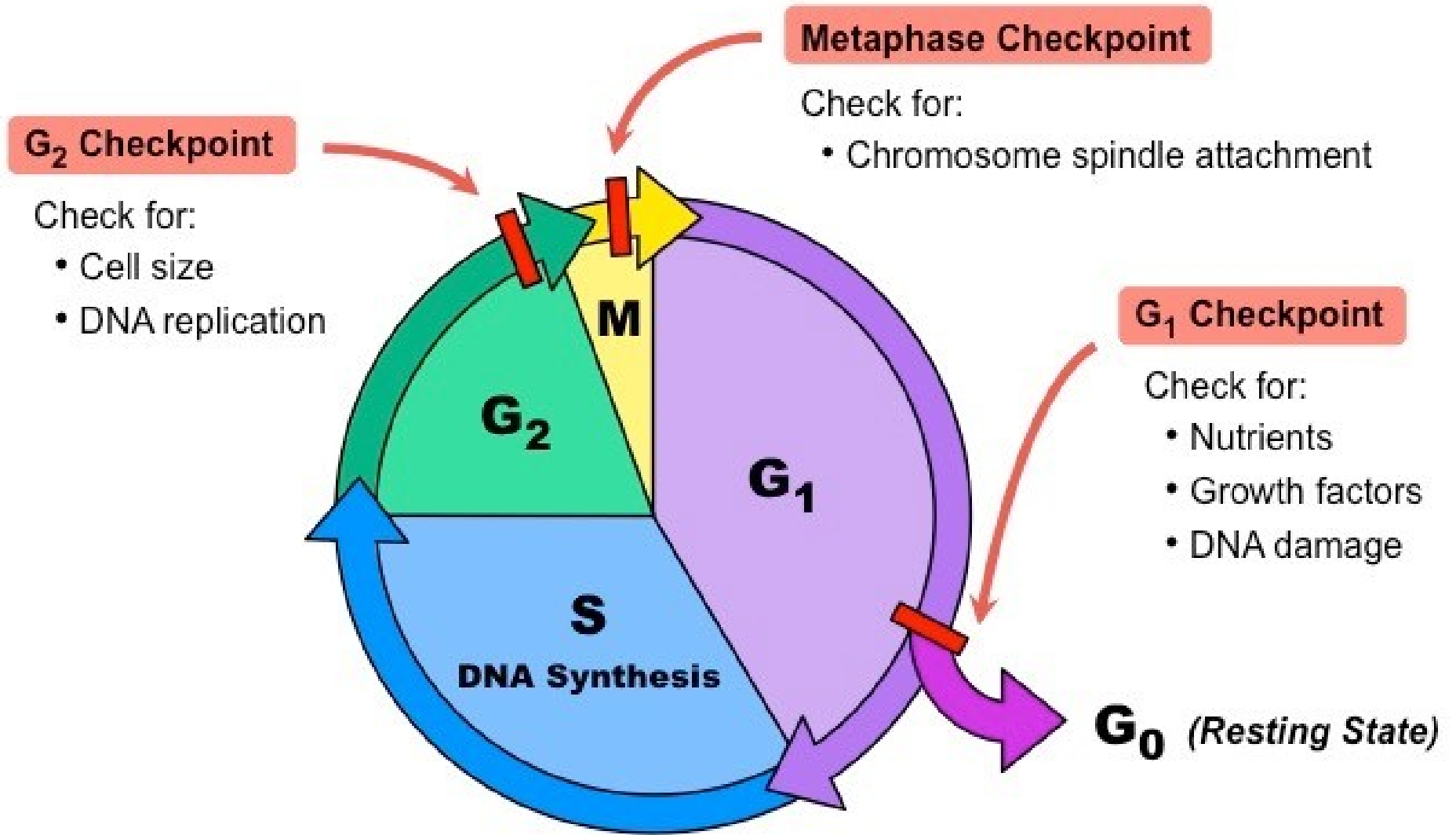


The Causes and Consequences of Genetic Heterogeneity in Cancer Evolution

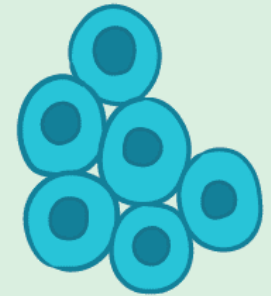
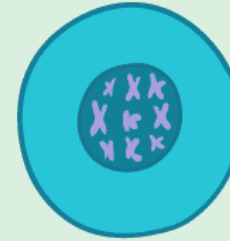
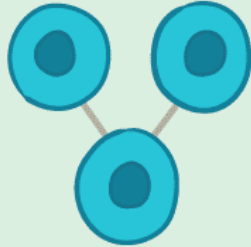
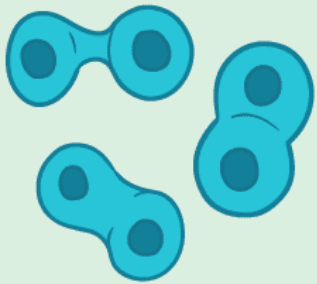
Burrell et al.

Nature, 2013

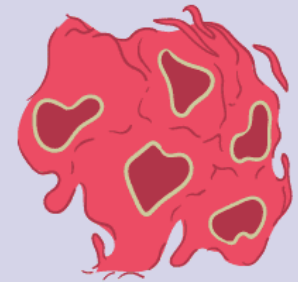
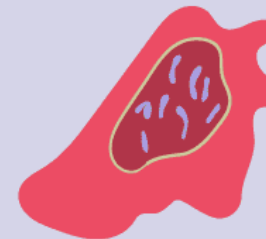
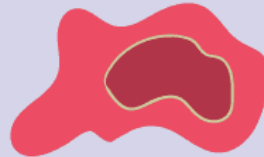
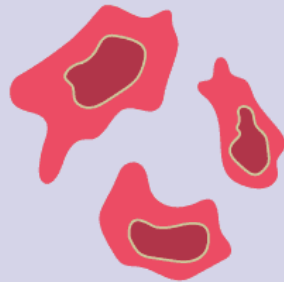
Cell Cycle



NORMAL CELLS



CANCEROUS CELLS



Many cells that
continue to grow
and divide

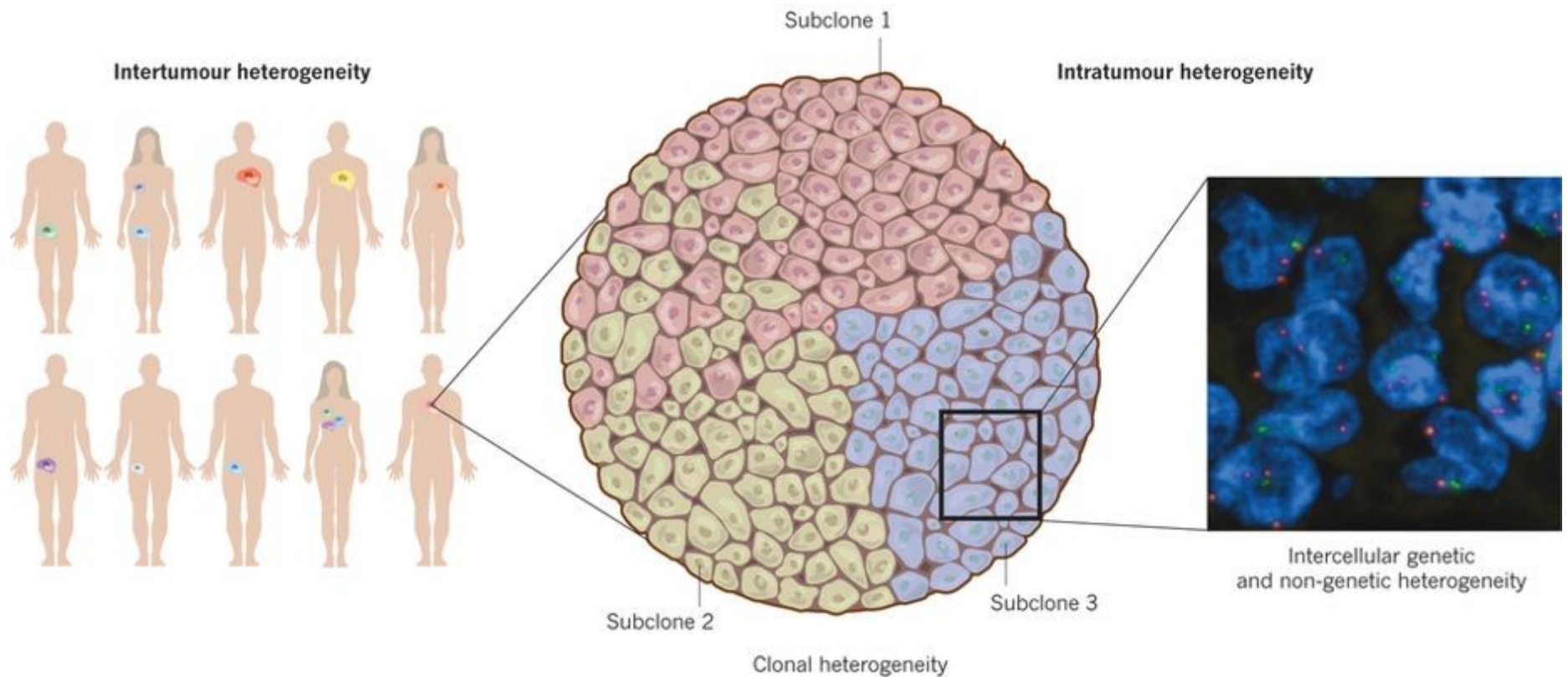
Variations in
size and shapes
of cells

Nucleus that
is larger and
darker than
normal

Abnormal
number of
chromosomes
arranged in a
disorganized
fashion

Cluster of
cells without a
boundry

Inter / Intra Tumor Heterogeneity



Why changes across tumors?

- genetic events of transformation interact with cell-intrinsic biological properties
- Distinct signalling pathways
- within a cohort of tumours, the same gene may be affected by point mutation, DNA methylation, copy number alteration, or a combination of the three

Intratumour heterogeneity and tumour evolution

- Diversity of expression of protein biomarkers
 - Intercellular genetic variation,
 - followed by selective outgrowth of clones that have a phenotypic advantage within a given tumour micro-environmental context
 - Linear Evolution: clonal sweep by a dominant subclone
 - Branched Evolution: subclones evolve in parallel
- genetically heterogeneous subclonal lineages in solid tumours could also be maintained by distinct stem cells

- At metastatic sites: new microenvironment
- the subclones occupying each niche evolve relatively independently of one another
- intermingled heterogeneous clones are observed within single biopsies.
- This intercellular heterogeneity increases **phenotypic variation**, broadening the pool of cells that are subject to **selection**, and therefore the likelihood of selective expansion of multiple different subclones and the **emergence** of a complex subclonal tumour architecture

Genomic Instability

- a prominent source of genetic diversity within tumours
- Cells are subject to selection in a given micro-environmental
- can arise through various routes, leaving distinct genomic footprints and differentially affecting tumour evolution

Genomic Instability and Tumor Evolution

- In normal cells, genome is replicated and divided with high fidelity.
- Most solid tumours and haematopoietic malignancies display at least one form of genomic instability
- Genome instability provides benefit to tumor evolution.
- leads to tumour regrowth after oncogene withdrawal.
- promotes loss of heterozygosity of tumour suppressor genes

Genomic feature	Description	Possible mechanisms
Whole-genome duplication	Duplication of the entire DNA complement	Cell fusions, cytokinesis failure, metaphase or anaphase defects, or endoreduplication ⁷²
Chromosomal loss and gain	Loss and gain of whole chromosomes and segments of chromosomes	Mitotic defects: abnormal spindle geometry ^{75,78,79} , centriole amplification ^{75,78} , mitotic checkpoint defects ^{73,74} or hyperstable microtubules ^{76,77} Pre-mitotic defects: cohesin mutations ¹¹⁸ , DNA replication stress ^{27,28,82,87} , DNA damage repair defects ⁸¹ or telomere dysfunction ^{80,95}
Chromothripsis	Extensive genomic rearrangements involving one or more chromosomes	Ionizing radiation, micronucleus fragmentation or replication defects ^{86,94,119}
Translocations	Chromosomal rearrangements resulting in fusion of two chromosome arms	Non-homologous end joining, aberrant lymphocyte DNA recombination mechanisms and cytokinesis-induced DNA damage ^{84,85,120}
Tandem duplications	Sequential copies of a genomic segment that often spans several genes	Unknown ^{121,122}
Loss of heterozygosity at fragile sites	Copy number imbalance or gene conversion at genomic loci that are particularly sensitive to replication stress	DNA replication stress ^{27,82}
Focal deletions	Deletion of less than 5 megabases	Chromosome breakage or DNA replication stress ⁸²
Focal amplification	Amplification less than 5 megabases	Double minute chromosomes generated through chromosome breakage ¹²³
Hypermutation	Elevated mutation rate, leading to abundance of somatic mutations	DNA mismatch repair defects ⁶⁸ , BRCA2 mutations ⁷⁰ and proofreading defects ⁶⁷
Kataegis	Localized hypermutation	AID/APOBEC activity ⁶¹
C·G>T·A transitions	Base changes	Ultraviolet radiation-damage ⁶³ , alkylating agents ⁷ and spontaneous deamination of methylated cytosines ⁵⁰
C·G>A·T transversions	Base changes	Base excision repair defects ⁶⁴ , tobacco-related DNA damage ²² and cytotoxic chemotherapy ⁶

Mechanisms of genomic instability

- Different mechanisms of instability can lead to particular distributions of point mutations
- replication stress is associated with an enrichment of mutations in large genes
- microsatellite instability may affect specific genes more frequently than others owing to the nucleotide composition of those genes
- Highly localized clusters of mutations that are associated with chromosomal rearrangement, known as kataegis, may be caused by the action of the a family of cytidine deaminases in breast cancer

Variation in genomic instability over time

- In a study of clear-cell renal carcinoma:chromosomally unstable metastases arise from a tetraploid subclone in the primary tumour
- In a study of breast cancer, researchers made use of variant allele frequencies and copy number events that were derived from whole-genome sequencing reads to dissect the temporal sequence of mutations
- temporally separated biopsies may give strikingly different pictures of a tumour's genomic landscape

Questions and Directions

- how heterogeneity affects tumour progression
- examine in greater depth the relationship between the rate of instability and the complexity of subclonal architectures
- approaches to limit cancer diversity, adaptation and drug resistance

Thank You.