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## Assessment and diagnostic relevance of novel serum biomarkers for early decision of ST-elevation myocardial infarction

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Blood transcriptome reflects the status of diseases and characteristic molecular signature provides a novel window on gene expression preceding acute coronary events. We aim to determine blood transcriptome-based molecular signature of acute coronary syndrome (ACS) and to identify novel serum biomarkers for early stage ST-segment-elevation myocardial infarction (STEMI). We obtained peripheral blood from the patients with ACS who visited emergency department within 4 hours after the onset of chest pain: STEMI (n=10), Non-ST-segment-elevation MI (NSTEMI, n=10) and unstable angina (UA, n=11). Blood transcriptome scans revealed that a characteristic gene expression change exists in STEMI resulting in 531 outlier genes as STEMI molecular signature (Welch's t test,  $P < 0.05$ ). Another analysis with a set of blood samples of patients with STEMI (n=7) before and 7 days after the primary percutaneous coronary intervention (n=7) and normal control (n=10) evidenced that STEMI molecular signature directly reflects the onset of STEMI pathogenesis. From the two sets of transcriptome-based STEMI signatures, we identified 10 genes encoding transmembrane or secretory proteins that are highly expressed in STEMI. We validated blood protein expression levels of these 10 putative biomarkers in 40 STEMI and 32 healthy subjects by ELISA. Data suggested that PGLYRP1, IRAK3 and VNN3 are more specific and sensitive diagnostic biomarkers for STEMI than traditional CK-MB or troponin. Blood transcriptome scans of ACS evidenced early stage molecular markers for STEMI. Here, we report novel biomarkers to diagnose STEMI at emergency department in hospitals by a simple ELISA method.

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