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### Proteogenomics-based identifying neoantigens in refractory cancers using xenograft mice

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Background

Recently, neoantigens have been paid great attention among cancer-specific antigens. Neoantigens are self-peptides that are displayed on major histocompatibility complexes (MHC) with cancer specific mutations that are never seen in normal tissues. We performed combined searching by the next generation sequencing (NGS) and mass spectrometry for MHC-associated neoantigens in the refractory cancers.

Methodologies

DNAs and RNAs are extracted and sequenced from cultured colon cancer cell lines and patient tissues (total 9 samples) from pancreatic and biliary cancers. Among the samples, 4 tissues are transplanted to mice to prepare xenograft mice. Proteins are extracted from the xenograft models, immunoprecipitated with anti-MHC antibody, and measured by a mass spectrometer. Peptide sequences are searched against database obtained from the exome and transcriptome from the identical tissue.

Findings

After a systematic examination of experimental conditions using the cultured cells, we have established a workflow that can detect above 1,000 MHC-associated peptides from 3 mg of protein lysates from xenograft mice. We have also identified several neoantigen candidates by DNA and RNA sequencing followed by peptide sequencing with mass spectrometric analysis.

Concluding

In identifying neoantigens, we have found that peptidomics have been added the detection confidence of the identified neoantigens. We are further improving sensitivity to the level to detect directly from patient tissues without xenograft formation. The identified neoantigen candidates are tested for immunogenicity *in vitro*.

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### Promotion of proteomic data sharing through a specialized data journal

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Background

Proteomics is a rapidly growing research area that produces large amounts of data, which has led to complex challenges around data management. Proteomics data and datasets need to become more Findable, Accessible, Interoperable, and Re-usable (FAIR[1]) to promote data sharing. To address these challenges and facilitate better proteome data management, the field needs to develop formal structures and procedures. To this end, the Japanese Proteomics Society decided to launch a new data journal – the Journal of Proteome Data and Methods (JPDM).

Preparations

In order to launch JPDM, we prepared the following documents: Publishing plan, Instruction to authors, Guide to reviewers, Ethics policies, License to publish form, and Frequently asked questions. All documents are available at https://www.jhupo.org/jpdm/. We also prepared a submission system (https://mc.manuscriptcentral.com/jpdm/) using the ScholarOne platform.

Features of JPDM

JPDM is a peer-reviewed and fully open access journal provided via the J-stage platform. JPDM publishes four article types: Data descriptors, Protocols, Data processing notes, and Reviews. The main content of the journal is Data descriptors, which is described detailed metadata of mass-based proteomics datasets. JPDM collaborates with ProteomeXchange[2] (PX), which is a consortium of proteome data repositories including jPOST[3], PRIDE[4], MassIVE, etc. When data producers register their datasets in a PX repository then post detailed metadata in JPDM, the journal sends a feedback to the PX repository. JPDM contributes to add a value for proteome datasets by providing detailed metadata.

Conclusion

We launched the new data journal for proteomics community named JPDM. The journal is peer-reviewed and fully open access, and the website is https://www.jhupo.org/jpdm/. JPDM realizes the FAIR principal in the proteomics field by providing rich information. JPDM welcomes lots of submission from community members.

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3. Moriya Y et al., The jPOST environment: an integrated proteomics data repository and database. Nucleic Acids Res. 47:D1218-D1224 (2019).