

The ecological imperative: Context and timing shape the path to colorectal cancer

Haoyu Duan,¹ Zhe-Yu Wen,¹ Jinju Lei,¹ Gong Chen,¹ and Dandan Lin^{1,*}

¹Cancer Center, Renmin Hospital of Wuhan University, Wuhan 430060, China

*Correspondence: lindandan@whu.edu.cn

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For over three decades, the "multi-hit" hypothesis, formalized by Fearon and Vogelstein,¹ has framed our understanding of colorectal cancer (CRC) pathogenesis. This linear paradigm describes tumorigenesis as a stepwise microevolution driven by the sequential accumulation of genetic alterations—classically initiating with *APC* inactivation. This model presumes driver mutations are inherently advantageous, enabling clones to outcompete wild-type neighbors. However, high-resolution lineage tracing and genomic sequencing now challenge this determinism. Normal tissues—including the colon, esophagus, and skin—are frequently colonized by clones harboring potent oncogenic drivers that nevertheless fail to progress. Conversely, many of the earliest lesions in the intestine present polyclonal structures that are not easily linearized. These paradoxes raise a fundamental question: Is oncogenic potential intrinsic to the mutation, or contingent upon tissue context and temporal order of acquisition?

Lourenço et al. recently resolved this paradox.² Leveraging mouse genetics and human genomic analysis, they reveal that most "driver" mutations fail to colonize the normal intestinal epithelium. Instead, these clones undergo rapid decay—driven by negative selection—unless the tissue has been "primed" by a permissive oncogenic background. This work reframes tumor initiation not merely as a linear accumulation of hits, but as an ecological phenomenon where context and chronology dictate whether a mutation becomes a lethal founder or is eliminated via negative selection (Figure 1).

To deconstruct this interplay, the investigators employed sophisticated, order-controlled murine mutagenesis paradigms. First, to mimic a pre-existing oncogenic field, they triggered specific priming events in murine intestinal epithelium—such as activating *Kras*^{G12D} allele or deleting *Pten/Trp53*. Subsequently, these mice were exposed to N-ethyl-N-nitrosourea (ENU), a chemical mutagen that rapidly scatters random point mutations. This "Priming-then-ENU" (TE) approach allowed the researchers to observe which random mutations could successfully colonize the pre-conditioned tissue. The outcome was striking: despite thousands of variants, potent WNT-activating mutations—particularly within *Ctnnb1*—were conspicuously absent. Lineage tracing revealed that in a homeostatic epithelium, these potent drivers do not act as super-competitors but are subject to negative selection. Thus, excessive WNT signaling is deleterious, precipitating negative selection via differentiation or apoptosis. However, priming fundamentally inverts this selective landscape. Oncogenic signaling of *Kras* may elevate the cellular threshold for WNT tolerance, buffering cellular stress and converting the previously lethal *Ctnnb1* mutations into potent drivers that fuel a 300-fold increase in tumor burden. This context dependence exhibits remarkable specificity. For instance, backgrounds with deficient *Pten* necessitated the selection of "weaker" *Apc* alleles retaining Armadillo repeats—an adaptation presumably required to constrain combined WNT/PI3K signaling within a survivable window. Rescue experiments provided definitive validation of this model by interrogating the temporal dependency of mutational fixation. When the experimental order was reversed—administering ENU prior to the priming event—a delay of merely 30 days resulted in a >90% collapse in tumor multiplicity. This observation indicates that in normal tissue, driver mutations are not dormant reservoirs but are actively eliminated, potentially due to rapid epithelial turnover. The opportunity for transformation is thus transient, mirroring a core tenet of evolutionary biology: a genetic adaptation is only advantageous if the immediate environment supports it.

Extending these insights to human disease, Lourenço et al. interrogated genomic data from >17,000 patients (GENIE project), identifying distinct mutational fingerprints corroborating the "priming" model. Tumors with mutant KRAS exhibited a pronounced skew toward APC truncations retain-

ing extra 20-amino acid repeats. Thus, human KRAS functions as a permissive buffer, licensing the fixation of APC variants that would otherwise be eliminated. This concordance indicates that mutation order imprints a distinct mutational signature. A mature tumor's genotype serves as a retrospective genomic indicator of tumor ontogeny; despite subsequent evolutionary adaptations, it retains traces of the ecological constraints governing its initiation.

Despite these revolutionary insights, critical questions persist regarding the translation of animal findings to human pathology. Reconciling the compressed kinetics of animal models with the decades-long evolution of human cancer poses a significant challenge. The mutational dynamics driven by an acute, high-dose ENU mutational shower differ markedly from the sporadic, chronic, and low-level mutational exposures (such as the clock-like mutational signature SBS1) characteristic of human colorectal tissue. How ecological priming operates under such prolonged, low-grade mutational pressure remains an open question necessitating higher-resolution clinical lineage tracing. While the authors establish *Kras* and *Pten* as permissive primers, the precise effectors enforcing the negative selection of mutants without being primed remain elusive. Does the swift elimination of *Ctnnb1*-mutant clones stem from apical extrusion, trophic competition, or microenvironmental attrition? Furthermore, establishing the generalizability of this "decay" model to other epithelia laden with phenotypically silent drivers—such as the esophagus and lung—is a priority.

If these ecological dynamics hold true in human pathogenesis, they suggest an intriguing hypothesis for future therapeutic intervention: what might be termed 'therapeutic un-priming'. If the survival of potent driver mutations is strictly contingent upon a permissive "scaffold" provided by an initiating lesion—such as KRAS activation—then it follows that dismantling this scaffold should not merely halt growth, but actively restore the tissue's innate negative selection pressures. Translating these findings into preventive strategies, however, requires extreme caution. It is crucial to acknowledge that the biological context of an established, complex tumor microenvironment differs fundamentally from early clonal selection in a mostly homeostatic epithelium; tumor suppression must not be conflated with the prevention of mutation fixation. Nevertheless, we might draw a conceptual analogy from emerging targeted therapies in advanced disease. For instance, the covalent KRAS(G12C) inhibitor AMG 510 accomplishes more than simple signaling blockade.³ As Canon and colleagues elegantly demonstrated, it fundamentally remodels the macroscopic tumor's ecological niche, converting an immunosuppressive "cold" state into a pro-inflammatory "hot" phenotype characterized by robust T-cell infiltration. By analogy, a true 'un-priming' agent designed for early interception would face a distinct and perhaps more formidable challenge: targeting morphologically normal but genetically 'primed' tissue. The goal here would not be tumor shrinkage, but rather dismantling the latent survival buffer provided by the priming event. This would, in turn, re-expose nascent driver mutations to the harsh attrition dynamics inherent to the wild-type epithelium. In principle, utilizing such agents to destabilize the oncogenic niche might eventually offer a pathway to 'sanitize' fields of precancerous potential, though actualizing this 'ecological engineering' in the clinic remains a distant challenge.

The rapid decay of unprimed clones raises the question of whether active immune surveillance plays a role in this elimination. While the initial explosive increase in tumor burden within p53-deficient contexts hints at a possible failure of immune surveillance or DNA damage responses, immune clearance is likely only one piece of a complex puzzle. The authors' findings necessitate further exploration into the intrinsic defense mechanisms of the homeostatic epithelium. For instance, the elimination of these potent,

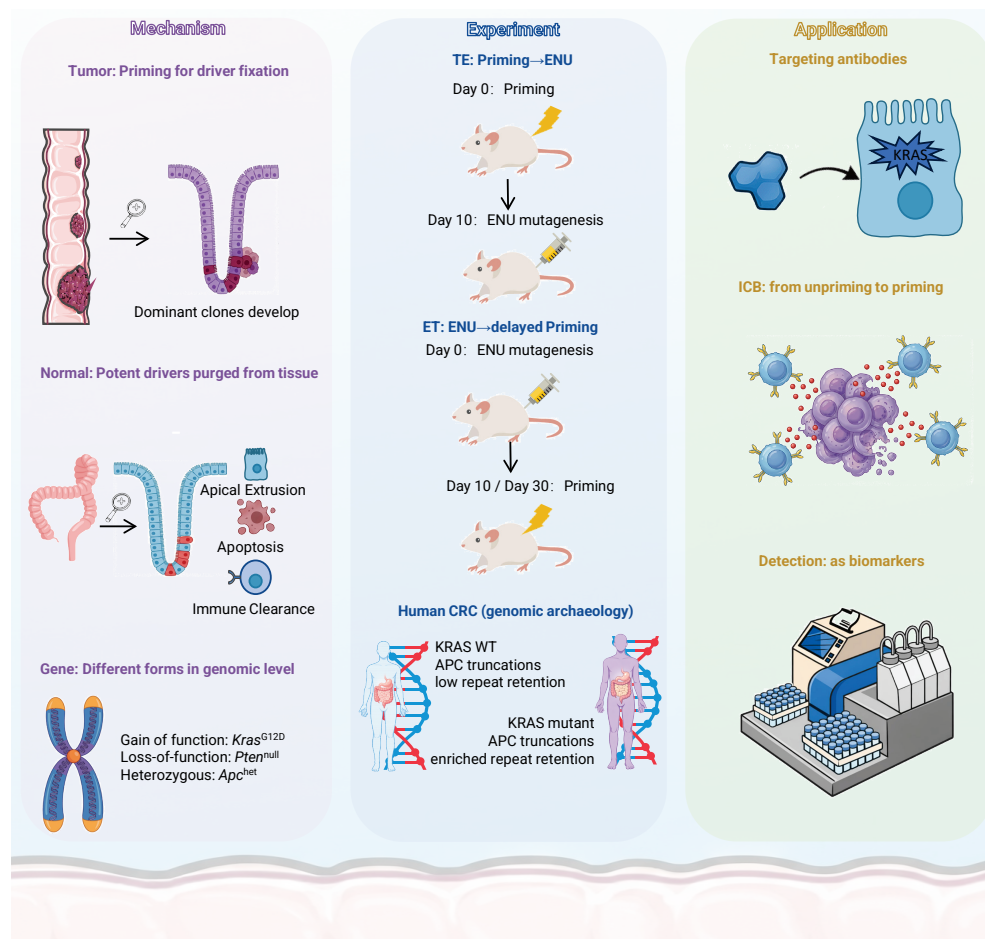


Figure 1. Ecological "priming" dictates the trajectory of intestinal transformation (Left) Mechanism: The homeostatic, unprimed intestinal epithelium is juxtaposed with its primed counterpart. In an unprimed state, the acquisition of potent driver mutations triggers negative selection, rapidly purging mutant clones via apical extrusion, apoptosis, and potentially immune clearance. Conversely, priming functions as a permissive scaffold that overrides negative selection and licenses the fixation of otherwise deleterious drivers. Genetically, priming encompasses gain-of-function (Kras G12D), loss-of-function (Pten null), or heterozygous (Apc het) alterations." (Center) Experiment: The temporal dependency of mutation fixation is interrogated via order-controlled murine mutagenesis. In the TE (Priming → ENU) paradigm, pre-existing priming licenses driver fixation. In the ET (ENU → delayed Priming) rescue paradigm, drivers arising in normal epithelium rapidly decay without prompt ecological support. In human CRC, genomic archaeology reveals that tumors with mutant KRAS exhibit enriched APC repeat retention, mirroring the temporal ecological constraints defined in mice." (Right) Application: Proposed clinical scenarios exploiting these dynamics. Strategies include therapeutic "un-priming" (e.g., targeted antibodies/inhibitors against KRAS) to dismantle the permissive scaffold; immune checkpoint blockade (ICB) to theoretically prevent the transition to a primed state or enhance latent clone clearance; and early detection modalities utilizing priming signatures as predictive biomarkers.

unprimed Ctnnb1-mutant clones might be governed by non-immune processes such as mechanical apical extrusion, WNT toxicity triggering localized apoptosis, or a competitive disadvantage during symmetric stem cell differentiation. Determining whether "priming" acts primarily by dampening immune alerting stress responses (e.g., cGAS-STING signaling) or by physically remodeling the niche to prevent epithelial extrusion remains an essential question for future studies.⁴

Finally, the recognition that a morphologically quiescent epithelium may conceal "primed" genetic fields mandates a reevaluation of our screening paradigms.⁵ Conventional white-light colonoscopy, predicated on the detection of macroscopic polyps, remains blind to the invisible molecular landscapes that precede morphological transformation. Just as high-resolution sequencing has revealed physiologically normal skin to be a patchwork of clones harboring driver mutations, the colon may similarly conceal "primed" reservoirs serving as silent launchpads for malignancy. Consequently, one major translational priority hinges upon developing ultrasensitive liquid biopsies or spatially resolved transcriptomics to chart these genetically volatile, yet visually unremarkable, regions.

CONCLUSION

In summary, Lourenço and colleagues have delivered a landmark study that deconstructs the long-held dogma of oncogenic determinism. They demonstrate that the path to malignancy is not an inevitable accumulation of hits, but a contingent evolutionary gauntlet where the chronological sequence of events dictates clonal survival. By recasting tumor initiation as a desperate race between mutation acquisition and homeostatic decay, this work provides a sophisticated molecular update to Paget's century-old "Seed and Soil" hypothesis: affirming that the "seed" of a driver mutation is impotent without the fertile "soil" of a primed niche. The "Big Bang" of cancer forma-

tion is thus not a solitary event triggered solely by a mutational spark, but a conditional expansion dependent on a highly permissive microenvironment. Ultimately, the frontier of precision oncology must expand beyond the targeted destruction of established tumors to

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AUTHOR CONTRIBUTIONS

H.D. led the resources, software, visualization, and the writing (original draft, review, and editing) of the manuscript. Z.-Y.W. contributed to the visualization, writing, and editing. J.L. and G.C. supported the resources and software. D.L. supervised the study and led the validation. All authors read and approved the final manuscript.

DECLARATION OF INTERESTS

The authors declare no competing interests.