species (H^-), there was a significant increase in both *Helicobacter* and *Odoribacter* species in the cohoused H^- mice concomitant with upregulated expression of MHC class II by IECs. Similarly, fecal transplantation from H^+ mice into germ-free mice resulted in increased MHC class II expression by IECs.

The regulation of intestinal MHC class II expression by commensal bacteria was shown to depend on pattern recognition receptor signalling and the inflammatory cytokine IFNγ. In particular, activation of TLR2 and NOD2 signalling, or IFNγ treatment, was sufficient to increase MHC class II expression by $LGR5^+$ ISCs. Levels of IFNγ were significantly reduced in the intestines of HFD-fed mice compared with control mice. Together, the results suggest that changes to the intestinal microbiome in response to a HFD attenuate MHC class II expression by ISCs as a result of reduced inflammatory gene expression, which was consistent with reduced immune cell infiltrates observed in the intestinal epithelium of HFD-fed mice.

The downregulation of antigen presentation that evades anti-tumour immune responses is a common feature of many cancers. Using inducible inactivation of the *Apc* tumour suppressor gene as a model of tumorigenesis, the authors showed that APC^{null} $LGR5^+$ ISCs had twofold greater tumorigenicity after in vivo transplantation if they lacked MHC class II expression, but that this difference between MHC class II negative and positive transplanted ISCs was not observed in recipient mice lacking B cells and T cells. Two further mouse models of intestinal tumorigenesis involving inducible deletion of MHC class II confirmed that loss of MHC class II specifically by $LGR5^+$ ISCs was associated with greater numbers of intestinal tumours. Thus, a HFD seems to disrupt MHC class II-dependent immune surveillance of tumour-initiating ISCs through effects on the intestinal microbiome.

Kirsty Minton

ORIGINAL ARTICLE Beyaz, S. et al. Dietary suppression of MHC class II expression in intestinal epithelial cells enhances intestinal tumorigenesis. *Cell Stem Cell* https://doi.org/10.1016/j.stem.2021.08.007 (2021)

Credit: Simon Bradbrook/Springer Nature Limited

in six mice developed small tumours. However, when recipient mice were treated with NRTIs or received xenograft cells with cGAS knockdown, all mice developed large tumours.

These findings led to the suggestion that RTE activation, owing to limiting DNMT1 activity, in premalignant BMR cells functions as a tumour suppressor mechanism. A similar situation may occur at early stages of carcinogenesis in other mammalian species when DNMT1 fails to keep up with rapid proliferation of premalignant cells. In agreement with this idea, growth of a human HeLa cell line xenograft in nude mice was repressed by DNMT1 knockdown, and HeLa cells stably transfected with LINE-1 showed induction of type I interferons and reduced proliferation in vitro and in vivo. Although cancer cells often have high levels of RTE expression, analysis of cancer cell databases showed a correlation between RTE expression and mutations affecting interferon, cGAS, STING and NF-κB pathways.

This study identifies a new anticancer mechanism to explain cancer resistance in BMRs; the naturally low level of DNMT1 expression in BMRs fails to maintain methylation-mediated silencing of RTEs during rapid cell proliferation. The consequent cytoplasmic accumulation of RNA/DNA hybrids triggers an interferon response through the cGAS–STING pathway and eliminates premalignant cells. The findings suggest that RTEs are not just selfish genomic parasites, but may serve as tumour suppressors.

Lucy Bird

ORIGINAL ARTICLE Zhao, Y. et al. Transposon-triggered innate immune response confers cancer resistance to the blind mole rat. *Nat. Immunol.* https://doi.org/10.1038/s41590-021-01027-8 (2021)

IN BRIEF

COVID-19

Fc-optimized monoclonal antibodies show superior efficacy

Monoclonal antibody (mAb) therapies have shown some use in patients with mild to moderate COVID-19, but have limited efficacy in preventing complications or death in patients with severe COVID-19. Reporting in *Nature*, Ravetch, Bournazos and colleagues now demonstrate that optimizing mAbs for the engagement of activating Fcγ receptors (FcγRs) significantly improves their ability to confer full protection in SARS-CoV-2 challenge models. Moreover, these mAbs are also highly potent at reducing mortality post-infection in animal models of severe COVID-19. These findings illustrate the importance of FcγR-mediated pathways in antibody-mediated antiviral immunity and have important implications for the development of more effective mAb therapeutics.

ORIGINAL ARTICLE Yamin, R. et al. Fc-engineered antibody therapeutics with improved anti-SARS-CoV-2 efficacy. *Nature* https://doi.org/10.1038/s41586-021-04017-w (2021)

COVID-19

Epitope mapping of spike identifies variant-resistant antibodies

One of the biggest concerns in the ongoing COVID-19 pandemic is the potential emergence of SARS-CoV-2 variants that evade immunity. A report in *Science* now presents a comprehensive map of antibody binding sites of the SARS-CoV-2 spike protein, which was generated using several hundred monoclonal antibodies (mAbs). Among 186 mAbs targeted at the receptor binding domain (RBD) of spike, the authors (a global consortium) identified seven mAb communities with distinctive footprints and competition profiles. Using pseudovirion-based neutralization assays to test mAb binding to mutant spike proteins (with either individual mutations or combinations of mutations, including those corresponding to variants α–ε), they were able to identify key classes of RBD-targeted antibodies that maintained neutralization activity against these mutants. The study may allow to predict and interpret the effect of new mutations and inform the selection of antibody cocktails against new variants.

ORIGINAL ARTICLE Hastie, K. M., Lie, H. et al. Defining variant-resistant epitopes targeted by SARS-CoV-2 antibodies: a global consortium study. *Science* https://doi.org/10.1126/science.abh2315 (2021)

COVID-19

Cross-reactive tissue-resident $CD8^+$ T cells may provide first line of defence against SARS-CoV-2

Cross-reactive $CD4^+$ T cells, likely induced by common cold coronavirus infections, are detected in 20–50% of peripheral blood samples from SARS-CoV-2 unexposed individuals. However, cross-reactive $CD8^+$ T cells are rarely detected in these samples. To study whether this may be because $CD8^+$ memory T cells are mostly located in tissues, Niessl at al. examined peripheral blood and tonsillar tissue samples from pre-2019. Indeed, they detected SARS-CoV-2 reactive $CD8^+$ memory T cells in 32% of tissue samples. Cross-reactive $CD4^+$ cells were detected at similar levels in blood and tissue, whereas cross-reactive memory $CD8^+$ T cells were largely absent in matched blood samples. Tissue-resident cross-reactive $CD8^+$ memory T cells displayed markers of follicular homing and tissue residency, and the authors speculate that these may enable rapid sentinel immune responses to SARS-CoV-2.

ORIGINAL ARTICLE Niessl, J. et al. Identification of resident memory $CD8^+$ T cells with functional specificity for SARS-CoV-2 in unexposed oropharyngeal lymphoid tissue. *Sci. Immunol.* https://doi.org/10.1126/sciimmunol.abk0894 (2021)