Editorial

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Integrative Analysis of Co-Morbid Multifactorial Diseases

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This special issue is based on the results of a German-Russian-Ukrainian project supported by the VolkswagenStiftung to analyze the biological mechanisms of co-morbid multifactorial diseases. One of the most urgent problems of modern medicine is related to the identification of molecular targets of drugs for the treatment of co-morbid diseases in humans. Achievements in various *omics* technologies have made it possible to study risks of diseases of interest at different molecular levels. Therefore, systems biology is developed to determine the effect of combined molecular pathways to build the causal link between genotype and phenotype. Such work showed that the diseases tend to exhibit co-morbidity if they share susceptibility genes. In this project the focus is hypertension and bronchial asthma as an example of common co-morbid diseases. Shared genes associated with the development of hypertension and asthma are identified, such as ADRB2, TNF, NOS, and many others. The goal of this project was to expand the knowledge on the mechanism and identify new drug targets for co-morbid diseases in humans using such frequently co-morbid observed pathologies as asthma and hypertension.

The project partner from Novosibirsk identified important genes that are involved in co-morbid links between asthma and hypertension by using text- and data-mining techniques. The result of this work is presented in Saik et al. relevant targets have been prioritized using well-known methods (ToppGene and Endeavor) and a cross-talk centrality criterion, calculated by analysis of associative gene networks from ANDSystem. Top 100 prioritized genes were found to exhibit significant positive dynamics in the frequency of mentioning them in scientific publications, suggesting increasing interest in the studies of these genes. The clinical and genetic data for this project came from the project partner of Tomsk National Research Medical Center of the Russian Academy of Sciences. Therefore, Bragina et al. are describing a genetic aspect of different clinical phenotypes. The single nucleotide polymorphisms (SNPs) of the identified genes by using bioinformatics approach were studied in patients with isolated and co-morbid diseases. It has been established that SNPs associated with co-morbidity differs from SNPs associated with isolated asthma and hypertension. Molecular links of comorbidity of asthma and hypertension may be due to genes TLR4, CAT, ANG. Furthermore, based on the clinical data and semi-automatic data mining approaches a new database was developed and implemented, which presents the positive and negative drug list for asthma and hypertension. This new database is presented in Shoshi et al. A web-based implementation of this database allows the access to this information via internet. Finally, Drevyt-ska et al. present pilot experiments and results about experimentally confirmed functionality changes of the target which was predicted *in silico* (Saik et al.) to be associated with both asthma and hypertension.

Ralf Hofestädt is the corresponding author.

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