

腸内細菌とその遺伝子による

ヒトマイクロバイオーム薬物代謝のマッピング

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中国の連携研究室で腸内細菌に関する研究を行う予定である。腸内細菌に活性のある化合物や植物（特に漢方薬）などを探索することを目的としている。近年、腸内細菌は漢方薬の代謝に関わることが考えられている。今回紹介する論文は腸内細菌の薬物代謝に関するものなので、腸内細菌に関する知識の勉強になると思い、この論文を選んだ。

紹介論文

Mapping human microbiome drug metabolism by gut bacteria and their genes

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要旨

Individuals vary widely in their responses to medicinal drugs, which can be dangerous and expensive owing to treatment delays and adverse effects. Although increasing evidence implicates the gut microbiome in this variability, the molecular mechanisms involved remain largely unknown. Here we show, by measuring the ability of 76 human gut bacteria from diverse clades to metabolize 271 orally administered drugs, that many drugs are chemically modified by microorganisms. We combined high-throughput genetic analyses with mass spectrometry to systematically identify microbial gene products that metabolize drugs. These microbiome-encoded enzymes can directly and substantially affect intestinal and systemic drug metabolism in mice, and can explain the drug-metabolizing activities of human gut bacteria and communities on the basis of their genomic contents. These causal links between the gene content and metabolic activities of the microbiota connect interpersonal variability in microbiomes to interpersonal differences in drug metabolism, which has implications for medical therapy and drug development across multiple disease indications.