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Sessions: Symposium K: Adding Value to Laboratory Medicine and Pathology Practice

A Novel evidence-based laboratory medicine in the era of the big data and AI

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After the International Human Genome Project, Genomic Medicine reveals that the allele pattern of disease susceptibility SNPs varies from individual to individual, and furthermore most diseases each of them has been enclosed by the same disease name, such as carcinomas and diabetes, are consist of multiple intrinsic subtypes. The scientific basis of traditional evidence based medicine (EBM) is population medicine that thinks that patients with the same disease name are homogeneous and that representative features appear by collecting a large number of cases. Entering the era of genomic medicine, its premise was broken away. On the contrary, one purpose of collecting big data actively is to comprehensively grasp how many intrinsic subtypes exist in the disease. Another purpose is cohort studies based on genomic information as well as environmental factors aimed at revealing the etiology of multifactorial diseases which are believed to be caused by a complicated interaction among them. Data gathered by these studies is nearly as many as 100 million attribute items and the number of measurable individuals is one million even in large scale biobanks. Since there are far more kinds of variables than the number of individuals, statistical analysis using correlations between variables is no longer possible. Deep Learning revolutionized the artificial intelligence of the multilayered neural network system and must be an extremely powerful analysis method for big data. Up to now, EBM practice based on conventional population medicine is already losing meaning. However, it is only one form of practice and should be adapted to technology advances. In the era of big data and AI, experts in laboratory medicine should take initiative in keeping with the philosophy of EBM.