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Biological variation of cardiac myosin-binding protein C in healthy individuals

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Abstract

Objectives: Cardiac myosin-binding protein C (cMyC) is a novel biomarker of myocardial injury, with a promising role in the triage and risk stratification of patients presenting with acute cardiac disease. In this study, we assess the weekly biological variation of cMyC, to examine its potential in monitoring chronic myocardial injury, and to suggest analytical quality specification for routine use of the test in clinical practice.

Methods: Thirty healthy volunteers were included. Non-fasting samples were obtained once a week for ten consecutive weeks. Samples were tested in duplicate on the Erenna ® platform by EMD Millipore Corporation. Outlying measurements and subjects were identified and excluded systematically, and homogeneity of analytical and within-subject variances was achieved before calculating the biological variability (CVI and CVG), reference change values (RCV) and index of individuality (II).

Results: Mean age was 38 (range, 21–64) years, and 16 participants were women (53%). The biological variation, RCV and II with 95% confidence interval (CI) were: CVA (%) 19.5 (17.8–21.6), CVI (%) 17.8 (14.8–21.0), CVG (%) 66.9 (50.4–109.9), RCV (%) 106.7 (96.6–120.1)/−51.6 (−54.6 to −49.1) and II 0.42 (0.29–0.56). There was a trend for women to have lower CVG. The calculated RCVs were comparable between genders.

Conclusions: cMyC exhibits acceptable RCV and low II suggesting that it could be suitable for disease monitoring, risk stratification and prognostication if measured serially. Analytical quality specifications based on biological variation are similar to those for cardiac troponin and should be achievable at clinically relevant concentrations.

Keywords: biological variation; cardiac myosin-binding protein C; index of individuality; reference change value.

Introduction

Cardiac myosin-binding protein C (cMyC) is a novel biomarker of myocardial injury that was first identified in cardiac venous effluent approximately 10 years ago [1]. More recently, a quantitative sandwich immunoassay was developed by selecting a pair of high-affinity mouse monoclonal antibodies to the N-terminal domain of cMyC. This assay can detect small quantities of myocardial injury in blood, equivalent to approximately 0.07 mg of the intact human heart, and less than 1% of the volume of myocardial necrosis needed to exceed the 99th percentile upper reference limit [2]. In the systemic circulation, cMyC concentrations rise more rapidly than hs-cTn after timed iatrogenic, as well as spontaneous, type 1 acute myocardial infarction (type 1 AMI) [3–5].

The kinetic profile of cMyC has been tested clinically and compared to cardiac troponins in a retrospective
analysis of 7,000 sera from approximately 2,000 patients in the Advantageous Predictors of Acute Coronary Syndromes Evaluation (APACE) cohort presenting with suspected non-ST-segment elevation myocardial infarction (NSTEMI) of whom 340 had an adjudicated AMI. Analysis, confined to the initial presentation blood sample, showed that cMyC is at least as good as cardiac troponin measured with the leading assays in predicting the diagnosis of AMI, mortality and future cardiovascular events [6]. Additionally, cMyC signalled improved triage over hs-cTnT of pre-hospital patients having blood drawn in the ambulance just 70 min after symptom onset [7]. In summary, cMyC shows promise as a biomarker of acute myocardial injury.

Understanding the long-term biological variation of an analyte has several applications including suggesting analytical quality specifications for routine assays, determining the number and frequency of sampling required to establish homeostatic set points of an individual, calculating the index of individuality, and determining physiological variations in consecutive results. The latter is useful for prognostication and risk stratification, chronic cardiovascular disease monitoring and detecting or predicting cardiac damage in the context of chronic non-cardiac conditions or long-term exposure to cardiotoxic agents. The EFLM suggest three different models for setting analytical quality specifications [8] of which biological variation seems the most applicable for novel markers, until a larger number of outcome studies or robust state of the art data become available [9]. The purposes of the current study are to examine the biological variation of cMyC in healthy individuals to (1) better understand its potential as a marker of chronic myocardial injury, and (2) provide data as for which analytical quality specification for routine use of the assay may be suggested.

Materials, subjects and methods

Ethics

This study was carried out according to the principles of the Declaration of Helsinki. The protocol was approved by the respective regional ethics committee at each centre: South Central – Berkshire Research Ethics Committee (London), and the Regional Committee for Medical and Health Research Ethics in Bergen (Bergen and Oslo). Unified informed consent from across centres was obtained from all volunteers.

Volunteers

Thirty healthy volunteers were recruited from London (King’s College London and Guys and St Thomas’ Hospital), Bergen (Haukeland University Hospital) and Oslo (University of Oslo and Akershus University Hospital), 10 volunteers were recruited from each centre.

The opportunity to participate in the study was advertised locally via posters and circulated “Research Opportunities” emails amongst the staff of each of the participating centres.

Screening, inclusion and exclusion criteria

Potential participants were screened according to the following criteria:

Inclusion criteria: healthy individuals of age between 18 and 75.

Exclusion criteria: any evident disease, current pregnancy, use of cardiac medications, previous history of acute or chronic cardiac illness, any chronic non-cardiac illness including cancer in remission during the past 5 years, or any of the following abnormalities on screening blood tests:

- eGFR<60 mL/min/1.73 m²
- NT-ProBNP>local reference limit
- Troponin T (hs-cTnT)>99th percentile value (>14 ng/L)

Sample collection, processing and analysis

To minimise pre-analytical variability, a unified Standard Operating Protocol (SOP) was used across all centres (see appendix). Venous blood sampling was performed weekly, on the same weekday ±1 day, for 10 consecutive weeks from October to December 2018. Non-fasting blood samples were drawn between 08.00 and 10.00 am. Smoking, alcohol intake and exercise were reviewed and documented during each visit.

Participants rested for 15 min before blood was collected into 3.5 mL plastic serum-separation Vacutainer SST II Advance gel tubes (Becton Dickinson) using a 21 Gauge winged blood collection set with flexible tube needle (Becton Dickinson). Samples were allowed to clot for 30 min at room temperature and then centrifuged at 2,200 × g for 10 min at 20 °C. Separated acellular serum (0.9 mL) was then aliquoted into matching cryovial tubes (1.5 mL Mikroröhre PCR-PT, SARSTEDT AG & Co. KG) before being frozen at −80 °C within 2 h after phlebotomy.
Samples were shipped simultaneously from all centres on dry ice for cMyC measurement.

Sample analysis

All serum samples were tested in duplicate on the Erenna® platform by EMD Millipore Corporation, Hayward California. LoD 0.4 ng/L; LoQ (20% CV) of 1.2 ng/L; intra-series precision (CV, 11 ± 3%) and inter-series precision (CV, 13 ± 3%) [3]. There were three missing samples.

Statistics

Data were analysed twice by two independent researchers: KMA and BA, using the following platforms: Excel 2016 and SPSS version 26.0 (KMA), and R version 3.6.1 (BA). Baseline characteristics were described using percentage, means or medians (standard deviation and first quartile-third quartile where applicable). Student’s t-test and Mann–Whitney U test were used for comparing groups as appropriate. Shapiro–Wilk test was used to verify the normality of distribution.

1. **Analytical outliers** were identified as per Burnett’s method [10]. An outlier was defined as a result, which lies further than some multiple, m (m is a constant determined by the sample size) of standard deviations from the mean.

2. **Stability of subjects**: Subjects that expressed a non-steady-state were identified with simple linear regression. The trend was calculated as a percentage of change from the first result. Individual slopes (per participant) of linear regressions were derived. Unstable trends (significantly deviating from 0, p<0.01) were identified and respective subjects were excluded. Then homogeneity of the remaining slopes was tested using linear mixed effect models. ANOVA was used to test whether introducing the slope as a random effect (allowing the slopes to vary) would improve the fit of the model. High ranked slopes were removed until homogeneity was achieved.

3. **Outliers in mean values of subjects** were defined according to Reed’s criterion which rejects extreme values if the difference between them and the next highest (or lowest) exceeds one-third of the range of all values [11].

4. The distribution of the residual data (means of duplicates) was tested using Shapiro–Wilk test. As data did not conform to a Gaussian distribution, values were transformed into natural logarithms [12].

5. **Homogeneity of analytical and between-subject variances (ln transformed data)**

   Analytical (n=residual duplicates) and between-subject (n=residual subjects) variances were calculated and ranked. Homogeneity of variances was tested using Cochran’s and Bartlett’s methods, outlying values were excluded until homogeneity was achieved [13].

   Calculations of $\sigma_A$, $\sigma_I$ and $\sigma_G$ were done (ln transformed data) using nested ANOVA. The $\sigma$ was thereafter retransformed into CV_A, CV_I, and CV_G using:

   $$ CV_{ln} = \sqrt{(\exp \sigma^2 - 1) \times 100} $$

   in which $\sigma$ is the estimated standard deviation for the ln-transformed data and CV_{ln} is the adjoining retransformed CV.

   The RCV values (with 95% confidence intervals) were calculated according to Fokkema et al. [12]. This method is applicable for skewed data as it will always return negative RCV data that are interpretable in clinical practice (not exceeding 100%).

   $$ RCV_{pos} = \left[ \exp \left(1.96 \times 2 \times (\sigma_A^2 + \sigma_I^2)^{1/2}\right) - 1 \right] \times 100 $$

   $$ RCV_{neg} = \left[ \exp \left(-1.96 \times 2 \times (\sigma_A^2 + \sigma_I^2)^{1/2}\right) - 1 \right] \times 100 $$

   in which $\sigma_A$ is the analytic standard deviation and $\sigma_I$ is the within-person standard deviation of the logarithmic data. Due to the CV_I exceeding 12%, we choose to also calculate the RCVs in the total cohort using the non-parametric method, as described by Røraas et al. [14]. This method is less precise compared to Fokkema, but fits all measurement distributions.

   The index of individuality II was calculated using the retransformed data as follows:

   $$ II = \sqrt{CV_A^2 + CV_I^2}/CV_G $$

   Separate calculations were performed in the total cohort, gender-stratified groups, using the methodology above for excluding the outliers and calculating biological variation, RCV and II.

Results

None of the samples had undetectable cMyC concentrations (below LoD). Baseline characteristics of participants contributing to total and gender-stratified cohorts are shown in Table 1. 16 participants were women (53%). Mean age was 38 (range, 21–64), there was no significant age
difference between women and men (mean age, 41 and 35 respectively; \( p=0.173 \)). Two participants were daily smokers. NT-proBNP concentrations were higher in women compared to men (61 ± 36.5 vs. 33 ± 15.7 ng/L, respectively; \( p=0.013 \)), however, none of the participants had NT-proBNP above the reference interval. Otherwise, both groups had similar baseline characteristics as listed in Table 1.

The distribution of cMyC concentrations across participants is shown in Figure 1.

**Total cohort**

In total, 216 samples from 22 participants (11 women and 11 men) were included in the calculation of biological variability, after the exclusion of outliers, as described in the method section, Figure 2 and Table 1, Supplementary Material. None of the excluded subjects were smokers. The following results were obtained:

\[
\begin{align*}
\text{CV}_A & = 19.5\% (17.8–21.6\%), \quad \text{CV}_I = 17.8\% (14.8–21.0\%), \\
\text{CV}_G & = 66.9\% (50.4–109.9\%), \quad \text{RCV} = 106.7\% (96.6–120.1\%)/-51.6\% (-54.6 to -49.1\%) \quad \text{and} \quad \text{II} = 0.42 (0.29–0.56) \\
\end{align*}
\]

Table 1: Baseline characteristics. Values displayed as mean (SD) unless stated otherwise.

<table>
<thead>
<tr>
<th></th>
<th>Total n=30</th>
<th>Women n=16</th>
<th>Men n=14</th>
<th>p-Value (women vs men)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age, mean (range)</td>
<td>38 (21–64)</td>
<td>41 (21–64)</td>
<td>35 (21–44)</td>
<td>0.173</td>
</tr>
<tr>
<td>BMI, kg/m²</td>
<td>22.8 (2.6)</td>
<td>22.35 (3)</td>
<td>23.38 (2.2)</td>
<td>0.303</td>
</tr>
<tr>
<td>Glucose, mmol/L</td>
<td>5.1 (0.6)</td>
<td>4.9 (0.5)</td>
<td>5.2 (0.6)</td>
<td>0.172</td>
</tr>
<tr>
<td>eGFR(CKD-EPIcreat), ml/min/1.73 m²</td>
<td>97.7 (14.7)</td>
<td>95 (13.7)</td>
<td>100.6 (15.9)</td>
<td>0.308</td>
</tr>
<tr>
<td>Troponin T, ng/L</td>
<td>3.3 (2)</td>
<td>3.3 (2.2)</td>
<td>3.3 (1.9)</td>
<td>0.917</td>
</tr>
<tr>
<td>NT-ProBNP, ng/L</td>
<td>47.9 (31.5)</td>
<td>61 (36.5)</td>
<td>33 (15.7)</td>
<td>0.013</td>
</tr>
<tr>
<td>Regular medications (%) ( ^b )</td>
<td>3.3</td>
<td>6.25</td>
<td>0</td>
<td>0.359</td>
</tr>
</tbody>
</table>

\( ^a \)Values below LoD were reported as 50% of the local lower limit of reportable result, 2 ng/L or 1.5 ng/L, respectively. \( ^b \)Non-cardiac drug.

When RCV was calculated using the non-parametric method, corresponding values were 100.1% and -50.5%, respectively.

**Gender-stratified subgroups**

A total of 118 samples from 12 women and 116 samples from 12 men were included in the calculation of gender-specific biological variability. The number of included individuals and samples were different from the total cohort, as the whole procedure of outlier exclusion was repeated in each gender-stratified data set (Table 1, Supplementary Material).

A significant difference in cMyC values between women and men was observed: median (Q1–Q3) 3.54 (2.47–5.25) vs. 4.58 (3.25–6.58) ng/L; respectively; \( p=0.007 \). The CV I was comparable across both groups, 19.7% (15.5–24.5%) and 20.3% (16.6–24.6%) for women vs. men, respectively. There was a trend for women to have higher CVA 20.2% (17.9–23.3%) vs. 16.8% (14.9–19.4%) and lower CVG 55.7% (37.9–110.8%) vs. 83.1% (55.6–195.9%).

Calculated RCVs were comparable in both groups, +117%/−54% vs. +106%/−51% for women vs. men,
respectively, however, women had higher II at 0.53 (0.30–0.78) compared to men 0.35 (0.20–0.52) (Table 2).

Table 2: Analytical and biological variation, RCV and II of cMyC.

<table>
<thead>
<tr>
<th></th>
<th>Total</th>
<th>Women</th>
<th>Men</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of participants</td>
<td>30</td>
<td>16</td>
<td>14</td>
</tr>
<tr>
<td>Number of participants*</td>
<td>22</td>
<td>12</td>
<td>12</td>
</tr>
<tr>
<td>Numbers of samples*</td>
<td>216</td>
<td>118</td>
<td>116</td>
</tr>
<tr>
<td>cMyC concentration, ng/L, median (Q1–Q3)</td>
<td>4.38 (2.75–5.97)</td>
<td>3.54 (2.47–5.25)</td>
<td>4.58 (3.25–6.58)</td>
</tr>
<tr>
<td>CVa, mean (95% CI), %</td>
<td>19.5 (17.8–21.6)</td>
<td>20.2 (17.9–23.3)</td>
<td>16.8 (14.9–19.4)</td>
</tr>
<tr>
<td>CVb, mean (95% CI), %</td>
<td>17.8 (14.8–21.0)</td>
<td>19.7 (15.5–24.5)</td>
<td>20.3 (16.6–24.6)</td>
</tr>
<tr>
<td>CVb, mean (95% CI), %</td>
<td>66.9 (50.4–109.9)</td>
<td>55.7 (37.9–110.8)</td>
<td>83.1 (55.6–195.9)</td>
</tr>
<tr>
<td>Positive RCV, mean (95% CI), %</td>
<td>106.7 (96.6–120.1)</td>
<td>117.2 (102.3–139.1)</td>
<td>106.2 (92.3–126.4)</td>
</tr>
<tr>
<td>Negative RCV, mean (95% CI), %</td>
<td>–51.6 (–54.6 to –49.1)</td>
<td>–54.0 (–58.2 to –50.6)</td>
<td>–51.5 (–55.8 to –48.0)</td>
</tr>
<tr>
<td>Index of individuality II</td>
<td>0.42 (0.29–0.56)</td>
<td>0.53 (0.30–0.78)</td>
<td>0.35 (0.20–0.52)</td>
</tr>
</tbody>
</table>

* After excluding the outliers.

Discussion

The main finding in this study is that the weekly biological variation, RCV of cMyC in healthy individuals, quantified with the Erenna® platform at EMD Millipore Corporation, is moderate and comparable to other cardiac ischemia markers (cardiac troponin). The II is low. No important gender differences were observed. These measures of variation are important to define the minimal magnitude of change in the concentration of cMyC beyond which pathological processes are likely to be present, and to help guide analytical performance.
The derived index in patients presenting to emergency department volunteers, i.e. measuring long-term RCV in patients with chronic stable heart failure or renal disease, and short-term RCV in patients with acute coronary syndrome, has also been used to assess the clinical relevance of the heart damage criteria for the assay when implemented in the routine laboratory. Our data demonstrate a within-subject CV of 15.8% (4.8–21.0%) and a between-subject CV of 17.9% (9.4–21.0%). Both fall within the range of CVs observed for cTn in similar long-term biological variation studies (Table 3) [15–23]. The derived index in patients rather than using population-based reference intervals since the later could increase the fraction of falsenegative results. The overlap between the 95% CI of the derived index calculated from long-term biological variation and RCVs demonstrated in the individual patient and the laboratory criteria for the assay when implemented in the routine laboratory.

### Table 3: Cardiac troponins’ long-term biological variation, RCV and II as reported in recent studies.

<table>
<thead>
<tr>
<th>Author</th>
<th>Yeara</th>
<th>n</th>
<th>Frequency</th>
<th>Period</th>
<th>Ageb</th>
<th>Assay</th>
<th>RCV (log-normal)</th>
<th>CVA (%)</th>
<th>CV (%)</th>
<th>CVB (%)</th>
<th>II (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>cTn</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lan et al. [13]</td>
<td>2020</td>
<td>20</td>
<td>Weekly</td>
<td>7 weeks</td>
<td>40</td>
<td>22–70</td>
<td>40.1 / 44–58.5</td>
<td>14.0</td>
<td>47.9</td>
<td>25.8</td>
<td>1.69</td>
</tr>
<tr>
<td>Ceriotti et al. [14]</td>
<td>2020</td>
<td>89</td>
<td>Weekly</td>
<td>10 weeks</td>
<td>20–60</td>
<td></td>
<td>50.1 / 45–53.4</td>
<td>11.6</td>
<td>16.6</td>
<td>13.9</td>
<td>0.3</td>
</tr>
<tr>
<td>Schindler et al. [15]</td>
<td>2016</td>
<td>10</td>
<td>Twice a week</td>
<td>3 weeks</td>
<td>50.9</td>
<td>51–64</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Aakre et al. [16]</td>
<td>2014</td>
<td>10</td>
<td>Weekly</td>
<td>10 weeks</td>
<td>61</td>
<td>46–68</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Vasile et al. [17]</td>
<td>2011</td>
<td>20</td>
<td>Daily</td>
<td>8 weeks</td>
<td>39</td>
<td>25–56</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Wu et al. [18]</td>
<td>2009</td>
<td>17</td>
<td>Fortnightly</td>
<td>8 weeks</td>
<td>19–58</td>
<td></td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td><strong>cTnT</strong></td>
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<td></td>
<td></td>
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</tr>
<tr>
<td>Meijers et al. [19]</td>
<td>2017</td>
<td>28</td>
<td>Monthly</td>
<td>4 months</td>
<td>43</td>
<td>13 [13]</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Corte et al. [20]</td>
<td>2015</td>
<td>11</td>
<td>Weekly</td>
<td>5 weeks</td>
<td>21–50</td>
<td></td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Aakre et al. [16]</td>
<td>2014</td>
<td>10</td>
<td>Weekly</td>
<td>10 weeks</td>
<td>61</td>
<td>46–68</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Frankenstein et al. [21]</td>
<td>2011</td>
<td>17</td>
<td>Weekly</td>
<td>5 weeks</td>
<td>32</td>
<td>22–59</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
<tr>
<td>Vasile et al. [17]</td>
<td>2010</td>
<td>20</td>
<td>Daily</td>
<td>8 weeks</td>
<td>39</td>
<td>25–56</td>
<td>40.1 / 37.4–43.4</td>
<td>10.9</td>
<td>13.9</td>
<td>14.5</td>
<td>0.40</td>
</tr>
</tbody>
</table>

*aYear published.*bNumber of subjects.*cExpressed in mean (range) or range only. F, females; M, males.
biological variation or RCVs. However, studies are encouraged to do so considering that gender-specific 99th percentile value of biomarkers are increasingly reported.

Until more data from outcome studies investigating the biomarker in different clinical situations become available analytical performance specifications might be based on biological variation. Our data suggest that the $CV_A$ for the cMyC assay at concentrations used for routine diagnosis should be below 9% (half of $CV_I$) [27], which is very similar to current recommendations for cTn. Our calculated $CV_A$ was 19.5% (17.8–21.6%), which is higher than $CV_A$ reported in the majority of long term cTn biological variation studies (Table 3). However, our $CV_A$% was obtained from duplicates with median cMyC of 4.38 (2.75–5.97) ng/L, which is considerably lower than median cMyC found in patient with adjudicated diagnosis of acute coronary syndrome 237 (71–876) ng/L in the APACE cohort [6], and only ~5% of the 99th percentile (derived from patients without coronary artery disease) [28]. Lower $CV_A$ should be expected at higher (more clinically relevant) concentrations, and we predict lower $CV_A$ with future automated assays of cMyC. Further, a higher ratio of mean cTn to respective assay-specific 99th percentile was reported in similar long-term cTns biological variation studies [16].

Finally, our data indicate that the desirable analytical bias (i.e. calculated as $1/4 \times (\sqrt{CV_I^2 + CV_G^2})$) should be 17% or lower. This is similar to what is commonly seen for lot variations for immunoassays. The allowable total error (precision and bias merged) should be below 28%.

This study has several strengths: (1) it is multi-centre, with unified protocol and standard operating procedure to minimise pre-analytical variability; (2) it included a relatively large number of participants, of which, 53% were women; (3) “healthy status” was clearly defined, (4) exclusion of outliers was performed systematically and is described in the manuscript; (5) gender-stratified variability, RCV and II were measured. The RCVs were calculated using two different models, ln transformed data and non-parametric method suggested by Røraas, the results were similar. The statistical analysis was performed by two independent researchers using two different software platforms.

The study also has limitations – the participant mean age was lower than in patients with chronic primary or secondary cardiac disease so the reported data may not be valid for cohorts with other characteristic. Samples were analysed 18 months after collection, however, these were continuously stored at −80 °C and thawed once for the analysis.

Conclusions

cMyC exhibits acceptable biological variation, RCV and low II suggesting that it could be suitable for disease monitoring, risk stratification and prognostication if measured serially. Analytical quality specifications based on biological variation data are similar to those for cTn and should be achievable at clinically relevant concentrations. However, testing the RCV in cohorts with chronic cardiac disease and reported/measured outcomes is necessary to testify its ability to monitor disease activity and predict outcomes. However, future use of the biomarker will determine if specification should be based on clinical needs or biological variation.

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Informed consent: Informed consent was obtained from all individuals included in this study.

Ethical approval: Research involving human subjects complied with all relevant national regulations, institutional policies and is in accordance with the tenets of the Helsinki Declaration (as revised in 2013). The protocol was approved by the respective regional ethics committee at each center: South Central – Berkshire Research Ethics Committee (London), and the Regional Committee for Medical and Health Research Ethics in Bergen (Bergen and Oslo).
References


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