

Matrix Proteins and Proteinases Network in Human Cardiovascular Diseases Explored By Cytoscape

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Abstract

Matrix proteins and proteinases altered extracellular matrix that involves in various pathogenesis of cardiovascular diseases. Systematic review selected matrix metalloproteinase-7 (MMP7), a disintegrin and metalloproteinase-17 (ADAM17), type I collagen (COL1), syndecan (SDC), and versican (VCAN). Their network was drawn by Cytoscape and Agilent Literature Search. MMP7, ADAM17, and SDC were grouped together. VCAN and COL1 had inadequate evidence to connect their human potential networks that were more evidence in animal models. The findings may provide clues for further laboratory investigations.

Keywords

Cytoscape, matrix proteins, metalloproteinase, network, cardiac disease

Introductions

As the extracellular matrix (ECM) plays pivotal roles in regulating cardiac structural and functional integrity (Chiao et al. 2012), any alteration of ECM by matrix proteins, proteinases, and related molecules may involve in the pathophysiological process of various cardiovascular disease. (Chiao et al. 2012, Etoh et al. 2001, Neill et al. 2015, Peterson et al. 2000, Vanhoutte et al. 2006, Zile et al. 2011) We would like to explore their network relationships in human for more laboratory workup.

Methods

Thorough systematic review was by using PubMed search. On Cytoscape 3.40 (<http://www.cytoscape.org>), we used Agilent Literature Search 3.11 to explore the molecular relationships. For the extraction control, the concept lexicon was “Homo sapiens”, and the interaction lexicon was set to “limited”. The network was drawn with GeneMANIA Force Directed layout. We screened most of the molecules available from systematic review and selected the most relevant ones for subsequent Cytoscape analysis.

Data resources

Systematic reviews with PubMed.

Online public-domain databases used by Cytoscape.

Results and discussion

From all the known and potential molecules relating to cardiovascular disease such as cardiomyopathy and transplant allograft rejection (Dupuis et al. 2015, Huet et al. 2015, Lu et al. 2000, Odenbach et al. 2010, Rickard et al. 2012, Wang et al. 2009), we selected matrix metalloproteinase-7 (MMP7), a disintegrin and metalloproteinase-17 (ADAM17), type I collagen (COL1), syndecan (SDC), and versican (VCAN). Their relational networks showed grouping of MMP7, SDC, and ADAM17 whereas only potential associations with COL1A1, COLA2, and VCAN (Fig. 1) With laboratory evidence from knock-out mice that showed interactions of COL1, VCAN, ADAM17, SDC, and MMP7, we are performing more laboratory works such as Western blotting, immunofluorescence staining, and rPCR to analyze tissue samples from human cardiomyopathy and transplant allograft rejection for validation.

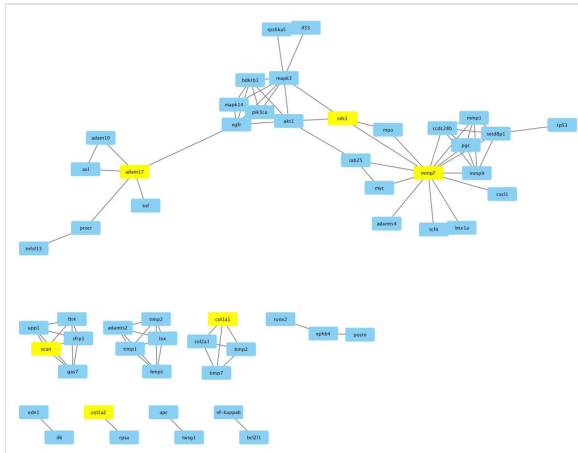


Figure 1.

Cytoscape network, derived from MMP7, ADAM17, SDC, COL1, and VCAN (see Abstract for full spellings of abbreviations).

Conclusions

Cytoscape network shows the interplaying roles of MMP7, ADAM17, SDC, COL1, and VCAN in the pathogenesis of cardiovascular diseases like cardiomyopathy and transplant rejection have been implied by the Cytoscape exploration. Further human laboratory experiments will be done to investigate the theoretical network.

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Hosting institution

National Taiwan University College of Medicine, Taipei, Taiwan

Ethics and security

Waived Institutional Review Board (IRB) review.

Author contributions

Chen RJC: concept, study design, analysis, and manuscripting; Yu WH: concept, revision, and supervision.

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