JSPCCS-Study Group for Cardiovascular Dev. Joint Session

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[JSCDJS-P1] 日本小児循環器学会・第25回日本心臓血管発生研究会 合同セッション（II-JSCDJS-P1）
ミニオーラル（eポスター）1

座長:白井 学(国立循環器病研究センター)
座長:岩瀬 晃康(東京大学アイソトープ総合センター)

[II-JSCDJS-P1-4] 自己免疫性血管炎における自己抗体プロファイリングのためのPhIP-seq基盤の構築

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Keywords：Autoimmune disease、PhIP-seq、Vasculitis

Introduction: Phage immunoprecipitation sequencing (PhIP-seq) enables high-throughput and unbiased identification of antibody-antigen interactions. Here, we report the construction and validation of a PhIP-seq platform designed for autoantibody profiling in autoimmune vasculitis.Methods: Human protein sequence data was obtained from the UniProt database and computationally divided into 62-amino acid peptides with 31-amino acid overlaps. Peptide sequences were reverse-translated into coding oligonucleotides and cloned into T7 phage DNA to generate a phage-display library. Serum samples or commercial antibodies were incubated with the phage library for immunoprecipitation, followed by amplification and next-generation sequencing (NGS) of enriched phage DNA to quantify peptide-specific antibody binding. Results: The library contained 352,000 peptides derived from 20,000 human proteins. NGS confirmed the presence of more than 98% of the designed peptide-coding sequences. Application of this platform to identical serum samples across independent experiments demonstrated reproducible enrichment of specific peptide signals. In addition, analysis using commercial antibodies successfully identified the corresponding target peptides, supporting robustness of the platform for detecting antigen-antibody interactions.Discussion: We established a PhIP-seq platform enabling unbiased, proteome-wide analysis of autoantibody repertoires. Ongoing analyses will apply this platform to serum samples from patients with autoimmune vasculitis to explore disease-associated autoantibody profiles.