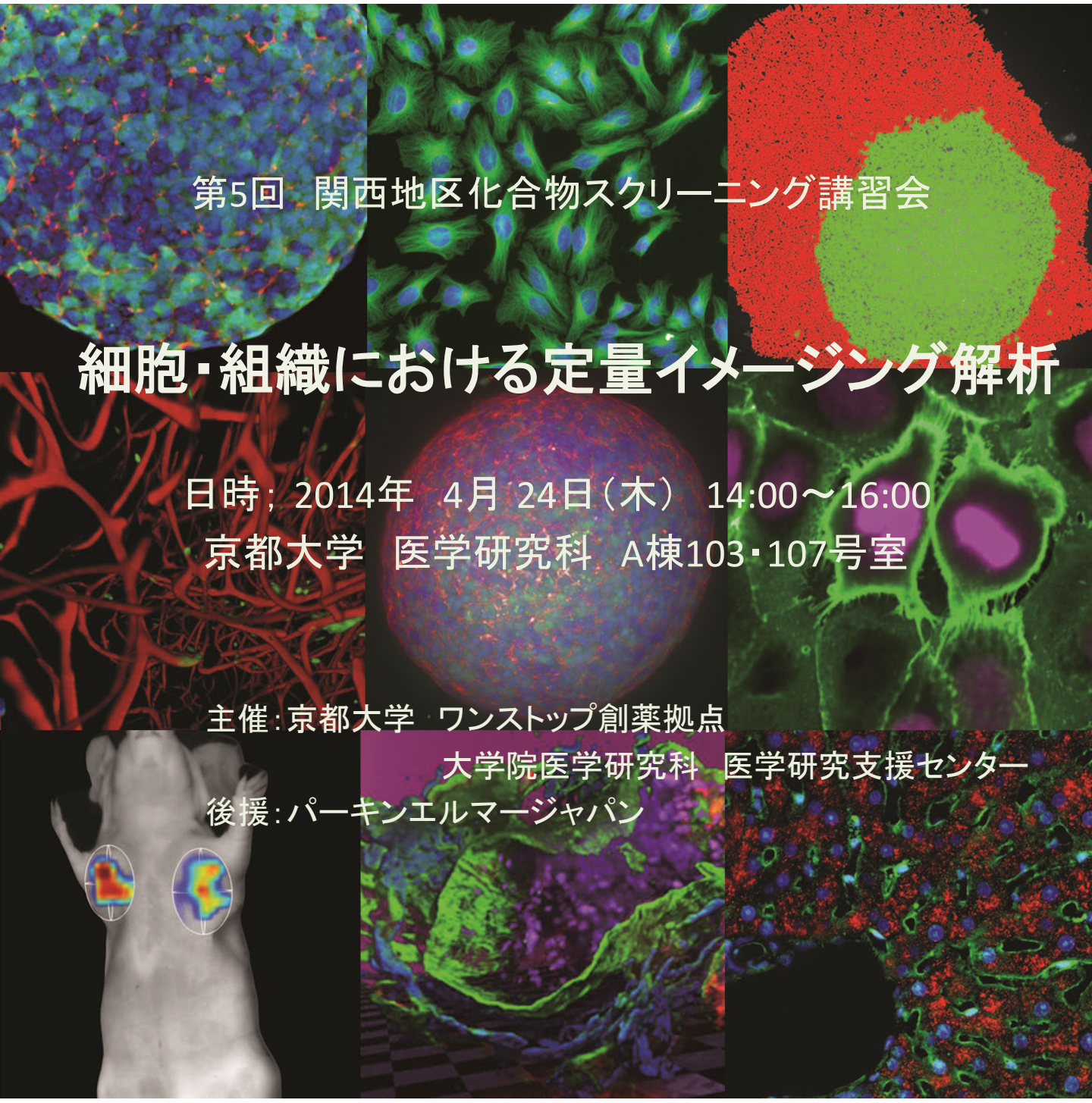

第5回　関西地区化合物スクリーニング講習会

細胞・組織における定量イメージング解析

日時；2014年　4月 24日（木）　14:00～16:00

京都大学　医学研究科　A棟103・107号室

主催：京都大学　ワンストップ創薬拠点

大学院医学研究科　医学研究支援センター

後援：パーキンエルマージャパン

参加希望の方は医学研究支援センターまでメールでご連絡ください（〆切：4月23日 17：00）

京都大学　大学院医学研究科　医学研究支援センター

担当：奥野（メール：info@support-center.med.kyoto-u.ac.jp

講演内容に関するお問い合わせ先：

株式会社パーキンエルマージャパン　ライフサイエンス事業部

担当：大渕（電話：06-6386-1771、メール：toru.ofuchi@perkinelmer.com）

Schedule and Abstracts

14:00-15:00

細胞の形態と機能 "Cellular Form and Function"

Chris Bakal, Ph. D,

Chester Beatty Laboratories腫瘍生物学分野チームリーダー・
ウェルカムトラスト リサーチキャリアデベロップメントフェロー(兼任)

Complex and highly coordinated changes in morphology occur during cancer cell metastasis. For example, metastatic cancer cells of epithelial origin lose cell-cell contacts and apical-basal polarity, engage once-dormant migratory machinery, remodel the extracellular matrix (ECM) and dynamically regulate integrin-based adhesion. Importantly, while there are common morphological aspects of metastasis, cells may also alternate between distinct modes of migration, such as mesenchymal versus amoeboid. Understanding how signalling networks that control shape are differentially rewired during oncogenesis is critical for developing safe and effective therapeutics. Given the recent advances in genomic profiling, we have an unprecedented opportunity to describe the genotype of cancer cells. However, a major challenge in the post-genomic era is to understand which genetic alterations are truly drivers of cancer cell phenotypes. For example, it is not clear which transcriptional changes underpin the ability of metastatic cells to migrate and invade secondary tissues. A number of studies have identified potential “master” regulators of metastatic phenotypes such as Twist, and RhoC, but the list of downstream effectors that lead to cell shape changes remains far from complete. One well-characterized example of a link between metastatic cell genotype and phenotype is the switch from E-cadherin to N-cadherin expression that results in a loss of cell-cell contacts and mesenchymal morphology in certain epithelial lines. But we hypothesize there are many more unknown genetic changes that are essential for the morphogenesis of metastatic cells. We are using methods we have previously developed in order to quantify cell shape in parallel with genome-wide microarray and comparative genomic hybridization techniques to determine how specific, quantitative differences in cell morphology in both 2D and 3D are driven by changes in gene expression and copy number variation.

15:00-16:00

組織切片分子マーカーの複数同時定量• 自動化と臨床応用に向けた展開

“Toward quantitative, automated, and multiplexed solutions for tissue biomarker discovery and clinical translation.”

Cliff Hoyt, Ph. D (パーキンエルマー　オンコロジーフェロー)

Simultaneous quantitation of 4 or more biomarkers in intact tissue specimens holds the key to many questions in the biological basis of health and disease. However, reliable detection remains elusive due to technical challenges from many sources including antibody cross reactivity, difficulty in balancing signals from rare and abundant targets, tissue autofluorescence and interference between fluorophores, especially for co-localized targets. In this Cliff Hoyt present Opal?, a practical method for highly multiplexed tissue biomarker analysis that addresses many of these challenges. Opal is an iterative process that incorporates the following:

- highly specific and reproducible results
- eight or more biomarkers may be imaged simultaneously in one tissue section
- covalent signal deposition followed by elution of the anti-target antibody allows detection of the next target without fear of cross reactivity
- typical 4-plex protocols may be completed in less than 1 day, compatible with standard immunohistochemical methods
- quantitative results are possible when Opal is combined with Multispectral Imaging

Cliff Hoyt will describe Opal in detail and provide examples demonstrating its use in the early identification of progenitor cells, cancer immunology, assessment of microenvironment, co-localization of markers within specific sub-populations of cells and tracking cell signaling pathways.