A more accurate approach to molecular genetics analysis in vascular disease.

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Abstract

Vascular disease (VD) and its complications are the leading cause of morbility and death in modern civilisations. Primary VD is a very complex and multifactorial process which is still not well understood. Recent studies provide clear and convincing evidences that genetic risk factors (gene polymorphisms) contribute significantly to the pathogenesis and expression of VD. Thus, we have to analyse the interaction of multiple polymorphisms in multiple genes coding for several proteins involved in the molecular etiopathogenesis of VD. All these polymorphisms are interacting among them, enhancing or antagonizing their pathogenic effects, and at the same time, their final phenotypic expression is constantly modulated by other non-genetic factors (environmental and behavioural). Thus, gene-environment interaction analysis would be crucial for the correct etiopathogenic evaluation. According to a particular assortment of positive and negative gene variants (alleles) present in their genetic pool some individuals develop VD without manifesting very extreme levels of any of the classical risk factors while other individuals remain free of disease despite exposure to several risk factors. Taking into account that this heterogeneity is due to their different genetic susceptibility it is necessary to make an analyse in deep including all genetic polymorphisms which have been involved in the vascular etiopathogenesis in order to design the most appropriate intervention strategy. Using a more accurate genetic polymorphism analysis it would be possible to predict complications in order to make prevention designing an individualized drug therapy on the basis of a person's genetic makeup. However, an accurate genetic testing is not being used as often as it is expected because there are so many polymorphisms to consider and DNA tests available to analyse them are usually dispersed throughout different laboratories because they are not included in an unified protocol. In this sense, DNA-Chip technology used as susceptibility (predisposition) testing has evolved into a powerful tool providing informative data from multiple loci in complex diseases like VD (where multiple genetic alterations contribute, but each on a small scale). This technology could greatly reduce health care costs by reducing the number of useless diagnostic tests making possible the genetic
dissection of complex human diseases. The proposed paper will discuss these topics with special
emphasis on how genetic polymorphisms influence in the individual susceptibility to develop vascular
disease and its complications as well as the way that may affect individual responses to several drugs
used in the VD management.