Ovarian Cancer Cytogenomics and Nuclear Motors

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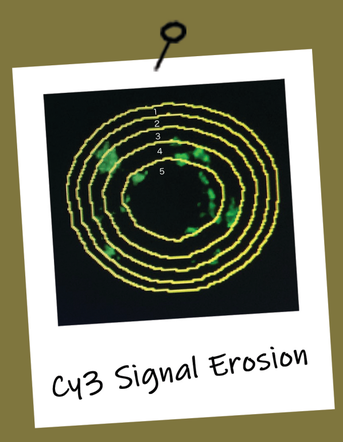
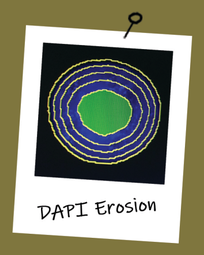
20% of women with ovarian cancer **CANNOT RECEIVE TREATMENT** due to late diagnosis and ineffective treament

The genome is **non-randomly** organised into **territories** but can **re-organise** in response to changes in physiological conditions and cell cycle. **Mis-localisation** can also occur in **disease** such as cancers.

Mapping chromosomes and gene loci position using **Fluorescence in-situ Hybridisation** (FISH) and erosion analysis.



Erosion analysis quantifies genome positions by dividing the nucleus concentrically towards the centre calculating the genome signal as a percent of the nuclear signal for each shell 1 to 5.



Investigate mis-localisation of chromosomes and genes to produce a **biomarker panel** for a **diagnostic** FISH kit.

Treat and **induce drug resistance** on ovarian cancer cell lines to investigate the possibility of **adaptive or faster** re-organisation.

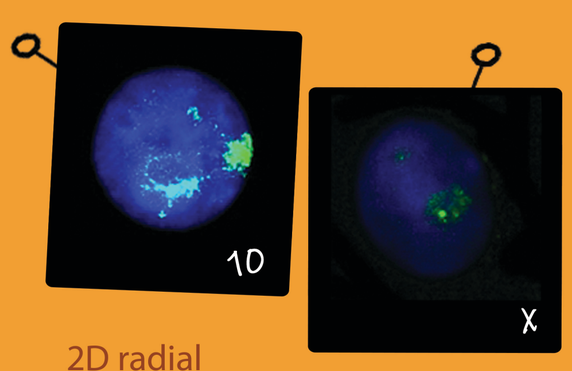
Temporarily remove the **motor ability** of the genome to re-organise via nuclear myosin RNA interference (RNAi) to **slow drug resistance**.

Diagnosing ovarian cancer **earlier** whilst **combating** drug **resistance** and **toxicity** using cytogenomics

Treatment assays to investigate **lower drug** doses of **chemo-toxic** drugs in **combination** with nuclear myosin RNAi.

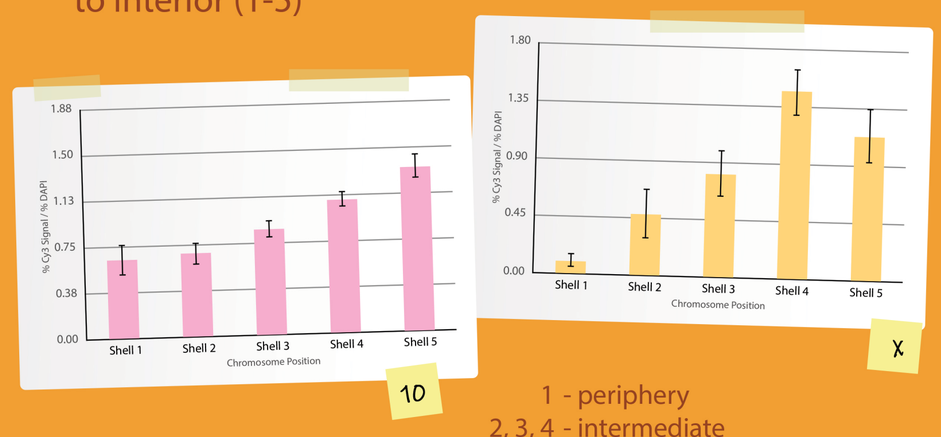
Monitor nuclear myosin **quantity** and **patterns** using western blot and indirect immunofluorescence

Results



2D radial positioning of chromosome 10 and X imaged using FISH

Chromosome 10 and X occupancy from periphery to interior (1-5)



1 - periphery
2, 3, 4 - intermediate
5 - central

Conclusion

Genome organisation represents another level of control; an **exploitable mechanism**, in which nuclear motor myosin may play a significant **clinical role** in future diagnostics, prognostics and therapy

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