SDOPDB: comparative standardized-protocol database for mouse phenotyping analyses

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Keywords: mouse phenotype, experimental protocol, comparative database, SOP, SDOP, data framework

1 Introduction

The mouse holds marked potential for studying mammalian gene function and human disease, offering an extensive toolkit for modifying genes and studying the phenotypic outcomes. Recognizing these advantages, large-scale mouse phenotyping projects such as Japan Mouse Clinic (JMC) [1] and European Mouse Disease Clinic (EUMODIC) [2] had been launched to catalog a subset of mutant mouse resources, and have been producing an enormous volume of phenotype data on morphology, behavior, pathology, etc. Because the phenotype data are generated through the execution of SOPs (Standard Operation Procedures), and are greatly influenced by the differences among them, it is essential to develop the information infrastructure which can easily and directly compare SOPs differences for the integration of the phenotype data with high reliability. For that purpose, we had developed SDOP (Standardized Description of Operating Procedures) format to provide the comparative standardized description framework of SOPs. Here we present a comparative standardized-protocol database named “SDOPDB (http://www.brc.riken.jp/lab/bpmp/SDOP/)”, which includes SDOPs for 16 mouse phenotypic analyses that are common between JMC and EUMODIC, and for other phenotypic analyses.

2 Method and Results

Development of SDOP format and its web interface

The SDOP format has been developed to allow for the easy and direct comparison of SOPs differences among institutes/laboratories (Figure 1). To form a tree diagram itemized and organized SOP contents, which is a vital portion of SDOP format, we first set up items which can become common data framework of SOPs for any phenotyping tests. Namely, the common items are set up according to the EMPReSS (the European
Mouse Phenotyping Resource for Standardized Screens [3, 4, 5] which is a comprehensive database of the validated SOPs for mouse phenotyping analyses in EUMODIC) style (e.g. items of Purpose, Equipment, Quality control, Notes, etc.) and a draft version of MIMPP (Minimum Information to describe Mouse Phenotyping Procedures) [6], which is proposed by Mouse Phenotype Database Integration Consortium (InterPhenome) [7] aimed to develop standards and data exchange formats for reporting a mouse phenotyping procedure. The MIMPP draft is further considered for more detailed item settings. Using the above set items as a common framework for the 16 phenotyping tests, each draft of SDOPs is developed according to the SOP descriptions of each phenotyping test. Finally, we complete each of SDOPs for the 16 tests by appropriately modifying, adding and deleting items and their descriptive contents, and altering item location through the discussion with JMC experts on their targeted mouse phenotyping tests. The dhtmlxTreeGrid, which is a cross-browser JavaScript user-interface component designed to represent tabular data in hierarchical view [8], is applied to represent each of SDOP formats on the web browser.

3 Discussion

The InterPhenome consortium has currently proposed draft version of MIMPP. As one of MIMPP data models, PPML (Phenotyping Procedures Markup Language), an XML schema to describe a phenotyping procedure, is in the process of international standardization [9]. The SDOP format represents compatibility with the PPML because it involves almost all items defined in the PPML. Actually, items in a SDOP format were used to development of the PPML format (personal communication). The SDOPs developed in this study enable the direct comparison of procedural differences to common mouse phenotyping analyses among institutes/laboratories. Therefore, the SDOPs would become essential for the standardized representation of detailed differences among specific mouse phenotyping procedures, as an example, procedural differences of clinical biochemical analysis between JMC and EUMODIC). Further, expansion of SDOPs taking ontological formalism will realize IMPC-aiming fully integration of mouse phenotype-related information.

References