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Review Article

Diseasome, a new fundamental genetic-based insight to diseases

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ABSTRACT:

Background: Genetic and environmental factors play an important role in human disease.

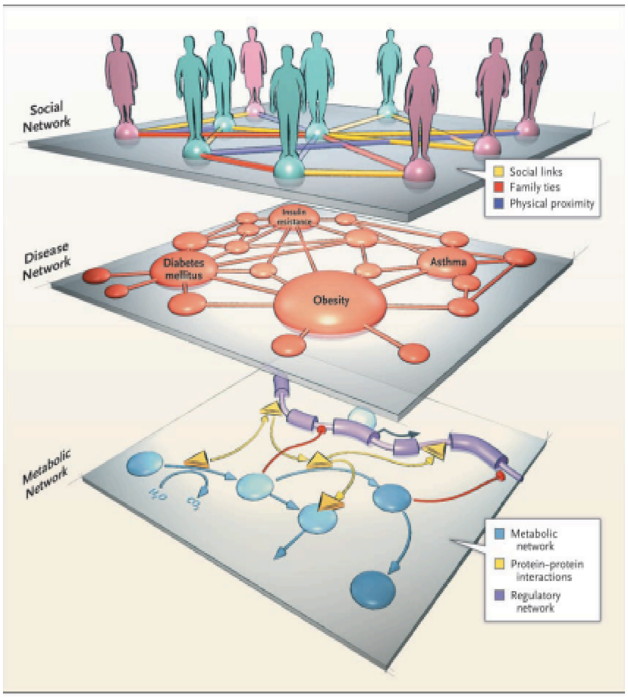
Epidemiological network model for disease or diseasome demonstrates a high degree of realism by including the details of interpersonal communication which are potentially capable of transmitting the disease in a social settingnetwork theory allows us to design a shortcut by which we can accurately predict the phenotype and genotype probability of various diseases have diverse and vice versa

Methods: In this review articlebetween 1990 to2012published indifferentjournals mostly in PubMed, Medline, OMIM and Gene Cardwere investigated.

Result and conclusion: Diseasome helps to better understand the relationship between etiologic factors and muscular efficiency and thus contributing to find related diseases.

BACKGROUND:

Genetic and environmental factors play an important role in human disease. Most common diseases influenced a large number of genetic and environmental etiologic factors which in themselves are effective in creating or modifying disease progression. In the present, in monogenic diseases have known several genetic etiologic factors that it is less about environmental factors. However, the network of genes involved in the formation of a specific disease phenotypes, certainly overlap, and indeed individual's genes may be simultaneously involved in the etiology of multiple disorders (1-8). Epidemiological network model for disease or diseasomedemonstrates a high degree of realism by including the details of interpersonal communication which are potentially capable of transmitting the disease in a social setting. However, taking into account the relationship between etiologic factors, communication network and their classification could be useful to explain their impact on health and disease.(Fig. 1)



In other words, network theory allows us to design a shortcut by which we can accurately predict the phenotype and genotype probability of various diseases have diverse and vice versa (3-9).

MATERIALS AND METHODS:

A search of relevant terms on PubMed, MEDLINE, OMIM, and GeneCards was conducted using a combination of key words (Muscle Strength ،Muscle ،Diseasesome, Gene ،Performance, Diseases ،GDF ،ACE ،GR ،PPARG ،VDR ،CNTF).

Our search included articles of all languagesPublished between 1990 till2012.The focus of this review was limited to those articles studying genes involved in muscle function and power; the article which were not relevant to our objectives nor had inadequate sample size nor validity were excluded.

To study the effect of the genes involved in muscle performance and power on a probable disease incidence or recovery, Odds Ratio ofthe studies for each gene were collected separately and the Cumulative Odds Ratio determined finallyby software Review Manager (RevMan) Then, using the software Gephi, a network or a model would be designed to illustrate the relation and association between the genes involved in muscle performance and power and also their roles in diseases.

RESULTS AND DISCUSSION:

Diseasome helps to better understand the relationship between etiologic factors and muscular efficiency and thus contributing to find related diseases.

In this regards, communication and the trade-off between diabetes and ACE gene polymorphism should be considered (6-28). (Fig.2)

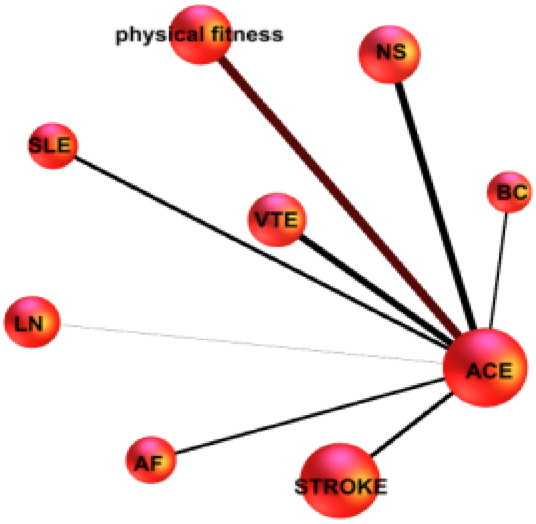


Fig. 2: disease related to ACE gene

Finally, the study results to be learned isthat genes and disease and more precisely both environmental and genetic etiologic factors can cause various diseases and perhaps overlap with herself in various diseases.That this overlapping and communicate in the best way possible through modeling theory is justifiable (12-36).As the results are visible forms and modules of genes involved in muscle strength and performance are responsible for creating multiple diseasesThat each of these diseases may be genetic etiology identical to the genes involved in muscle strength and performance therefore, the turning point of the overlapped and their connections to Find the answers in the screening, treatment and prevention of these disorders may occur (17-40).

Conclusions: Whensix genes associated with physical performance were examined all of related diseases genes in a figure consisting of 100 patientswas drawn(Fig. 3), to the possible association of genes in a cell matrix 600 CI (confidence interval), 95% to be considered for the communication network. It is interesting that in this network by using a circular (circular layout) well seenACE gene is the most centrum which together have created specific modules. (Fig. 4)

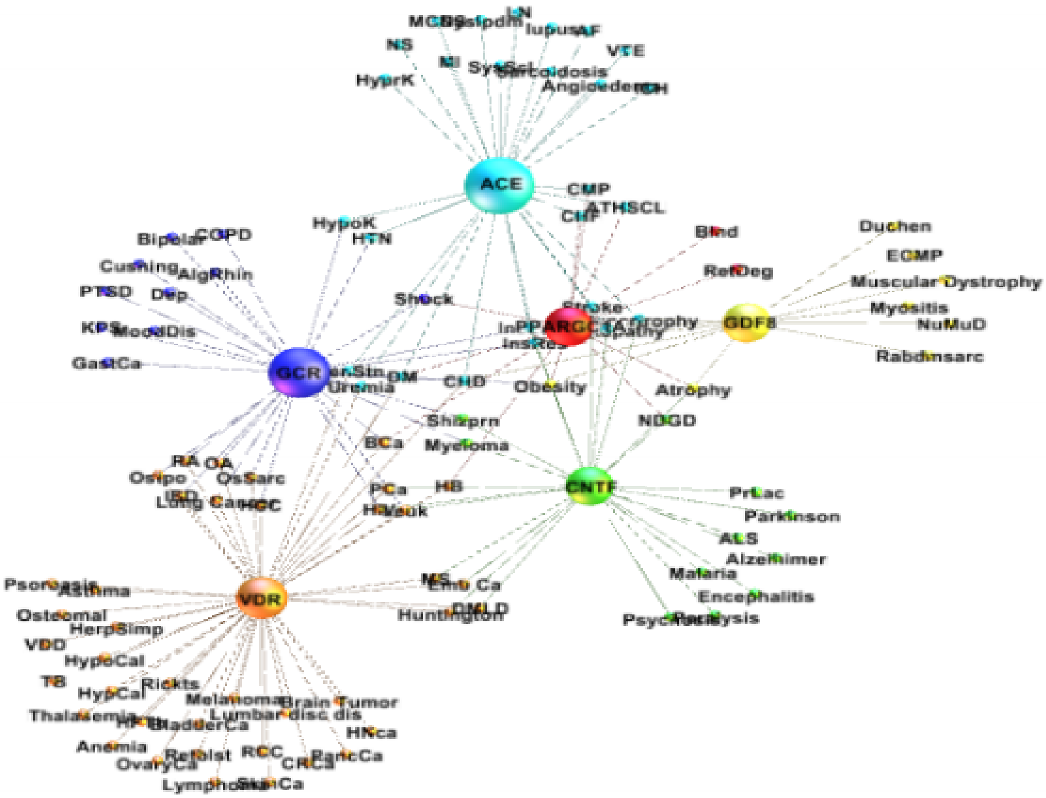


Fig.3 Disease-Gene-Network (DGN)

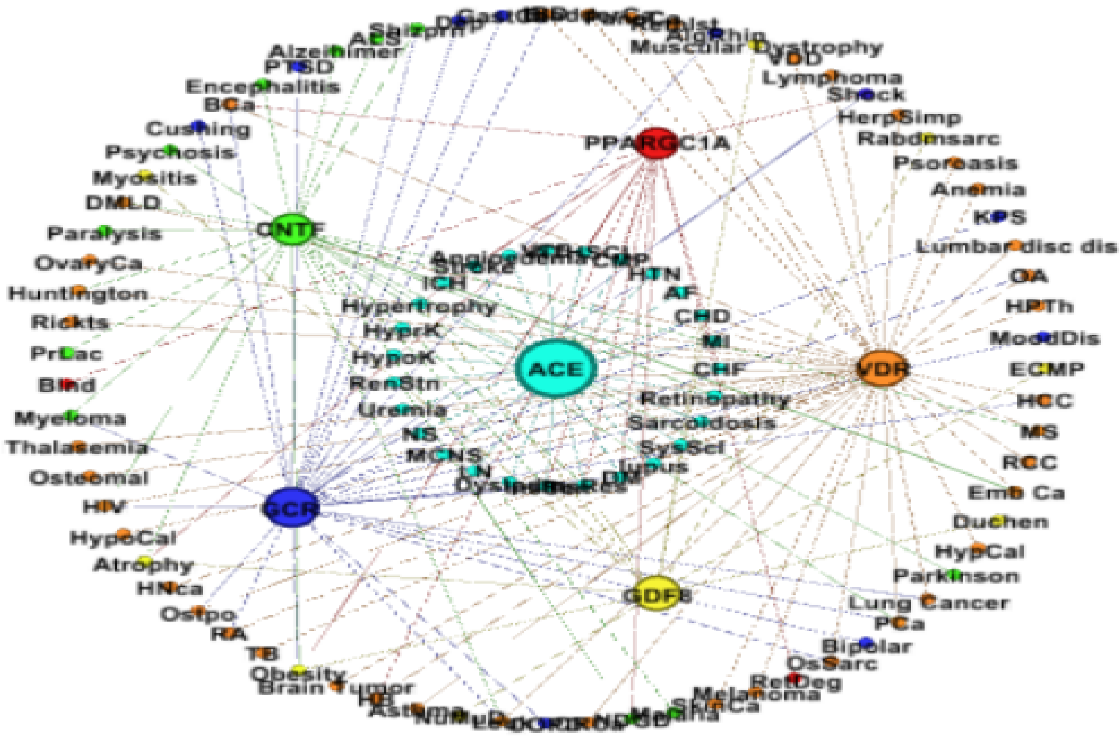


Fig4. Six genes and 100 disease

The designed network (diseasome) Shows muscle efficiency, beautiful cluster of communication between patient and etiologicalfactors with the mean (average degree)graph 4/7 and clustering coefficient of the mean (average clustering coefficient) 0/6. The designed network havetwo clusters of the disease, diabetes and other onecancers Which of the two, diabetes had more power and centrum.

In the case of other diseases associated with physical inactivity gene showed that the disease is strongly influenced by a strong association network module cancersa strong core network that is more relevant to FOK1. This link leads to the highest clustering coefficient for the set of cancers.

There is no conflict of interest.

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