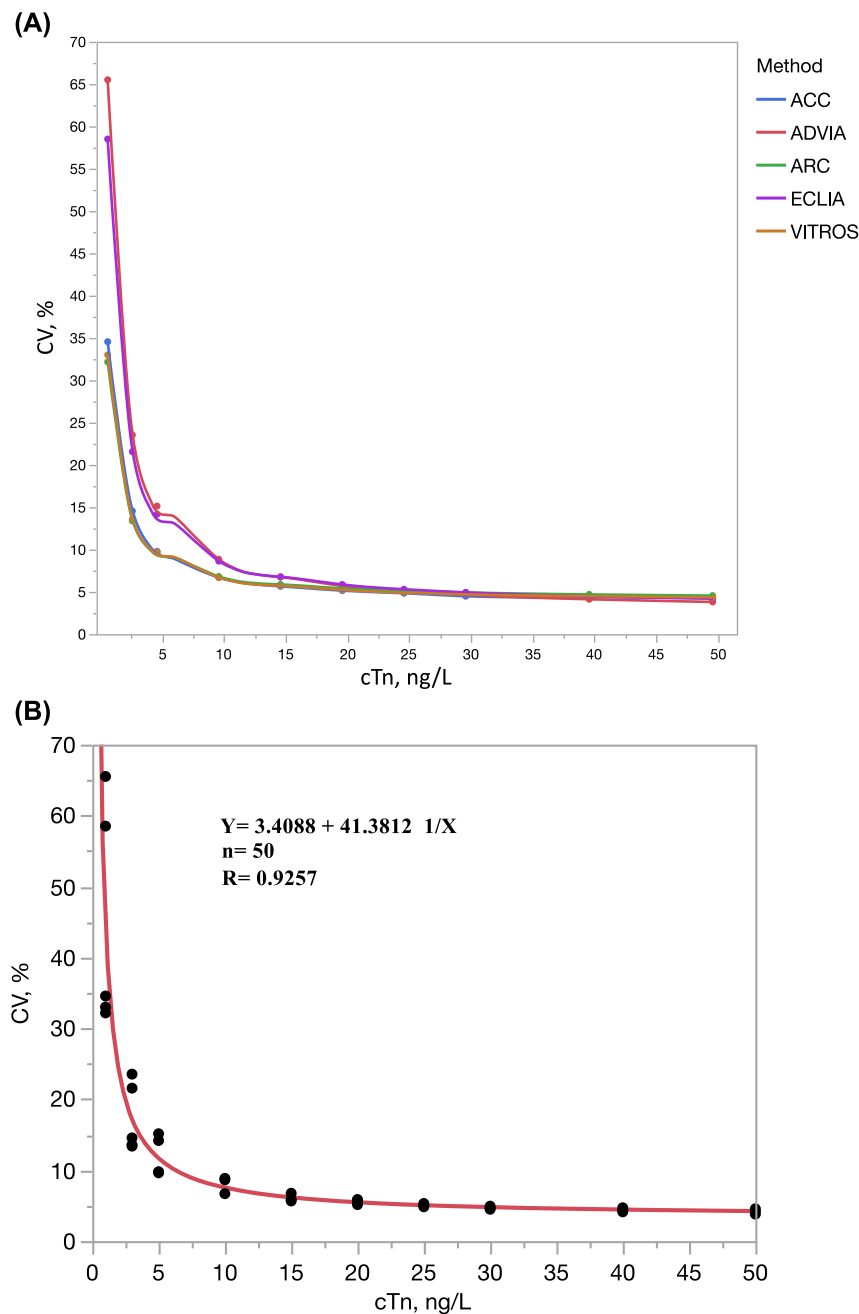


Figure 2: Imprecision profiles of hs-TnI and hs-cTnT methods. (A) The Figure shows the imprecision profile of the five most popular hs-TnI and hs-cTnT methods utilized by the clinical laboratories of European and North American countries. (B) The Figure shows the mean imprecision profile calculated from the five hs-cTnI and hs-cTnT methods reported in (A). The curvilinear fitting, using a reciprocal function, is calculated among the data related of imprecision profile of the five hs-TnI and hs-cTnT methods using the JMP-17 statistical software (SAS, statistical discovery LLC, 920 SAS Camp Drive Cary, NC 27513).

kinetics is based on cut-offs expressing the absolute difference between concentrations at baseline and at 1 or 2 h, defined as the delta (Δ) change. These cut-off values are sex independent but assay specific. In accordance with the 2023 ESC guidelines [102], these cut-off values were derived and validated in large multicentre diagnostic studies using central adjudication of the final diagnosis for all currently available hs-cTn assays [103–125]. These rapid algorithms were developed from large derivation cohorts and then validated in large independent validation cohorts [102]. The optimal rule-out thresholds were chosen to provide a

negative predictive value (NPV) of at least 99 %, while the optimal rule-in threshold should be chosen to provide a positive predictive value (PPV) of at least 70 % [102]. Both the IFCC document 2021 [10] and the NICE guidelines [46] state that sex- and method-specific cut-offs are preferable, as many studies have shown that sex-based differentiation allows a more accurate diagnosis of NSTEMI-ACS, especially when hs-cTnI methods are used in female patients [125–130]. A relevant clinical finding is the time from symptom onset, which is used to evaluate the change in concentration levels measured by the hs-cTnI and hs-cTnT methods [3, 45, 98, 131].

The Fourth Universal Definition of Myocardial Infarction (3) identifies a specific group of patients who are admitted to the ED more than 12 h after the onset of symptoms of myocardial ischaemia (i.e., referred to as “late presenters”). These patients may be admitted to the ED when the peak concentration has already been reached and the circulating levels of the biomarker are therefore decreasing (i.e. the descending phase of the biomarker peak) [3, 45, 98, 131]. The decrease in cardiac troponins is usually much slower than the increase detected within the first 24 h after the onset of ischaemia. Accordingly, the late presenters may have hs-cTnI and hs-cTnT changes that are too small to be detected over a few hours (as in the 0 h/1 and 0 h/2 h algorithms), especially if the areas of myocardial necrosis due to the acute ischaemia are also small [3, 45, 98, 131]. Furthermore, late presentation is particularly prevalent in elderly patients presenting to the ED, where 36–50 % of patients aged >65–70 years who do not have AMI often present with hs-cTnI or hs-cTnT levels consistently above the 99th percentile URL value for the presence of some comorbidities, such as diabetes mellitus, chronic kidney disease and heart failure or cardiac amyloidosis [3, 45, 98, 131–135].

According to the document 2021 of the IFCC Committee on Clinical Applications of Cardiac Biomarkers [45], patients presenting late to the ED often have hs-cTnI and hs-cTnT concentrations that may not change significantly (i.e. <30 %) over 1–2 h because they are in the declining phase after the peak of the biomarker. Already in 2013, Bjurman et al. [131] suggested that 26 % of patients with a definitive diagnosis of AMI might not show dynamic changes in hs-cTnT concentrations according to the guidelines in use at that time. Specifically, these authors reported that after 6 h of observation, the relative change in hs-cTnT levels remained <20 % in 26 % and the absolute change remained <9 ng/L in 12 % of NSTEMI patients [131]. The cut-off of all hs-cTnI and hs-cTnT methods for the diagnosis of myocardial damage (i.e. the 99th percentile URL value) usually shows values ≥ 10 ng/L [6, 15, 62, 73]. According to the data shown in Figure 2B, all hs-cTnI and hs-cTnT methods show an approximately constant analytical error of about 5 CV% for biomarker concentrations >10 ng/L. Considering formula (1), if the CV_i is 10 % and the CV_a is 5 %, then the RCV for two consecutive samples is 31 %. Of course, an RCV value of 31 % is significantly higher than the <20 % increase in hs-cTnT values observed in the 26 % of some patients with a definitive diagnosis of NSTEMI included in the study by Bjurman et al. [131].

The estimated CV_i values reported in the literature range from 4.2 to 63 % (mean 13.1 %) for the hs-cTnI methods and from 1.3 to 16.0 % (mean 8.2 %) for the hs-cTnT method

[41, 77]. However, these values vary widely depending on the time frames used in the experimental studies to estimate RCV, which can vary from 1 h to 9 months in 10 different studies [41, 77]. As mentioned above, myocardial damage corresponds to an elevated hs-cTnI or hs-cTnT value with at least one value above the 99th URL and is considered acute if there is an increase and/or decrease in hs-cTnI or hs-cTnT values. As the 99th percentile URL values vary widely between hs-cTnI methods, cTnI should always be measured with the same hs-cTnI method and preferably in the same laboratory. Sex-specific 99th percentile URL values should be used for the pathophysiological and clinical interpretation of temporal hs-cTnI variations, as suggested by several clinical studies, expert documents and international guidelines [2, 3, 5, 11, 14, 39, 41, 45, 46, 72]. On the contrary, there is currently only one hs-cTnT assay commercially available in European and North American countries for automated platforms commonly used in clinical laboratories [6, 8, 10, 72, 73]. The manufacturer of this hs-cTnT assay indicates a cut-off for the diagnosis of myocardial injury that is not sex-specific (i.e. 14 ng/L), although several studies have reported significant sex differences between the 99th percentile URL values of hs-cTnT [6, 8, 10, 72, 73].

Evaluation of hs-cTnI and hs-cTnT kinetics is relevant in some common clinical conditions, including 1) patients undergoing major non-cardiac surgery [99, 136–144]; 2) patients undergoing cancer therapy with cardiotoxic drugs [100, 145–154]; 3) cardiovascular risk assessment in pregnant women [155–162], the general population or athletes [31, 38, 39, 99, 101]. In all these clinical conditions, the detection of myocardial damage by hs-cTnI and hs-cTnT testing is associated with a worse outcome and an increased incidence of major adverse cardiovascular events (MACE) [31, 38, 39, 99, 100]. Although there are currently no specific recommendations from international guidelines, the authors believe that it is necessary to perform a baseline measurement of hs-cTnI/hs-cTnT in every patient to evaluate any significant changes in biomarker levels following therapy or during and after surgery. Some patients may have elevated hs-cTnI and hs-cTnT prior to drug administration or surgery, particularly those over 75 years of age or with cardiovascular disease.

As recently reviewed [101], several studies have evaluated the clinical relevance of cardiac troponin assays in women with pregnancies complicated by diabetes, hypertension, eclampsia or cardiomyopathy [155–162]. In particular, some studies reported a significant association between elevated cardiac troponin levels in pregnancy and a higher risk of cardiovascular complications, dystocia and fetal distress [155, 156, 158–162].

As a general indication, given the large difference between biomarker levels measured by the different hs-cTnI and hs-cTnT methods, it is advisable to repeat biomarker measurements using the same immunoassay method and possibly in the same laboratory to reduce analytical error. In particular, this approach is necessary to accurately assess the temporal variation of hs-cTnI and hs-cTnT concentrations in the same individual or patient, whether at home or in hospital [6, 31, 41, 77, 99, 100].

Take-home messages

- Several studies have suggested that assessment of hs-cTnI and hs-cTnT kinetics is relevant in some common clinical conditions, including: 1) patients undergoing major non-cardiac surgery [99, 136–144]; 2) patients receiving cancer therapy with cardiotoxic drugs [100, 145–154]; 3) cardiovascular risk assessment in pregnant women, the general population or athletes [31, 38, 39, 99, 101].
- The European Society of Cardiology (ESC) guidelines 2020 [4] and 2023 [102] recommend the most rapid algorithms (0–1 h or 0–2 h) for the diagnosis of MI in patients presenting to the emergency department with suspected ACS.
- A relevant clinical finding is the time from the onset of ischaemic symptoms in patients admitted to the ED for the diagnosis of NSTEMI-ACS, which is used to evaluate the change in concentration levels measured by the hs-cTnI and hs-cTnT methods [3, 45, 98, 131].
- Some patients who present to the emergency department more than 12 h after symptom onset of myocardial ischaemia (i.e., referred to as “late presenters”) may be in the declining phase of biomarker levels because the peak concentration has already been reached and therefore the circulating levels of the biomarker are slowly decreasing (variations <30 %) [3, 45, 98, 131].
- Due to the systematic differences between the immunoassay methods, it is always necessary to measure the hs-cTnI and hs-cTnT levels of the same individual/patient using the same method and possibly in the same laboratory in order to reduce analytical errors as much as possible and also to more accurately estimate the variations in biomarker concentrations [6, 31, 41, 77, 99, 100].
- Although there are currently no specific recommendations from international guidelines, the authors believe that it is clinically important to perform a basal

measurement of hs-cTnI/hs-cTnT before surgery or administration of cardiotoxic drugs in order to correctly assess any significant changes in biomarker levels [41, 77, 99, 100].

Artificial intelligence and hs-cTnI and hs-cTnT variants

Biological systems are extremely complex, and their analysis requires considerable clinical experience for the human brain to accurately weigh all the multiple factors when making complex decisions [163, 164], such as those related to health sciences and laboratory medicine [165–169]. In particular, laboratory medicine can now benefit from the use of some innovative technologies of network science, such as digitisation, big data, artificial intelligence (AI) and machine learning (ML) [165–169].

AI may promise to further advance the management of patients with chest pain [165]. The diagnosis of AMI is currently based on clinical presentation, ECG, hs-cTnI and hs-cTnT measurements, and cardiac imaging data [4, 10, 11, 45, 46, 165, 166]. Since 2000 [1], several clinical algorithms have been proposed for the diagnosis and management of ACS-NSTEMI in patients presenting to the ED with chest pain [4, 10, 11, 45, 46, 165, 166], but the clinical performance of these algorithms can still vary with patient age, sex and ethnicity, and the time of blood sampling from symptom onset and between samples. This heterogeneity cannot be explained solely by differences in cTnI and hs-cTnT cut-off values or clinical stratification of patient groups into two to four cardiovascular risk groups [165]. In addition, AI algorithms have been used to enhance the diagnostic accuracy of transdermal sensors, as highlighted above [69].

Network analysis can integrate data from different techniques to reveal relationships between biological and clinical factors and analyse underlying and fundamental structures [163, 164]. ML is a quantitative and reproducible way to combine and integrate a large amount of information derived from multiple variables to improve predictive accuracy, and therefore this approach may be very useful for the analysis of large data provided by clinical laboratories [163–170].

In this context, it is important to consider not only the quality of the data collected, but also the pipelines used to validate the algorithms developed [167, 171]. Furthermore, the integration of health data between laboratories and across clinical disciplines is crucial to improve the effectiveness of AI algorithms [171]. Several recent studies have demonstrated that

these innovative approaches (usually based on ML) are able to process and efficiently integrate the information produced by laboratory methods (including data on hs-cTnI and hs-cTnT assays) with those available from large datasets on socioeconomic, demographic and clinical data related to the general

population and/or patients with cardiovascular disease [42–44, 172–195]. Here, we discuss only those studies that consider the combined contribution of hs-cTnI or hs-cTnT assay and ML approach, specifically for the diagnosis of AMI. Table 2 summarizes the results of some multicentre (or very large

Table 2: Clinical studies, evaluating the combined hs-cTnI and hs-cTnT assay and Machine Learning (ML) approach for the diagnosis of SCA-NSTEMI in patients admitted to ED.

Study	Study aims	Studied populations	Results
Björkelund A, et al. J Am Coll emerg physicians open 2021 [177]	Authors aimed to assess the predictive accuracy of machine learning algorithms based on paired hs-cTnT concentrations with varying sampling times, age, and sex in order to rule in or out AMI. Authors compared the performance of an artificial neural network with ESC guideline-recommended 0/1- and 0/3-h algorithms for hs-cTnT and with logistic regression without interaction.	Authors enrolled 5,695 chest pain patients at 2 hospitals in Sweden 2013–2014. Patient data on chief complaint, age, and sex and laboratory data on hs-cTnT and discharge diagnosis were extracted from the EXPECT database.	ML algorithms and logistic regression had similar (95 %) areas under the receiver operating characteristics curve. Machine learning algorithms allow for flexibility in sampling and have the potential to improve risk assessment among chest pain patients at the ED.
Liu N, et al. BMC med res methodol 2021 [178]	Authors aimed to investigate if ML dimensionality reduction methods can improve performance in deriving risk stratification models.	A retrospective analysis was conducted on the data of patients >20 years old who presented to the ED between September 2010 and July 2015. 795 chest pain patients were enrolled in this study, of which 247 (31 %) patients had MACE within 30 days of presentation to the ED.	Dimensionality reduction models showed marginal value in improving the prediction of 30-day MACE for ED chest pain patients. Moreover, they are black box models, making them difficult to explain and interpret in clinical practice.
Liu WC, et al. EuroIntervention 2021 [179]	Authors aimed to develop a deep learning model (DLM) as a diagnostic support tool based on a 12-lead electrocardiogram.	The retrospective cohort study included 1,051/697 ECGs from 737/287 coronary angiogram (CAG)-validated STEMI/NSTEMI patients and 140,336 ECGs from 76,775 non-AMI patients at the emergency department. The DLM was trained and validated in 80 and 20 % of these ECGs.	The AUC of the DLM for STEMI detection was 0.976 in the human-machine competition, which was significantly better than that of the best physicians. Furthermore, the DLM independently demonstrated sufficient diagnostic capacity for STEMI detection (AUC=0.997; sensitivity, 98.4 %; specificity, 96.9 %). Regarding NSTEMI detection, the AUC of the combined DLM and hs-cTnI increased to 0.978, which was better than that of either the DLM (0.877) or hs-cTnI (0.950).
Emakhu J, et al. Comput methods programs Biomed 2022 [183]	Authors aimed to develop an ensemble learning-driven framework as a diagnostic support tool to prevent misdiagnosis. An analytical framework equipped with many well-developed algorithms was applied to improve the data quality by addressing missing values, dimensionality reduction, and data imbalance.	This single-center study included 31,228 patients, of whom 563 (1.8 %) had ACS and 30,665 (98.2 %) had alternative diagnoses. 11 features, including systolic blood pressure, BNP, chronic heart disease, coronary artery disease, creatinine, glucose, heart attack, heart rate, nephrotic syndrome, red cell distribution width, and cTn levels, was found to be significantly contributing risk factors.	The proposed framework successfully classified the cohorts of patients with sensitivity and AUROC as high as 86.3 and 93.3 %. The evaluated model's accuracy, precision, and specificity, were: 85.7 %, 86.3%, 93%, and 80 %.
Ke J, et al. Am J emerg med 2022 [185]	The purpose of this single-center study was to identify the risk factors of in-hospital mortality in patients with ACS and to evaluate the performance of traditional regression and ML prediction models.	6,482 ACS patients were included in the study with an in-hospital mortality rate of 1.88 %. The study used univariate and multivariate logistic regression analyses to identify risk factors for in-hospital mortality of ACS patients.	The AUC ROC values of the models developed by logistic regression, gradient boosting decision tree, random forest, and support vector machine for predicting the risk of in-hospital mortality were: 0.884, 0.918, 0.913, and 0.896, respectively. Evaluation of changes in NT-proBNP, D-dimer, killip score, cTnI, and LDH values was found to improve clinical outcomes of ACS patients.

Table 2: (continued)

Study	Study aims	Studied populations	Results
Doudesis D, et al. Nat med 2023 [42]	Authors developed ML models that integrate hs-cTnI values at presentation or on serial testing with clinical features and compute the collaboration for the diagnosis and evaluation of acute coronary syndrome (CoDE-ACS) score that corresponds to an individual's probability of myocardial infarction.	The validation cohort consisted of 10,286 patients (median age 60 years, 35 % women) with possible AMI pooled from seven prospective cohort studies enrolling patients across six countries. In 8,664 and 1,622 patients with and without myocardial injury at presentation, the final adjudicated diagnosis after serial cardiac troponin measurements was AMI in 1,032 and 267 patients, respectively.	The CoDE-ACS model showed an AUC for AMI of 0.953 (95 % CI: 0.947–0.958), and identified more patients at presentation as low probability of AMI than fixed hs-cTnI assay (61 vs. 27 %) with a similar NPV and fewer as high probability of having AMI (10 vs. 16 %) with a greater PPV. Patients with a low probability of AMI had also a lower rate of cardiac death than those with intermediate or high probability at both 30 days and 1 year ($P < 0.001$).
Neumann JT, et al. Clin res Cardiol 2023 [192]	Authors aimed to build a digital tool to directly estimate the individual probability of AMI, allowing for numerous hs-cTn assays.	In 2,575 patients presenting to the ED with suspected AMI, two ensembles of ML models using single or serial concentrations of six different hs-cTn assays were derived to estimate the individual AMI probability (ARTEMIS model). Model performance was validated in an external cohort with 1,688 patients and tested for global generalizability in 13 international cohorts with 23,411 patients.	11 routinely available variables including age, sex, cardiovascular risk factors, electrocardiography, and hs-cTn were included in the ARTEMIS models. In the validation and generalization cohorts, excellent discriminative performance was confirmed, superior to hs-cTn only. For the serial hs-cTn measurement model, AUC ranged from 0.92 to 0.98. Good calibration was observed. Using a single hs-cTn measurement, the ARTEMIS model allowed direct rule-out of MI with very high and similar safety but up to tripled efficiency compared to the guideline-recommended strategy.
Lopez-Ayala P, et al. Lancet digit health 2024 [43]	Authors validated the myocardial-ischæmic-injury-index (MI3), which is a novel machine learning algorithm for the early diagnosis of type 1 non-ST-segment elevation myocardial infarction (NSTEMI), using serial hs-cTnI measurements.	Authors enrolled 6,487 patients (median age 61.0 years [IQR 49.0–73.0]; 2,122 [33 %] female and 4,365 [67 %] male) from April 21, 2006, to Feb 27, 2019 in 12 centres from five european countries (Switzerland, Spain, Italy, Poland, and Czech republic), presenting to the ED with symptoms suggestive of AMI. 882 of these patients (13.6 %) had a definitive diagnosis of NSTEMI.	Model performance showed an AUC ROC curve of 0.961 (95 % CI 0.957 to 0.965). The model identified 4,186 (64.5 %) patients as low probability of having a type 1 NSTEMI (sensitivity 99.1 % [95 % CI 98.2 to 99.5]; NPV 99.8 % [95 % CI 99.6 to 99.9]). A model score of 49.7 or more identified 915 (14.1 %) patients as high probability of having a type 1 NSTEMI (specificity 95.0 % [94.3 to 95.5]; PPV 69.1 % [66.0–72.0]).
Boeddinghaus J, et al. Circulation 2024 [44]	The CoDE-ACS model was validated as a clinical decision-support tool that uses ML with or without serial hs-cTnI measurements at a flexible timepoint to calculate the probability of AMI.	Patients with possible AMI without ST-segment elevation were enrolled at 12 sites in five countries and underwent serial hs-cTnI measurements at 0, 1 and 2 h. In total 4,105 patients (age 61 [19, 50–73] years, 32 % women) were included where 575 (14 %) had type 1 AMI.	Overall, the CoDE-ACS model performs consistently irrespective of the timing of serial hs-cTnI assay identifying more patients as low-probability with comparable performance to international ESC 0/1 h, ESC 0/2 h and High-STEACS guidelines recommended pathways for AMI.

single-centre) studies aimed at evaluating the contribution of hs-cTnI or hs-cTnT assay and ML approach to the diagnosis of acute coronary syndrome [42–44, 175, 178, 183, 185, 187]. Other studies have used the ML approach in combination with the hs-cTnI or hs-cTnT assay to better estimate cardiovascular risk in general or heterogeneous populations [184, 186] and in patients with heart failure [189, 190] or stable coronary artery disease [186]. In particular, several studies have suggested that the ML

approach in combination with hs-cTnI or hs-cTnT assay significantly improves the accuracy of diagnosis of AMI [42–44, 175, 179, 183, 185]. More specifically, the CoDE-ACS model identifies more patients as low-probability with comparable performance to the international ESC 0/1 h, ESC 0/2 h and High-STEACS guidelines recommended pathways for AMI [4, 47], with consistent performance regardless of the timing of serial hs-cTnI testing [44]. Another very recent ML approach is the

ARTEMIS model [192], which is based on heterogeneous global data and has been calibrated for European, Australian, New Zealand, North American and Japanese settings for worldwide application. This model integrates data from two POCT hs-cTnI (i.e. Pathfast and Atellica VTLi), the hs-cTnT and 3 hs-cTnI methods (i.e. Access, Architect and Atellica) [192]. Using these POCT hs-cTnI methods, the ARTEMIS model can be applied in the outpatient setting and could improve diagnostic accuracy and speed in the outpatient setting, thereby reducing hospital admissions [192]. The results obtained with the CoDE-ACS and ARTEMIS models indicate that the innovative ML approach can overcome the drawbacks due to different cut-off values and timing related to the hs-cTnI and hs-cTnT assays, and thus may provide a faster, safer and more efficient diagnostic workup of patients with chest pain [43, 44, 192].

Several authors have recently discussed various theoretical issues, ethical challenges and other concerns regarding the application of AI in clinical and laboratory medicine [7, 167–172], [194–201]. The main ethical issues relate to the role of laboratory professionals, the automatic generation of data and the use of patient data [167–169, 195, 196]. In addition, the fundamental question of whether laboratory professionals are ready for the routine use of AI remains unanswered [167–172, 195–199]. The potential application of ML models to laboratory data could be relevant, but there is an urgent need to adapt expertise within clinical laboratories and also to improve the collaboration between laboratory medicine and AI experts [169–174, 199–202].

Take-home messages

- The integrated use of innovative strategies based on AI promises to refine the management of patients with chest pain [165].
- ML is a quantitative and reproducible way to combine and integrate large amounts of information from multiple variables to improve predictive accuracy, and so this approach may be very useful for analysing the large data provided by clinical laboratories [167–169]. However, careful consideration should be given to data collection and handling, which are of paramount importance for the effectiveness of the algorithms.
- Some recent studies have shown that the ML approach combined with hs-cTnI or hs-cTnT assay can significantly contribute to improve the accuracy of diagnosis of AMI [42–44, 175, 179, 183, 191].
- However, while the potential application of ML models to laboratory data may be relevant, there remains an urgent need to adapt expertise within clinical

laboratories and improve collaboration between laboratory medicine and AI experts in order to manage the change and uncover additional benefits for patient care [167–171, 198, 199].

Conclusions

Over the past decade, hs-cTn assays have dramatically reduced the time required to diagnose AMI to less than 3 h in most cases [4]. This improvement in diagnostic speed has allowed for faster clinical decisions and interventions, especially in rule-out AMI [4, 9–11, 45, 46, 99]. In addition, new hs-cTn POCT methods [9–11, 15, 17] can further reduce laboratory turnaround times. POCT methods also have the advantage that they can be used in outpatient clinics, ambulances and even in the home [9–11, 15, 17].

Despite these advances, challenges remain in standardising hs-cTn methods and interpreting small temporal changes in biomarker levels [41, 202]. In particular, low-molecular-weight troponins, which are often released after strenuous physical activity or in patients with end-stage renal disease, present complexities in the accurate interpretation of hs-cTn results because the methods available to date are unable to distinguish between the different molecular forms of troponin circulating in the blood [26, 27, 2–33]. Furthermore, the challenge of accurately determining the 99th percentile URL for hs-cTn assays remains unresolved [71–74]. In fact, the 99th percentile URL values, which are crucial for clinical diagnosis, vary significantly not only between hs-cTnI and hs-cTnT assays, but also due to some individual conditions, in particular: age, sex and body structure [72–74]. Although the hs-cTn assay using wearable technology is not fully mature, this new technique represents an exciting frontier in continuous monitoring and early detection of myocardial injury [17, 21]. Another promising area of innovation is the integration of ML algorithms with hs-cTn assays [167–173]. Several studies have shown that these algorithms can improve the accuracy of AMI diagnosis, particularly in emergency departments [43, 189, 190, 193, 194]. In conclusion, after 25 years of continuous research and technological improvements, the task of refining and standardising analytical performance and expanding the use of hs-cTnI and hs-cTnT methods in clinical practice is not yet complete [202].

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