

第 708 回

千葉県がんセンター研究局集談会



**演題: Progress in evolutionary genomics**

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日時: 平成 23 年 1 月 21 日 (金) 午後 3 時 00 分 - 午後 4 時 00 分

場所: 千葉県がんセンター 研究局カンファレンスルーム

**要旨:**

Progress in evolutionary genomics is tightly coupled with the development of new technologies to collect high-throughput data. Next generation sequencing platforms are now paving the way to make numerous genomic measurements. Using next generation sequencing platform such as Illumina/HiSeq 2000 we could get an all-round view of human disease at DNA level, RNA level, and epigenetic level. In DNA level, whole genome, exome, target region sequencing can be done for human disease and pharmacogenetics research to discover SNPs, insertions and deletions (InDels), copy number variations (CNVs). Nowadays, whole genome exome sequencing as the most cost effective method has been well used in discovery functional variations that are responsible for various diseases. In RNA level, transcriptome, RNA-Seq, DGE-tags profiling, small RNA sequencing can be used to discover aberrant splicing and fusion transcripts. Epigenetic sequencing can be used to discover aberrant DNA methylation, histone modifications and so on. In brief, high throughput cost and accuracy next generation sequencing begins a new era for modern translational medicine and personalized healthcare.

多数の御来聴、御討論をお願いいたします。世話人: 中川原