J Comput Sci Syst Biol 2016, 9:5 (Suppl)
http://dx.doi.org/10.4172/0974-7230.C1.015

Analyses of selective influence on partial genes in domestication of *Gallus gallus domesticus*

Tangjie Zhang
Yangzhou University, China

To research effects of the artificial selection of *G. gallus* on *G. domesticus*' nucleotide diversity of immune genes, sequence polymorphisms of *G. domesticus* (23 genes), *G. gallus* (23 genes), *Gallus lafayetti* (17 genes), and *G. sonneratii* (17 genes) were obtained from GenBank. The data set included 819 polymorphisms. Immune gene polymorphism and selection efficiency in the data from those four species of *Gallus* were calculated. By calculating the θ_w (Watterson's estimator) of each site, an average θ_w for each species, and the minimum number of re-combinations in each species and estimating the selection efficiency for *G. domestics* and *G. gallus*, no significant nucleotide diversity nor genetic diversity θ_w difference was found between *G. domesticus* and *G. gallus*. The results indicated that the patterns of genetic diversity in *G. domesticus* were strongly influenced by recombination and because Tajima's D has a negative value, recombination was the main mechanism responsible for the immune gene evolution of *G. gallus*.

slx@yzu.edu.cn

An unbiased, weighted network intersects with experimental approach to define the functions of PSMD10, an assembly chaperone of the proteasome

Prasanna Venkatraman[1], **Indrajit Sahu**[1], **Padma Nanaware**[1], **Meenal Mane**[1] and **Soumen Roy**[2]
[1]Tata Memorial Centre, India
[2]Bose Institute, India

PSMD10, a proteasomal assembly chaperone, when overexpressed induces gene expression changes in HEK293 cells. A weighted network approach was employed to gain biological insights from these differentially expressed genes. Key network properties such as degree centrality and edge betweenness were identified. The top 30 edges (interactions) indicated that PSMD10 might be involved in cell fate decisions that commits stem cells to differente into neurons and/or astrocytes. Pathway analysis of the upregulated genes indicated a strong signature for the activation of neuroactive ligand receptor interaction pathway and Wnt signaling. Two hypothesis emerged from these comprehensive analysis: The presence of a neuronal differentiation program that includes genesis of astrocyte and neurons regulated by the source node PSMD10 and; the probability that PSMD10 may skew cell fate decision towards the formation of neurons. We tested these possibilities and provide preliminary and yet a compelling experimental evidence for the involvement of PSMD10 in the preferential differentiation of a neural progenitor cell line into neurons.

vprasanna@actrec.gov.in