PRIZE ESSAY

TRANSLATIONAL MEDICINE

# Metabolic markers as cancer clues

## Changes in branched-chain amino acids may be first sign of certain cancers

*By* **Jared R. Mayers**

The study of cancer metabolism began almost a century ago when Otto Warburg noted that cancerous tissues metabolize glucose differently from their normal counterparts (*1*). It has since become widely understood that cancer cells, and proliferating cells more broadly, carry out a metabolic program that favors the accumulation of new biomass components by synthesizing amino acids, lipids, and nucleotides necessary for the generation of daughter cells (*2*).

Contemporary studies have focused on cell-autonomous metabolic alterations in cancer, using cell culture models to dissect the contributions of different oncogenes and tumor suppressors to observed metabolic phenotypes (*3*). These systems have yielded numerous promising therapeutic targets (*4*), although their nonphysiologic nature raises the question of how broadly findings may apply to patients (*3*). In fact, models deviating from standard culture conditions have uncovered previously underappreciated metabolic flexibility within cancer cells (*2*), and growing the same cell line either in culture or in animals alters the fuel these cells use (*5*).

### SEARCHING FOR CANCER'S SIGNAL

Based on these findings, we posited that evaluating metabolism in mouse models of cancer and in human subjects might better identify metabolic weaknesses in cancer cells that could be exploited therapeutically. Specifically, we sought to determine how cancer can influence whole-body metabolism through interactions with normal cells and the tissue microenvironment, particularly in early-stage disease.

Initially, we focused on pancreatic cancer, a leading and increasingly common cause of cancer death in the United States (*6*). Pancreatic cancer is disproportionally associated with systemic metabolic alterations such as insulin resistance (*7*) and cachexia, a condition characterized by wasting of muscle and fat, which is commonly seen in end-stage disease (*8*). Although these phenotypes are well documented, it was unknown whether more subtle metabolic changes, such as alterations in circulating nutrient levels, could yield insight into earlier time points of disease development.

### A METABOLIC INDICATOR OF EARLY PANCREATIC CANCER EMERGES

We used mass-spectrometry metabolomics to analyze samples from four prospective human cohorts and found an association between elevated plasma levels of branched-chain amino acids (BCAAs) and future diagnosis of pancreatic cancer (*9*). Intriguingly, this association was strongest 2 to 5 years before diagnosis, a period hypothesized to overlap with occult disease (*10*). Thus, although these cohort studies are traditionally used to identify risk factors for future disease development, our findings indicated that BCAA elevations might instead represent a marker of early pancreatic cancer.

We recapitulated these observations in two mouse models of pancreatic cancer driven by mutations in *Kras* and *Trp53* and confirmed our hypothesis from the human data that the changes occurred during the earliest histologic stages of invasive disease. Using stable isotope–based labeling, we demonstrated that elevated plasma BCAAs resulted from increased systemic protein turnover, most likely due to protein degradation in the muscle. This suggested that the process of tissue breakdown that is associated with cachexia during end-stage disease likely begins years earlier in humans than previously thought (*9*).

In this study, we used a reverse-translational approach, taking human data into mouse models, which allowed us to dramatically shift how we study prospective human cohorts and to exploit the variable lengths of time from blood draw to cancer diagnosis to study early disease. As a result, we were able to understand a mechanism of early disease progression and not just predictors of disease development and diagnosis.

### CIRCULATING INDICATORS OF ALTERED METABOLISM ARE ALSO PRESENT IN LUNG CANCER

After demonstrating that one type of cancer could drive whole-body metabolic alterations, we wondered whether these effects might occur across other cancer types. To allow for a direct comparison, we chose to investigate plasma metabolite alterations in another *Kras*- and *Trp53*-driven model of cancer: non–small-cell lung carcinoma (NSCLC).

In contrast to our observations in the isogenic pancreatic cancer model, plasma levels of BCAAs were decreased in NSCLC tumor-bearing mice (*11*). Using stable-isotope BCAA tracers, we observed that NSCLC cells, but not pancreatic cancer cells, take up more free BCAAs compared with their respective tissues of origin.

NSCLC cells incorporate plasma BCAAs into proteins and additionally use them as a source of nitrogen for de novo synthesis of nonessential amino acids and nucleotides (*11*). This activity drives the decreased plasma BCAA levels observed in this model (see the figure). Pancreatic cancer cells, on the other hand, rely more on the uptake and metabolism of material from the surrounding stromal environment to obtain

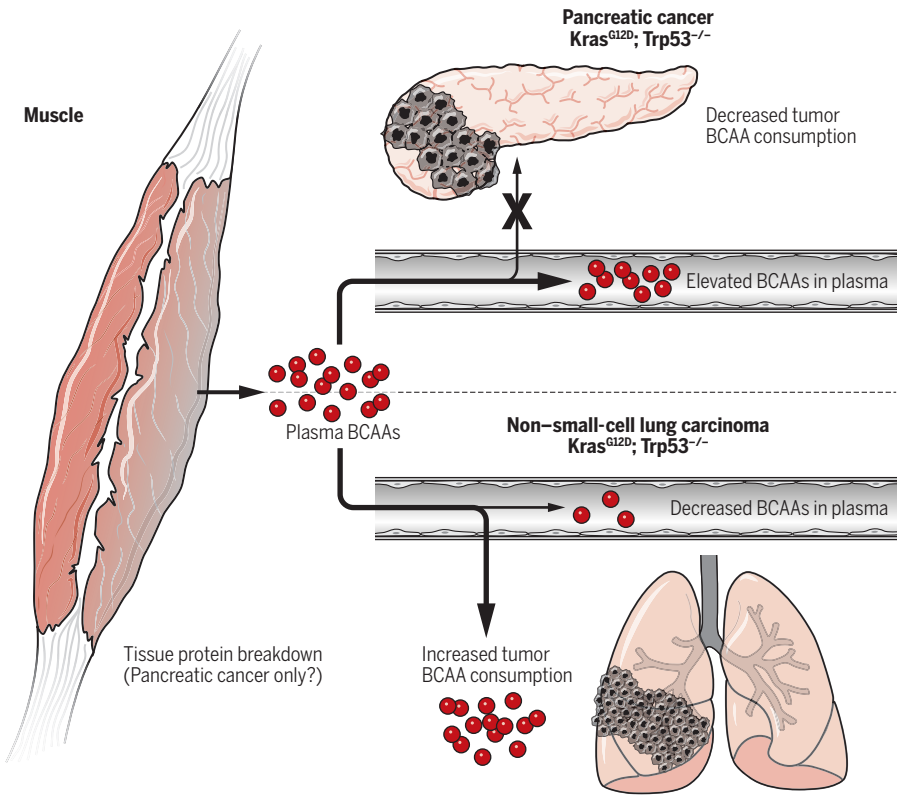
PHOTO: ALENA HEATH

FINALIST: TRANSLATIONAL MEDICINE

**Jared Mayers**

Jared Mayers is a resident in internal medicine at Brigham and Women's Hospital in Boston, MA, working toward a career that balances basic science research with clinical practice. After completing his undergraduate degree at Williams College, he earned an M.D. from Harvard Medical School and a Ph.D. in biology from the Massachusetts Institute of Technology. His research interests center on identifying and understanding the mechanisms driving whole-body metabolic alterations and tissue interactions in early disease states. Outside of the hospital and lab, he enjoys running and spending time with his family.

www.sciencemag.org/content/358/6368/1265.1




## Branched-chain amino acids and cancer

Early pancreatic cancer and non–small-cell lung carcinoma (NSCLC) are associated with distinct changes in plasma branched-chain amino acids (BCAAs). In pancreatic cancer, increased protein turnover and muscle breakdown with concurrent low utilization by tumor cells drive increased levels of BCAAs. In contrast, NSCLC cells take up more free BCAAs, resulting in decreased concentrations.

amino acids (*11*–*13*). These distinct phenotypes were reflected in expression levels of BCAA metabolic enzymes in both human and mouse NSCLC. Deletion of the enzymes responsible for nitrogen extraction blocked formation of NSCLC, but not pancreatic tumors, in mice despite having no effect on proliferation of either cell type in culture (*11*). This study revealed an in vivo, NSCLC-specific metabolic vulnerability.

### BEYOND GENETICS: TISSUE OF ORIGIN AND TUMOR ENVIRONMENT MATTER, TOO

In the clinic, both the selection of patients for some treatments and the development of new therapies relies heavily on the underlying genetic profile of a particular tumor (*14*). Implicit in this approach is the hypothesis that specific mutations produce predictable phenotypes that can be targeted by a single method in a variety of cancer types. This hypothesis has also been applied to metabolism, where stereotyped driver mutation-metabolic phenotype relationships based largely on in vitro studies have been described (*15*–*17*). Our findings, however, suggest that tissue of origin and tumor environment, in addition to genetics, are important factors that influence metabolic weaknesses for a given tumor. Consistent with this idea, administration of chemotherapies that target nucleotide metabolism has historically been based on tumor type rather than genetics (*18*).

Using mouse and human data, we have explored metabolic interactions between nascent tumors and their host environment, both local and distant, which measurably influence whole-body metabolism. Exploring the mechanisms driving these changes has altered our interpretation of prospective human cohort data, opening new avenues of investigation into early disease. Additionally, our work on the combined influence of mutational status and tissue context on a tumor's metabolic preferences resulted in our identification of a previously unappreciated, cancer-type–specific metabolic vulnerability that could be targeted therapeutically.

Our work expands the promise of precision-medicine approaches to targeting cancer metabolism. Continued investigation with in vivo systems remains our best hope, both to understand the metabolic features of early cancer development and to develop strategies to exploit these features therapeutically. ■


### REFERENCES AND NOTES

1. O. Warburg, K. Posener, *Die Naturwissenschaften* **12**, 1131 (1924).
2. R. J. Deberardinis, N. S. Chandel, *Sci. Adv.* **2**, e1600200 (2016).
3. J. R. Mayers, M. G. Vander Heiden, *Trends Biochem. Sci.* **40**, 130 (2015).
4. U. E. Martinez-Outschoorn, M. Peiris-Pages, R. G. Pestell, F. Sotgia, M. P. Lisanti, *Nat. Rev. Clin. Oncol.* **14**, 11 (2016).
5. S. M. Davidson *et al.*, *Cell Metab.* **23**, 517 (2016).
6. American Cancer Society, *Cancer Facts and Figures* (American Cancer Society, Atlanta, 2017).
7. B. M. Wolpin *et al.*, *J. Natl. Cancer Inst.* **105**, 1027 (2013).
8. S. J. Wigmore, C. E. Plester, R. A. Richardson, K. C. Fearon, *Brit. J. Cancer* **75**, 106 (1997).
9. J. R. Mayers *et al.*, *Nat. Med.* **20**, 1193 (2014).
10. S. Yachida *et al.*, *Nature* **467**, 1114 (2010).
11. J. R. Mayers *et al.*, *Science* **353**, 1161 (2016).
12. S. M. Davidson *et al.*, *Nat. Med.* **23**, 235 (2017).
13. O. Olivares *et al.*, *Nat. Comm.* **8**, 16031 (2017).
14. L. A. Garraway, *J. Clin. Oncol.* **31**, 1806 (2013).
15. E. White, *Genes Dev.* **27**, 2065 (2013).
16. C. V. Dang, *Cell* **149**, 22 (2012).
17. O. Maddocks, K. H. Vousden, *J. Molec. Med.* **89**, 237 (2011).
18. P. M. Wilson, P. V. Danenberg, P. G. Johnston, H. J. Lenz, R. D. Ladner, *Nat. Rev. Clin. Oncol.* **11**, 282 (2014).



### ACKNOWLEDGMENTS

I am grateful to all members of the Vander Heiden laboratory and my collaborators, past and present, whose wisdom, help, and friendship shaped my thesis work. In particular, thanks to my Ph.D. adviser, M. Vander Heiden, for his timely advice and incredible enthusiasm for science and medicine.

10.1126/science.aar2001


GRAPHIC: ADAPTED BY A. KITTERMAN/*SCIENCE*