

# Engineering Cures Through Genes (MicroArray に代わる遺伝子発現解析と安全性評価)

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## 1. 緒言

キュラジェン社は1991年に米国コネチカット州に設立されたベンチャー企業です。GeneCalling™, SeqCalling™, PathCalling™, GeneScape® という4つの遺伝子解析技術プラットフォームを持っており、新規遺伝子の探索、毒性の解析、パーソナライズド・メディスン等をサポートしております。

- 特徴 1) CuraGen はどの生物にも応用可能な、遺伝子発現解析手段を有しています。  
2) 新しい薬のターゲットを発見できます。  
3) 薬によって影響される遺伝子を発見できます。  
4) 新しい薬の毒性や効能の指標(マーカー)を発見できます。  
5) 効率のよい創薬・開発に貢献します。

## 2. 発表内容

### Pharmacogenomics and Pharmacogenetics: Identifying Response Genes and Variants to Facilitate Personalized Medicine

A paradigm shift in how we view genetics and genomics in drug development will soon usher in the era of personalized medicine, the goal of which is to give the right drug to the right patients. The completion of the human genome sequencing project will enable scientists to examine the effects of genetic variation on drug response in a way not previously possible. However, the sheer abundance of genomic information is likely to overwhelm any effort to correlate genetic variation with variable biological response. Thus, it is imperative to focus on only those genes of relevance in any particular system, whether drug-induced or disease-associated. CuraGen has developed a suite of technologies that is providing a high-throughput, intelligent means of identifying the genes of interest, and the genetic variations within those genes. Our technology for rapid analysis of global gene expression, GeneCalling™, has been applied to the identification of drug-response and disease-associated genes. For example, we have identified a set of genes regulated by SSRI compounds that appear to correlate with cardiotoxicity. Drug response genes may also uncover mechanism of action or efficacy, as we have demonstrated in studies of PPAR ligands and of cell cycle inhibitors. In parallel to the gene expression studies, we have employed SeqCalling™, a high-throughput process of sequencing transcribed genes, to identify cDNA-based single nucleotide polymorphisms (cSNPs). By linking GeneCalling™ and SeqCalling™, we will demonstrate the value of defining genetic variation in drug-response genes as a way of understanding variable response to drugs during and following clinical development.

問合せ先

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