IN THIS ISSUE
Highlighted research articles .................................. 211

NEWS IN BRIEF
Important news stories affecting the community .......... 214

NEWS IN DEPTH
How Cancer Vaccine Tech Shaped COVID Response ........ 218

RESEARCH WATCH
Selected highlights of recent articles of exceptional significance from the cancer literature ...................... 219

ONLINE
For more News and Research Watch, visit Cancer Discovery online at http://cancerdiscovery.aacrjournals.org/CDNews.

VIEWS
In The Spotlight
Lower Airway Dysbiosis Exacerbates Lung Cancer ....... 224
L. Zitvogel and G. Kroemer
See article, p. 293

Shedding Light on Mutant Clonal Dynamics and Cancer Risk in the Skin ......................... 227
M. De Dominici and J. DeGregori
See article, p. 340

A Presynaptic Protein Is a Net Gain for Pancreatic Tumor Progression .......................... 230
M.H. Sherman
See article, p. 446

Science in Society
Priority COVID-19 Vaccination for Patients with Cancer while Vaccine Supply Is Limited .............. 233

RESEARCH BRIEFS
Somatic HLA Class I Loss Is a Widespread Mechanism of Immune Evasion Which Refines the Use of Tumor Mutational Burden as a Biomarker of Checkpoint Inhibitor Response ............ 282

Précis: Across cancer types, loss of heterozygosity at the locus encoding HLA-I was an independent prognostic factor for response to immune checkpoint blockade, and its predictive power improved when combined with measures of tumor mutation burden.

Lower Airway Dysbiosis Affects Lung Cancer Progression ....... 293

Black in Cancer: Championing Diversity in Cancer Research and Medicine .................. 237
H.J. Henderson and S. Bell

In Focus
A Call to Action: Dismantling Racial Injustices in Preclinical Research and Clinical Care of Black Patients Living with Small Cell Lung Cancer ....... 240

REVIEWS
Modes of Regulated Cell Death in Cancer ................. 245
E. Koren and Y. Fuchs

Fueling the Fire: Inflammatory Forms of Cell Death and Implications for Cancer Immunotherapy ........... 266
S.R. Rosenbaum, N.A. Wilski, and A.E. Aplin

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Black in Cancer: Championing Diversity in Cancer Research and Medicine .................. 237
H.J. Henderson and S. Bell

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A Call to Action: Dismantling Racial Injustices in Preclinical Research and Clinical Care of Black Patients Living with Small Cell Lung Cancer ....... 240

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Lower Airway Dysbiosis Affects Lung Cancer Progression .......................... 293
Précis: Lower airway dysbiosis characterized by excessive colonization with oral commensal microbes, particularly Veillonella parvula, was a predictor of poor prognosis in lung cancer, and in vivo experiments supported a role for V. parvula colonization in decreasing survival.

See commentary, p. 224

Genetically Defined, Syngeneic Organoid Platform for Developing Combination Therapies for Ovarian Cancer


Précis: Organoids representing high-grade serous ovarian cancer were developed; these organoids exhibited varying sensitivities to chemotherapy drugs and elicited different immune responses, suggesting they may serve as a novel platform for discovery.

See commentary, p. 227

RESEARCH ARTICLES

Personalized Antibodies for Gastroesophageal Adenocarcinoma (PANGEA): A Phase II Study Evaluating an Individualized Treatment Strategy for Metastatic Disease


Précis: In a phase II clinical trial, personalized antibodies plus molecularly targeted chemotherapy improved median overall survival and the one-year survival rate in patients with gastroesophageal adenocarcinoma relative to historical survival data.

Clinicogenomic Analysis of FGFR2-Rearranged Cholangiocarcinoma Identifies Correlates of Response and Mechanisms of Resistance to Pemigatinib


Précis: In patients with cholangiocarcinoma harboring FGFR fusions or rearrangements, response to the FGFR1-3 inhibitor was equally likely regardless of the type of genomic alteration, and resistance mutations affected the FGFR2 kinase domain.

Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site


Précis: Genetic analyses of healthy aged human epidermal cells revealed skin site-specific mutational signatures, with common skin cancer sites exhibiting more potentially oncogenic mutations and with high variability in mutations under positive selection among sites.
Timed Ang2-Targeted Therapy Identifies the Angiopoietin-Tie Pathway as Key Regulator of Fatal Lymphogenous Metastasis .......................... 424
Précis: A hindrance to the study of metastasis via lymphatic vessels with lymph nodes as intermediate sites was overcome using a genetically engineered mouse model–derived allograft model, the use of which uncovered the Ang2–Tie2 pathway as a critical dependency.

Netrin G1 Promotes Pancreatic Tumorigenesis through Cancer-Associated Fibroblast-Driven Nutritional Support and Immunosuppression ...................... 446
Précis: The glutamatergic presynaptic protein Netrin-G1 was found to be a major contributor to the metabolic and immunosuppressive tumor microenvironment in pancreatic ductal adenocarcinoma, and blocking Netrin-G1 in vivo suppressed tumorigenesis.
See commentary, p. 230

The RNA m6A Reader YTHDF2 Maintains Oncogene Expression and Is a Targetable Dependency in Glioblastoma Stem Cells ........................................... 480
Précis: In glioblastoma stem cells, YTHDF2 (which reads mRNA for the modified nucleotide N6-methyladenosine) stabilized MYC and VEGFA transcripts via an IGFBP3-mediated mechanism, and blocking IGF–IGF1R signaling in vivo hindered glioblastoma growth.

The Hepatic Microenvironment Uniquely Protects Leukemia Cells through Induction of Growth and Survival Pathways Mediated by LIPG .................. 500
Précis: Liver-infiltrating leukemia stem cells in mice acquired a proliferative, chemotherapy-resistant phenotype characterized by over-expression of the gene encoding the lipase LIPG, which was sufficient to induce the same phenotype in non–liver-infiltrating leukemia cells.

Correction
Correction: Impact of PD-1 Blockade on Severity of COVID-19 in Patients with Lung Cancers ................................. 520

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The risk of skin cancers such as basal cell carcinoma and squamous cell carcinoma varies greatly across the body, and it is known that healthy aged skin cells often harbor cancer driver mutations, but whether these observations are connected has not been determined. Fowler and colleagues discovered that the mutation density in healthy human skin differed from location to location across the body. Common sites for skin cancer, such as the forearm, bore more mutations than uncommon sites, and the mutation profile suggested UV radiation as a cause. Interestingly, not only was there selection for cancer-associated mutations in healthy skin, but the DNA repair mechanisms used varied based on site. For more information, see the article by Fowler and colleagues on page 340.