DNA-Damage Response during Mitosis Induces Whole-Chromosome Missegregation

S.F. Bakhoum, L. Kabeche, J.P. Murnane, B.I. Zaki, and D.A. Compton

Précis: Activation of the DNA damage response during mitosis leads to whole chromosome segregation defects via PLK1/Aurora A–mediated stabilization of kinetochore–microtubule attachments.

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L-2-Hydroxyglutarate: An Epigenetic Modifier and Putative Oncometabolite in Renal Cancer


Précis: Accumulation of L-2-hydroxyglutarate in renal cell carcinoma as a result of somatic L2HGDH deficiency is associated with alterations in DNA and histone methylation.

Brain Tumor Cells in Circulation Are Enriched for Mesenchymal Gene Expression


Précis: Circulating tumor cells with invasive mesenchymal characteristics can be detected in patients with glioblastoma and may prove useful in disease monitoring.

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The Androgen-Regulated Protease TMPRSS2 Activates a Proteolytic Cascade Involving Components of the Tumor Microenvironment and Promotes Prostate Cancer Metastasis


Précis: The serine protease TMPRSS2 enhances androgen-driven prostate cancer metastasis by inducing HGF cleavage and activation of c-MET signaling, and may represent a potential therapeutic target.

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The Genomic Landscape of Pediatric Ewing Sarcoma


Précis: Pediatric Ewing sarcoma is characterized by few somatic alterations at diagnosis but frequently exhibits loss of STAG2 expression, which is correlated with metastatic progression.

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Using next-generation sequencing, Crompton, Stewart, and colleagues found that Ewing sarcoma tumors were relatively genetically stable, but exhibited recurrent loss of stromal antigen 2 (STAG2) expression, which was associated with metastatic progression. In addition, relapsed tumors displayed an increased mutation rate compared with tumors at diagnosis. Using whole-genome sequencing, Tirode, Surdez, and colleagues also detected few somatic alterations in Ewing sarcoma and identified STAG2 as the most frequently mutated gene. STAG2 mutations were mutually exclusive with CDKN2A deletion, but often coexisted with TP53 mutations, were associated with poor outcome, and expanded at tumor relapse. Together, these findings provide insight into the genomic landscape of Ewing sarcoma and suggest potential therapeutic targets. For details, please see the article by Crompton, Stewart, and colleagues on page 1326 and the article by Tirode, Surdez, and colleagues on page 1342.