# Cardiac myosin-binding protein C as a biomarker of acute myocardial infarction

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Cardiac myosin-binding protein C (cMyBP-C, MYBPC3, cMyC; UniProtKB—Q14896) is a 140 kDa sarcomeric protein that is loosely associated with both myosin and actin. It was identified in the coronary effluent from ischaemic myocardium about 10 years ago and after systematic screening of monoclonal antibodies a sensitive sandwich immunoassay was formulated. Using this assay, cMyC has been measured in a variety of patient groups and directly compared to cardiac troponin T (cTnT) and cardiac troponin I (cTnI) measured in the same blood samples using high-sensitivity assays. 1

Direct comparisons of cMyC with cTnI/T have established the following:

- (1) cMyC is more abundant than cTnT/I and consequently it is possible to measure smaller volumes of myocardium undergoing injury, based on spiking human heart into human blood.<sup>1</sup>
- (2) After myocardial injury cMyC can be detected in the blood earlier, and its concentration rises more rapidly, than cTnT/I or novel RNA biomarkers.<sup>1,2</sup>
- (3) Based on blood samples taken at presentation in patients with a suspected acute coronary syndrome, the diagnostic accuracy for acute myocardial infarction of cMyC, cTnl, and cTnT are similar, but cMyC is more efficient at rapid rule out.<sup>3</sup>
- (4) Despite cMyC having a sarcomeric location and kinetic profile that differs from cTnT/I, its concentration is similarly increased by chronic myocardial injury and acute (non-ischaemic) myocardial injury.<sup>3,4</sup>

Based on these results the diagnostic performance of cMyC is similar to cTnT/I. Whilst this is a remarkable accomplishment, the question remains whether cMyC has sufficient distinctive advantage to possibly replace cTnT/I or add enough incremental value to be used in conjunction with cTnT/I? Figure 1 shows the location of cMyC and cTn within the cardiac sarcomere and their migration into the bloodstream. One of the difficulties with any new biomarker of myocardial injury is that

cTnT/I is not just the comparator, but also to some extent the referee—since the final adjudicated diagnosis of acute myocardial infarction is heavily reliant on its use—creating strong confirmation bias. This is particularly problematic in real-world studies where treatment decisions, such as early discharge and lack of subsequent blood samples, are driven by the comparator. One possible way to overcome this bias is to perform randomized controlled diagnostic trials where the biomarker concentration drives treatment decisions and the endpoints are clinical events (not biomarker determined). Such trials require enormous resource and superior analytic sensitivity does not necessarily translate into a clinically meaningful advantage. For these reasons, current research efforts focus on further improving the specificity of the cMyC assay for acute myocardial infarction caused by sudden reductions in myocardial blood supply.

In summary, cMyC is a myocardial injury biomarker that behaves similarly to cTnI/T but is more sensitive. However, this advantage is being challenged by the combination of confirmation bias, the evolving analytic sensitivity of the cTn assays and methodological difficulties in translating improvements in analytic sensitivity into reductions in hard clinical endpoints.

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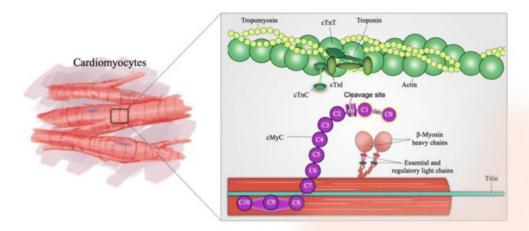
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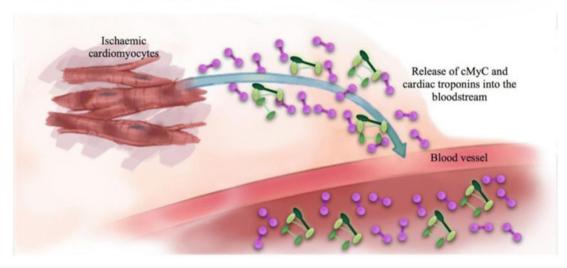
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## A Structure of cMyC and cardiac troponins



# B Ischaemia-induced cardiomyocyte damage



**Figure 1** Structure of cMyC and relationship with the cTn complex from ref.<sup>1</sup> . Panel A depicts the location of the troponins (cTnC, cTnI and cTnT) and cardiac myosin binding protein C (cMyC) within the sarcomere of a cardiac myocyte. cMyC undergoes clevage to generate an amino-terminal fragment containing the C0 and C1 domains. The clevage of cMyC is a regulated process and is prevented by phosphorylation of key amino acids by stress-responsive kinases such as protein kinase A. Panel B depicts the forms of cTn and cMyC that enter the circulation from the damaged cardiomyocyte. The image is simplified since the biomarkers circulate as complexes of full-length proteins as well as various fragments.

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