

















expanded TICs in culture and thereafter injected them in larger numbers than those contained in the PDX transplants. Regarding intratumor heterogeneities, our PDXs and spheroids that derived from separate subregions of the same tumor were almost identical as others reported (5, 26, 27).

Second, the PDSX method allowed us to reduce variances in the tumor growth rate. As noted above, TIC spheroids consisted of only proliferating cancer epithelial cells. In case of PDXs, on the other hand, the engrafted tumor fragments upon passages were likely to be heterogeneous regarding the number of live TICs and their microenvironment (e.g., the extent of differentiation and coexisting stromal cells, respectively). In fact, we had significantly fewer mice excluded in the PDSX groups than in PDX upon preparations for drug-dosing tests, indicating that PDSX method is less wasteful in xenograft formation.

Third, and most importantly, PDSXs gave chemosensitivity data statistically more significant than PDXs in drug-dosing tests. Accordingly, it is expected that the clinical responses can be predicted more reliably with PDSX mice than with PDX. To date, many methods have been proposed that predict patient responses to cancer chemotherapeutics (28). These include mutational analyses, gene expression signature analyses, as well as *in vitro* sensitivity tests with cancer organoids similar to spheroids (14, 29). For example, colorectal cancer that retains intact Ras signaling with wild-type RAS genes responds to EGFR inhibitors at a high probability (25, 30). However, there is always a sizable fraction in the patient population that does not respond to the indicated regimen(s). Although it is beneficial to each patient if a regimen is efficacious, the patient will lose precious time and QOL if not. Thus, more reliable prediction methods are awaited. To this end, direct tumor grafts to immunodeficient mice (i.e., PDXs) have been proposed as a straightforward method of drug sensitivity evaluation personalized to the respective patients (3, 4).

Our current results provide a rationale for PDSXs as a more improved method than PDXs, overcoming the drawbacks of the latter. Namely, the results of PDSX drug-dosing tests demonstrated a strong correlation with the clinical responses (Figs. 3–5; Supplementary Figs. S6–S9), and paralleled with those of PDXs (Supplementary Table S3). Therefore, these results suggest a strong predictive power in chemosensitivity when applied to personalized prospective studies. To this end, our PDSX method also helps expedite preparation of test mice for drug-dosing tests. Namely, it took only 2 to 3 months to setup groups of PDSXs for testing several regimens. Notably, however, some types of cancer may be excluded that take very rapid downhill courses such as pancreatic cancer. It can be more practical to test the sensitivity of spheroids *in vitro* for such types. Along this line, *in vitro* cultures of spheroids/organoids have been proposed to be used in drug screening as well as in personalized chemosensitivity tests (9, 31). Such *in vitro* sensitivity tests may provide quicker, although limited, answers for a class of chemotherapeutics that directly target cancer cell proliferation. In other words, there are occasions in which xenografts can provide more practical prediction of the clinical courses as exemplified by irinotecan sensitivity in Fig. 4. Although irinotecan resistance was reported to correlate with the expression level of DNA topoisomerase I (32), our expression analysis did not provide enough data that allowed personalized predictions.

Taken together, the PDSX method should allow us to design personalized chemotherapy regimens for patients with advanced colorectal cancer in a prospective manner. We would like to propose introduction of personalized PDSX-based chemosensitivity tests as "personalized preclinical prediction" (PPP) trials. For testing already established regimens, they can be designated as PPP phase 3.5X trials (X for xenograft) because the drugs had completed phase III clinical trials. When the tests can be performed using *in vitro* culture of spheroids/organoids, they may be PPP phase 3.5V (V for *in vitro*). If candidate drugs for repurposing are used, they can be PPP 1.5X or 1.5V trials, and so on. We encourage further discussion among those who participate in cancer chemotherapy development.

Notably, PDSXs have some limitations common to PDXs because both lack key immune responses and have different stromal microenvironment from that of human hosts. Technical improvements to humanize the mouse immune system and mimic the patient tumor microenvironment in mice appear to be in progress, although multiple difficulties still remain (4, 33, 34). Despite such limitations, PDX has been one of the best preclinical models owing to their predictive power for a variety of chemotherapeutics (3, 4).

In conclusion, we have demonstrated that PDSXs are reliable "preclinical" models for personalized colorectal cancer chemotherapies. Our methods of TIC spheroids and PDSXs are straightforward, reliable, and well formulated. They also meet the timeline in most colorectal cancer clinical courses. In addition, PDSXs may be applied to chemotherapies of not only colorectal cancer, but also other types of cancer when the primary tumors are available. It is worth noting that applications of the PDSX method can be extended to evaluations of off-label uses of therapeutics and compassionate uses of yet-unapproved drugs.

#### Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

#### Authors' Contributions

**Conception and design:** H. Maekawa, H. Miyoshi, T. Yamaura, M.M. Taketo  
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**Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.):** H. Maekawa, H. Miyoshi, T. Yamaura, Y. Itatani  
**Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis):** H. Maekawa, H. Miyoshi, M.M. Taketo  
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**Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases):** Y. Itatani, K. Kawada, Y. Sakai  
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