＜シンポジウム 14＞神経ゲノミクスの最先端

Aim

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Technologies of genome analysis is making breath-taking progresses. Positional cloning developed in the last decades in the 20th century brought discoveries of a large number of genes for Mendelian diseases to fruition. After the accomplishment of the Human Genome Project and Hap Map Project in this decade, DNA microarray technology enabled us to identify genetic factors of common diseases by genome wide association studies. Recently, a new technology, next generation sequencing, has emerged, which can reveal a whole genome nucleotide sequence of an individual (personal genome), and, that is, all genome sequence variations. The symposium focuses on a large-scale genome analysis using next generation sequencers, and the frontline of genomics research on neurological diseases.

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