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Cell microarray as a powerful tool to accelerate cancer research: focus on drug screening

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Abstract

Background: Designing reliable *in vitro* assays is crucial to attain impactful results in oncology research. Cell Microarray (CMA) has become a key tool to accelerate cancer research as many samples can be evaluated at the same time in a single slide, allowing the evaluation of many prognostics, diagnostics, and therapy response biomarkers. Previously, we described a model of drug combination using antineoplastic and repurposed drugs to find alternative oncology regimens [1,2]. **Objective:** The purpose of this study is to adapt a histology-based method to evaluate the changes on biomarkers expression during drug efficacy tests and explore the mechanisms of therapy resistance in a chip-like tool such as a CMA. **Methods:** Two chemoresistant ovarian cancer models, i.e., OVCAR8 (Carboplatin-resistant) and OVCAR8 PTX RP (Carboplatin and Paclitaxel-resistant) cell lines [3] were incubated for 48 h with Carboplatin and Paclitaxel, alone and combined with repurposed drugs (Pitavastatin, Metformin and Ivermectin), using their half-maximal inhibitory concentration (IC_{50}) previously assessed. Next, we collected the cells subjected to all assay conditions and constructed a CMA, gathering all the conditions in a single paraffin block [3-5]. **Results:** CMA have the potential to accelerate cancer research studies since it allows the evaluation and comparison of a variety of cell culture conditions, such as several cell lines, time-points, and different therapeutical conditions, on a single microscope slide [4,5]. **Conclusions:** This approach represents a rapid and cost-effective screening tool to accelerate anti-cancer drug efficacy studies, allowing the discovery of biomarkers capable to predict therapy responses and to unveil the mechanism of action of new drugs, repurposed drugs, and drug combinations.

Keywords: biomarkers; cancer research; cell microarray; cell cultures; drug screening

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