expression. Knock-down of EJC components therefore should be expected to have a systemic impact on gene expression, resulting in major disturbance of plant growth and development. Indeed, RNAi lines of several EJC genes have demonstrated strong pleiotropic phenotypes. Proteomic DIGE analysis indicated large groups of proteins with altered levels of expression in RNAi lines. A systematic analytical and modelling approach is being developed to unify localisation, protein–protein interaction and function of EJC proteins.

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CSS.19
Modelling aspects of solid cancer growth

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The modelling of cancer provides an enormous mathematical challenge because of its inherent multiscale nature. For example, in vascular tumours, nutrient is transported by the vascular system, which operates on a tissue level. However, it affects processes occurring on a molecular level. Molecular and intra-cellular events in turn affect the vascular network and therefore the nutrient dynamics. Our modelling approach is to model, using partial differential equations, processes on the tissue level and couple these to the intercellular events (modelled by ordinary differential equations) via cells modelled as automaton units. Thusfar, within this framework we have modelled structural adaptation at the vessel level and the effects of growth factor production in response to hypoxia. We have also investigated the effects of acid production, mutation and phenotypic evolution driven by tissue environment. These results will be presented.

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CSS.20
Spatial and temporal information encoding by the NF-κB system

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Signalling through NF-κB involves its release from an IκB in the cytosol, followed by translocation into the nucleus. NF-κB regulation of IkBa transcription represents a delayed negative feedback loop that drives oscillations in NF-κB translocation. Single cell time-lapse imaging and computational modeling of NF-κB (RelA) localization showed asynchronous oscillations following cell stimulation that decreased in frequency with increased IkBa transcription. Transcription of target genes depended on oscillation persistence, involving cycles of RelA phosphorylation and dephosphorylation. We used timed stimulation of cells with pulses of Tumour Necrosis Factor alpha (TNFa) at differing doses to investigate the response of the NF-κB system. These studies suggested that the system has a reset time after which a full amplitude pulse of NF-κB nuclear occupation is observed when a 5 min pulse of TNFa is applied. Repetitive pulses at regular intervals leads to synchronous oscillations in the cell population assisting biochemical analysis for example by Western blotting ChIP and analysis of differential target gene expression. These studies confirmed that cyclical phosphorylation occurs at RelA Ser536. Refitting of computational models to these data has made predictions about the role of the A20 feedback loop in regulating NF-κB signalling. Previously, we have studied the key canonical pathway proteins RelA and IκBa. However, NF–κB signalling involves a further set of negative and positive feedback loops, including through IκBe and RelB. We have used a stochastic 3 feedback computational model to suggest that noise in IκBe expression may have a role in increasing cell to cell oscillation asynchrony.

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CSS.21
To be confirmed

M. Levine (UC Berkeley MCB)

To Be Confirmed

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CSS.22
Partial purification and characterization of tyrosinase extracted from mushroom (*Agaricus bisporus*)

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Tyrosinase from mushrooms (*Agaricus bisporus* (J.E.Lange) Imbach) was partially purified and characterized. The enzyme exhibited both monophenolase and diphenolase activities that were measured spectrophotometrically using L-tyrosine and pyrogallol as substrates. A two-fold purification in both activities was achieved by ammonium sulfate fractionation. The monophenolase activity was 3.35 EU/ml, and the diphenolase activity was 189.3 EU/ml. Tyrosinase was relatively stable at −15 °C for 44 days. The enzyme was not very heat stable, and its activity decreased when incubated at the temperatures higher than 35 °C. Tyrosinase activity showed two pH optima, at 5.3 and 7.0 at 25 °C when pyrogallol was used as the substrate. Mono-, di- and triphenols were substrates for tyrosinase. Using Vmax/Km as a specificity constant, pyrocatechol was the better substrate followed by pyrogallol. The kinetic parameters of the enzyme were: Vmax=78 EU/min/ml, Km=1.4 Mm and KS=250 mM for pyrogallol and Vmax=168 EU/min/ml, Km=0.40 mM and KS=270 mM for the pyrocatechol. Of the inhibitors tested, competitivetype inhibition was observed with benzoic acid and sodium azide. A mixed-type inhibition was observed with L-cysteine and sodium fluoride.

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CSS.23
Anoxia resistance in vertebrates: Metabolomics of brains and heart that never stop

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The capacity to tolerate extended anoxia is restricted to only a few vertebrates. These include some North American freshwater turtles and two cyprinid fishes, the crucian carp (*Carassius carassius* L.) and