www.beatson.gla.ac.uk/ross_cagan

BIOLOGY OF THERAPEUTICS

Group Leader

Ross Cagan

Research Scientists
Hammed Badmos
Bojie Cong
Shree Roychowdhury
Harshit Shah
Kimmi Stephens

Scientific Officer
Evangelia Stamou

Graduate Students
Björk Aston
Sindhura Gopinath
Teena Thakur

University of Glasgow

Translating therapeutics from the bench to the bedside has proven a challenge. Focusing on cancer and rare genetic diseases, my laboratory explores the 'biology of therapeutics': why do some therapies make the successful leap from pre-clinical to clinical while others fail? We use Drosophila as our lead tool to explore these questions, focusing on developing genetically complex models and using these to develop lead therapeutics including fly-to-bedside clinical trials.

Our laboratory uses Drosophila along with a variety of complementary tools to explore why some therapies succeed and others fail. We then use this information to develop network- and whole animal- based candidate therapies. We have been testing these ideas in experimental fly-to-bedside clinical trials as well as building a new generation of lead therapeutic compounds for cancer and RASopathies.

Colorectal cancer

A key unmet need in the cancer field is effective, durable treatments for solid tumours, the major focus of the laboratory. A particular challenge is tumours with oncogenic RAS isoforms, contributing to ~30% of all solid tumours and perhaps 30,000 cancer deaths annually in the UK alone. *KRAS* mutations are associated with poor patient outcome, and RAS pathway inhibitors have proven ineffective for most solid tumours.

As part of an experimental fly-to-bedside clinical trial *(NCT02363647)*, we recently reported a fly-based treatment of a CPCT patient with an advanced KRAS-mutant treatment-resistant colon adenocarcinoma. Building a patient-matched 9-hit 'personalised fly avatar', we identified a combination of trametinib plus zoledronate as effective in rescuing avatar viability (Figure 1) and a strong partial response in the patient (Figure 1) that exceeded 11 months. We are currently using genetic, expression, and metabolite studies to match this and other unique drug combinations to genetic profiles. Our goal is to predict drug response based on a patient's tumour profile.

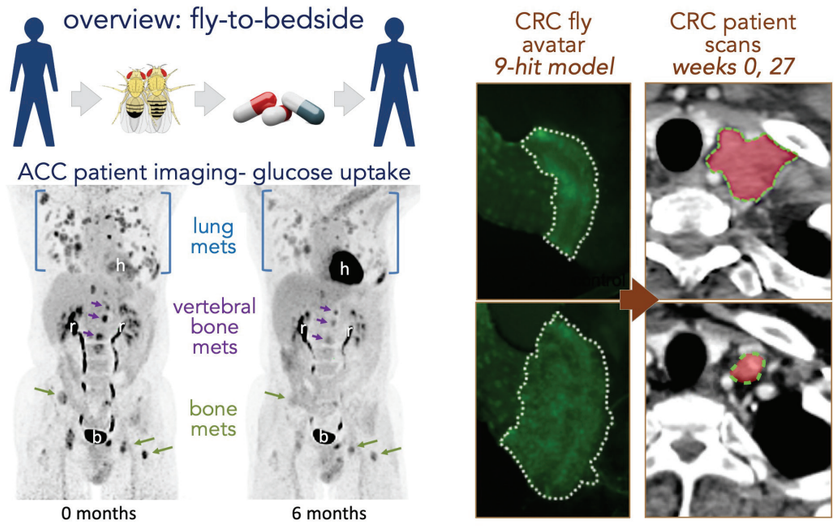
Exploring our set of patient based colon cancer 'fly avatar' lines more deeply, we found evidence that increasing genetic complexity gave rise to multiple avenues of drug resistance. For example, we have identified upregulation of detoxification pathways when specific cancer genes were paired. Blocking these emergent networks is sufficient to reveal a drug's full activity, leading to tumour shrinkage. We are taking both multi-drug and medicinal chemistry approaches to circumvent these resistance networks in flies and organoids. Leaning into our biology tools, we are further connecting these resistance networks to fundamental biological processes such as 'cell competition', broadening our understanding of the relationships between complex mutation profiles, cell competition, and drug response.

Adenoid cystic carcinoma

Adenoid Cystic Carcinoma (ACC) is the most common malignant tumour of the minor salivary glands and the second most common of the major salivary glands. Unfortunately, once disseminated there are currently no effective therapies.

As part of our fly-to-bedside clinical trial, we reported treatment of an ACC patient presenting with treatment-resistant metastatic disease (Figure 1). We used a full omic tumour analysis to develop a 5-hit 'personalised fly avatar'; the resulting fly exhibited multiple aspects of transformation. Our robotics-based approach identified the novel three-drug combination tofacitinib-vorinostat-pindolol, which proved effective: the patient displayed partial response for 12 months on treatment, with tumour burden reduced by 49% across all lung and bone marker lesions (Figure 1). Our recent work has identified key pathways that are required for tumour progression; drugging these pathways with clinically relevant drugs and drug cocktails showed broad efficacy across our set of ACC avatars. We are now exploring whether our most broadly acting drugs are likely to show efficacy in ACC clinical trials.

Figure 1
Our fly-to-bedside, which led to successful treatment of adenoid cystic and colorectal cancer patients.



RASopathies

Rasopathies are a family of rare Mendelian diseases characterised by mutations that activate RAS pathway signalling. There are currently no treatments approved for RASopathies, a common situation for inherited diseases. Further, accruing sufficient Rasopathy patients for clinical trials is challenging and, ideally, a trial would accept a broad cross-section of Rasopathy patients.

To compare different RASopathy isoforms, we collaborated with Bruce Gelb's laboratory to develop 29 Drosophila models that express human RASopathy isoforms including *PTPN11, KRAS, HRAS, BRAF, RAF1*, and *MEK1*. Different isoforms showed distinct phenotypes as well as different levels of RAS activity as assessed with phosphorylated ERK (pERK), mirroring differences in RASopathy patients. Our models indicated these signalling differences have consequences: while several drugs worked against one or a few fly models, few drugs worked with multiple fly RASopathy models, emphasising the unique whole-body challenge presented by the RASopathies. We have identified promising lead therapeutics that act broadly across our models; we are currently working with Maria Kontarides to explore these compounds in mouse RASopathy models, as well as a drug company to help advance our most promising leads towards clinical trials.

Drug development

Despite exciting new advances, targeted therapies are effective in less than 30% of solid tumours. A particularly vexing problem is the identification of an effective and durable drug for RAS-mutant solid tumours. One approach is 'polypharmacology': single agents that target multiple points along a disease network to optimise efficacy and minimise liabilities including toxicity. Polypharmacology is challenging, and several laboratories including my own are working to bridge this chemistry gap. For example, we have established a 'drug evolution' platform designed to attack disease networks through 'rational polypharmacology', a whole animal version of Quantitative Structure/Activity Relationship (QSAR). We combine fly genetics with medicinal and computational chemistry, 'evolving' leads that are tuned for whole body efficacy (Figure 2). The results can be striking when tested in standard mammalian models. To date we have used our platform to evolve lead compounds for RET-dependent thyroid and lung cancers, RAS-mutant colorectal cancer, hepatocellular carcinoma, and RASopathies. We are currently working with Lee Cronin's laboratory to further advance this technology through advanced automation, merging chemical evolution and 'chemputer' technologies.

Publications listed on page 103

Figure 2
Platform to 'tune' therapeutic leads.