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Stem cell informatics

幹細胞インフォマティクス

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The iPS cell technology has brought us a break-through in both drug discovery and regenerative medicine. I would like to talk on two topics: i) computational toxicology based on embryonic body (EB) system, and ii) SHOGoin: Human Omics database for the Generation of iPS and Normal cells.

In (i), we have developed a high-accuracy prediction system for difficult-to-predict late-onset developmental toxicity, such as abnormalities, caused by well-known drugs, including thalidomide and methylmercury, using only EBs without differentiation. The prediction accuracies are as high as 97.5%-100% for three representative toxicity categories.

In (ii), we are developing a new generation of digital dictionary of human cells, which is an extension of previously reported CELLPEDIA (Hatano et al. Database 2011), trying to provide "reference cell" information as much as possible, in order to function as the compass for cell engineers in the related fields. As a secondary product, the complete set of human reference cell data will enable us to extract "rules" for human cell types as well as evolutionary clues to cell speciation mechanisms.

Keywords: stem cell, drug discovery, large-scale analysis, single-cell, database

キーワード: 幹細胞、創薬、大規模解析、シングルセル、データベース