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Genetic polymorphisms of human cardiac troponins as an unrecognized challenge for diagnosing myocardial injury



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Human cardiac specific troponin I (cTnI), the inhibitory subunit of the troponin complex, is encoded by the *TNNI3* gene, located on chromosome 19q13.4. The final transcript is a 200 amino acid protein (Fig. 1), with a predicted molecular mass of 24 kDa [1]. Human cardiac specific troponin T (cTnT), the tropomyosin-binding subunit of the troponin complex, is instead encoded by the *TNNT2* gene, located on chromosome 1q32. The final transcript is a 298 amino acid protein (Fig. 1), with a predicted molecular mass of 35.9 kDa [1].

The measurement of cardiac specific troponins, thus entailing cTnI and cTnT, has now become the cornerstone for diagnosing a wide spectrum of ischemic and non-ischemic cardiac injuries. In particular, their assessment is pivotal for diagnosing non-ST elevation myocardial infarction (NSTEMI), where electrocardiographic findings are understandably lacking. The recent development of novel and more analytically sensitive immunoassays for measuring these important biomarkers (i.e., contemporary-sensitive and high-sensitivity methods), has substantially improved the efficiency of cardiac injury detection, wherein modestly increased concentrations of cTnI and cTnT can now be detected more efficiently and precociously than with previous methods [2].

Although, these technical advancements have allowed to achieve a final diagnosis of acute myocardial infarction (AMI) within 2–3 h from the onset of symptoms in the vast majority of patients [3], the sensitivity and negative predictive value of contemporary-sensitive and high-sensitivity immunoassays remain suboptimal, and a variable percentage of patients – ranging from 6 to 23% – has normal levels of cardiac specific troponins at presentation, even when measured with high-sensitivity immunoassays [4].

Various hypotheses have been proposed to explain the modest but meaningful number of “false negative” cardiac specific troponin tests in patients who are then finally diagnosed as having an AMI, which include preanalytical issues (i.e., sample misidentification, spurious hemolysis), analytical errors (instrument malfunctioning, reagent deterioration) and interference (e.g., heterophilic antibodies and rheumatoid factor) [1]. Another potential and virtually unrecognized source of false negative test results is then represented by genetic polymorphisms of cardiac troponin genes. The various contemporary-sensitive and high-sensitivity immunoassays contain a heterogeneous cocktail of (monoclonal) antibodies for the capture and detection of the molecules (Table 1), which specifically react against targeted domains of the proteins [5]. It is hence predictable that natural variants of both cTnI and cTnT containing single nucleotide polymorphisms (SNPs) that involve (and structurally modify) any of the epitopes recognized by these antibodies, would decrease or even impair the binding properties of the commercial antibodies. We have hence performed a search on the database of UniProt, which is a comprehensive and high-quality resource of protein sequence and functional information [6], to identify all SNPs in the *TNNI3* and *TNNT2* genes that may involve antibody-binding domains of either cTnI or cTnT. This search identified 19 and 4 of such polymorphisms in the sequence of *TNNI3* and *TNNT2*, respectively. We also found that 71% (i.e., 12/17) of commercial cTnI immunoassays, as well as all four cTnT immunoassays, contained antibodies targeting SNP-containing domains in the *TNNI3* and *TNNT2* genes (Table 1) [7–16]. In some cases, the monoclonal antibodies recognized regions of the proteins containing more than one single SNP. Even more interestingly, the vast majority of these SNPs were associated with inherited cardiac disorders, namely idiopathic dilated cardiomyopathy, familial hypertrophic cardiomyopathy and familial restrictive cardiomyopathy, whereas two SNPs of the *TNNT2* gene have been reported to be clinically silent so far (Table 2). It is noteworthy that the vast majority of these

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cTnI

10 20 30 40
MADGSSDAAR EPRPAPAPIR RRSSNYRAYA **TEPHAKKKSK**

50 60 70 80
ISASRKLQLK TLLLQIAKQE LEREAEERRG **EKGRALSTRC**

90 100 110 120
QPLELAGLGF AELQDLRQL HARVDKVDEE RYDIEAKVTK

130 140 150 160
NITEIADLTQ KIFDLRGKFK **RPTLRRVVIS ADAMMQALLG**

170 180 190 200
ARAKESLDLR **AHLKQVKKED TEKEHREVGI WRKNIIALSG**

210
MEGRKKKFES

cTnT

10 20 30 40 50 60
MSDIEEVVEE YEEEEQEEAA VEEEDDWRD EDEQEAAEE DAEAEAETEE TRAEDEEEEE

70 80 90 100 110 120
EAKAEDGEM EESKPKRSF MPNLVPPKIP DGERVDFDDI HRKRMEKDLN ELQALIEAHF

130 140 150 160 170 180
ENRKKEEEL VSLKDRIER **RA**ERAEQQRI RNEREKERQN RLAEERARRE EENRRKAED

190 200 210 220 230 240
EARKKKALSN MMHFGGYIQK **QAQ**TERKSGK RQTEREKKKK ILAERRKVLIA IDHINEDQLR

250 260 270 280 290
EKAKELWQSI YNLEAEKFDL **QEK**FKQKYE INVLRNRIND NQKVSCTRKG AKVTGRWK

Fig. 1. Amino acid sequence of cardiospecific troponin I (cTnI) and cardiospecific troponin T (cTnT). The single nucleotide polymorphisms (SNPs) that may impair the immunoreactivity of the molecules are shown in bold and underlined.

inherited conditions are characterized by incomplete penetrance, variable expressivity and seldom late onset (i.e., not rarely after the fifth–sixth decade of life) [17].

According to this data, it is hence nothing but unlikely that carriers of one or more of these SNPs may suffer from AMI or other acquired cardiac injuries earlier than the onset of symptoms of cardiomyopathy, and may hence be misdiagnosed and potentially mistreated due to a false negative cardiospecific troponin test. It may hence be advisable that the next generation of cardiospecific troponin immunoassays should be designed to contain antibodies reacting not only with the more stable region of the proteins, but also against domains that do not contain known SNPs (Fig. 1).

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