

## A need of convergence between personal genomics and Korean medicinal typology

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### ABSTRACT

Advances in individual genome sequencing technology and next generation sequencing technology have allowed for widespread research of human genome, which would give us opportunities not only to change our focus from the experience-based Korean medicine including typology and Sasang constitution to the evidence-based Korean medicine but to provide effective tailored medical care and Tang theory.

**Keywords** human genome, Korean medicine, tailored medicine, typology, Tang

Human genome, which was completely sequenced in 2012, is the entire set of human genetic information. The increased speed of individual genome sequencing technology and next generation sequencing technology has enabled scientists in various fields to research about human genome. (Zheng-Bradley and Flícek, 2012).

In truth, the research landscape of genetics has been translated in to the medical purposes. Accordingly, even genome researches in different fields have been consistently applied to medical purposes, and the knowledge learned from sequencing of individual genomes and NGS into the decision-making process of medical care brought a wide range of anticipation for the advancement of diagnosis and treatment of diseases. Many reports about genetic variations of single nucleotide polymorphism (SNPs) and copy number variation have suggested the genetic mechanisms for various phenotypes of diseases. For instance, Corder et al., (1994 and 1993) demonstrated the strong association between apolipoprotein E (ApoE) polymorphisms and Alzheimer's disease. To give other examples, Walsh et al., (2012) revealed that six SNPs from six genes have 90% or more accuracy for blue and brown eye colors in European populations. Kayser et al., (2008) practiced a genome wide association study on quantitative eye color extracted from digital eye images and found three new eye color genes.

Advances in human genetic study have enabled researchers to carry out effective personalized medicinal treatment and predictive medicine. In Korean medicine, the personalized medicinal treatment has been the important characteristic for a long time. According Donguibogam, written by Hur Joon (1539-1615) in the 17<sup>th</sup> century, the Korean Medicinal doctor has diagnosed illness based on observations of patient's specific body shape and feature to focus on the individual patient's clinical signs and symptoms, and medical history. Also, the medication has been applied to each individual patient with well-documented particular prescription which is called Tang in Korean medicine.

Until now, only few cautious convergence studies have been accomplished between Korean medicine and genome study. Jung et al., (2011) reported results of a study about angiotensin I converting enzyme (ACE) I/D SNPs. They found that ACE I/D polymorphism is significantly associated with Korean female asthma patients applied to symptomatic classification. After that, they suggested that the symptomatic classification by Differentiation-Syndrome can be useful in evaluation of the pathogenesis of asthma. In Korean medicine, the individual humans have been classified into one of four constitutional types (Taeum, Soeum, Soyang, and Taeyang) based on Sasang constitution medicine (Chae et al., 2003). These four types of persons are characterized to distinct personalities, body shape patterns and disease types. Kim et al., (2012) presented the association between genome-wide SNP profiles and the categorization of the four constitutional types.

If the Korean Medicinal diagnostic profiles and Tang theory efficiently combine with human genomics, these will provide opportunity for effective tailored and personalized medical care in Korean Medicine.

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### CONFLICT OF INTEREST

The authors have declared no conflict of interest.

### REFERENCES

Chae H, Lyoo IK, Lee SJ, Cho S, Bae H, Hong M, Shin M. An alternative way to individualized medicine: psychological and physical traits of Sasang typology. *J Altern Complement Med.* 2003;9:519-528.

Corder EH, Saunders AM, Risch NJ, Strittmatter WJ, Schmechel DE, Gaskell PC Jr, Rimmeler JB, Locke PA, 2013 / Volume 3 / Issue 2 / e11

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Conneally PM, Schmader KE, Small GW, Roses AD, Haines JL, Pericak-Vance MA. Protective effect of apolipoprotein E type 2 allele for late onset Alzheimer disease. *Nat Genet.* 1994;7:180-184.

Corder EH, Saunders AM, Strittmatter WJ, Schmechel DE, Gaskell PC, Small GW, Roses AD, Haines JL, Pericak-Vance MA. Gene dose of apolipoprotein E type 4 allele and the risk of Alzheimer's disease in late onset families. *Science.* 1993;261:921-923.

Jung SK, Ra J, Seo J, Jung HJ, Choi JY, Cho YJ, Hong MS, Chung JH, Kim J. An Angiotensin I converting enzyme polymorphism is associated with clinical phenotype when using differentiation-syndrome to categorize korean bronchial asthma patients. *Evid Based Complement Alternat Med.* 2011; 2011:498138.

Kayser M, Liu F, Janssens AC, Rivadeneira F, Lao O, van Duijn K, Vermeulen M, Arp P, Jhamai MM, van Ijcken WF, den Dunnen JT, Heath S, Zelenika D, Despriet DD, Klaver CC, Vingerling JR, de Jong PT, Hofman A, Aulchenko YS, Uitterlinden AG, Oostra BA, van Duijn CM. Three genome-wide association studies and a linkage analysis identify *HERC2* as a human iris color gene. *Am J Hum Genet.* 2008;2:411-423.

Kim BY, Yu SG, Kim JY, Song KH. Pathways involved in sasang constitution from genome-wide analysis in a Korean population. *J Altern Complement Med.* 2012;18:1070-1080.

Walsh S, Wollstein A, Liu F, Chakravarthy U, Rahu M, Seland JH, Soubrane G, Tomazzoli L, Topouzis F, Vingerling JR, Vioque J, Fletcher AE, Ballantyne KN, Kayser M. DNA-based eye colour prediction across Europe with the IrisPlex system. *Forensic Sci Int Genet.* 2012;6:330-340.

Zheng-Bradley X, Flicek P. Maps for the world of genomic medicine: the 2011 CSHL Personal Genomes meeting. *Hum Mutat.* 2012;33:1016-1019.