

Abstract

Food Quality Control: Nutrition and Immunity in Intestinal Homeostasis

Zuri Ayana Sullivan

2020

The gastrointestinal (GI) tract is a multi-kingdom cellular ecosystem that facilitates the procurement of nutrients from the environment. In constant contact with the external world, it is at once a point of exposure to lethal pathogens and toxins, and the locus of absorption for nutrients that are essential for life. Consequently, this tissue is tasked with the challenge of balancing its primary functions of nutrient uptake and host defense in response to a complex and constantly changing environment.

This challenge is particularly significant for omnivores, whose diets change on daily, seasonal, and lifelong timescales, alongside encounters with ingested toxins, enteric pathogens, and commensal microbes. Omnivorous lifestyles therefore require that the GI tract of such animals be adaptable to the dynamic nature of their environments. This dissertation explores the cellular and molecular mechanisms that confer this adaptability.

Chapter 1 provides an ecological perspective on the physiology of the gastrointestinal tract, and defines the major cellular players in nutrient uptake and host defense in this tissue. Chapter 2 presents a conceptual framework for understanding the basis of immunological responses to food, and describes how systems that monitor the quality of food become exaggerated in allergic disease. Chapter 3 explores the intestinal epithelial response to

nutrient sensing, and provides evidence that diet can alter the cellular composition of the intestinal epithelium. Chapter 4 details the contribution of a poorly understood subset of intestinal lymphocytes, $\gamma\delta$ T-cells, to the on-demand induction of digestive and absorptive machinery in response to diet. Chapter 5 examines mechanisms by which hosts may monitor the state of their commensal microbiota, using diet as a tool to perturb the microbial ecosystem. Finally, in Chapter 6, I propose a set of principles to explain how the intestine adjusts the balance between nutrient uptake and host defense in response to environmental change.

PREVIEW

Food Quality Control:
Nutrition and Immunity in Intestinal Homeostasis

A Dissertation
Presented to the Faculty of the Graduate School
of
Yale University
in Candidacy for the Degree of
Doctor of Philosophy

by
Zuri Ayana Sullivan

Dissertation Director: Ruslan Medzhitov, Ph.D.

December 2020

© 2021 by Zuri Ayana Sullivan

All rights reserved.

PREVIEW

Table of Contents

Abstract	i
Title Page	iii
Acknowledgements	vii
Dedication	xi
List of Figures	xii
List of Abbreviations	xiii
Chapter 1: Introduction	1
<i>Ecological physiology of the gastrointestinal tract</i>	<i>1</i>
<i>Intestinal epithelium</i>	<i>6</i>
<i>Intestinal lymphocytes in defense and homeostasis</i>	<i>13</i>
<i>Commensal microbiota</i>	<i>18</i>
<i>Summary and Study Objectives</i>	<i>24</i>
Chapter 2: Food Quality Control Systems	27
<i>Introduction</i>	<i>28</i>
<i>Food composition</i>	<i>30</i>
<i>Sensing food components</i>	<i>31</i>
<i>Learned behavior in food selection</i>	<i>38</i>
<i>Allergic defenses: protective versus pathological</i>	<i>42</i>
<i>Immune system and food quality control</i>	<i>43</i>
<i>Defensive neuronal reflexes</i>	<i>44</i>
<i>Autonomic nervous system in allergic defenses</i>	<i>46</i>
<i>What makes an allergen an allergen?</i>	<i>48</i>
<i>Food allergens and food quality control</i>	<i>50</i>
<i>Conclusions and Perspectives</i>	<i>57</i>
Chapter 3: Epithelial Response to Nutrient Sensing	62
<i>Introduction</i>	<i>62</i>
<i>Results</i>	<i>63</i>
High carbohydrate diet induces expression of carbohydrate transcriptional program in the small intestine and pancreas	63
Diet alters the cellular composition of the intestinal epithelium	64
Signals required for induction of the carbohydrate transcriptional program	66
Inflammation regulates expression of carbohydrate transcriptional program	67
<i>Summary & Discussion</i>	<i>68</i>

Chapter 4: $\gamma\delta$ T-cells Regulate Intestinal Response to Nutrient Sensing	79
<i>Introduction</i>	<i>79</i>
<i>Results</i>	<i>79</i>
$\gamma\delta$ T-cells are required for induction of carbohydrate transcriptional program	79
Diet alters tissue localization of $\gamma\delta$ T-cells	81
Diet alters transcriptome of $\gamma\delta$ T-cells	82
Intestinal $\gamma\delta$ T-cells form 4 transcriptionally distinct clusters	82
Signals regulating $\gamma\delta$ T-cell response to diet	82
$\gamma\delta$ T-cells regulate carbohydrate transcriptional program through regulation of IL-22 by ILC3s	84
Tuft cells regulate epithelial transcriptional response to diet	85
<i>Summary & Discussion.....</i>	<i>86</i>
Chapter 5: Host Responses to Dietary Manipulation of Commensal Microbiota.....	104
<i>Introduction & Background.....</i>	<i>104</i>
<i>Results</i>	<i>105</i>
Diet rapidly alters the composition and tissue localization of the commensal microbiota.....	105
Host responses to dietary manipulation of commensal microbiota	106
AhR and PXR are required for host response to dietary manipulation of commensal microbiota.....	107
<i>Summary & Discussion.....</i>	<i>107</i>
Chapter 6: Summary & Perspectives	114
<i>Introduction</i>	<i>114</i>
<i>Principles of adaptability in the small intestine epithelium</i>	<i>115</i>
<i>Conclusions.....</i>	<i>122</i>
<i>Questions for Future Study.....</i>	<i>125</i>
Chapter 7: Materials and Methods.....	134
Appendix 1: Custom Animal Diet Nutritional Information	149
Appendix 2: qPCR primers	150
References	153

Acknowledgements

This dissertation would not have been possible without the support and encouragement of my incredible community of mentors, colleagues, friends, and family.

First, to my mentor, Dr. Ruslan Medzhitov – you are a brilliant, inspiring, and creative scientist. You have encouraged me to think outside convention, to explore beyond what is fashionable, and to never be limited by the boundaries of what others believe is possible. Thank you for teaching me how to identify important questions, how to synthesize complex ideas, how to elegantly and precisely test a hypothesis, and how to effectively communicate the complexities of the natural world to others. I will be forever grateful to you for your mentorship and support – being your student has been the opportunity of a lifetime.

To my thesis committee – Dr. Andrew Goodman, Dr. Andrew Wang, Dr. Fred Gorelick, and Dr. Noah Palm – thank you for your wisdom, generosity, patience, and encouragement. Each of you has inspired me, challenged me, and helped me grow as a scientist. I have learned so much from each of you; thank you for the countless hours of committee and one-on-one meetings, for your feedback on my ideas and advice on experiments. I feel incredibly fortunate to have had such a talented group of scientists guiding me over the past five years.

I am grateful to each and every member of the Medzhitov Lab, past and present. You are a brilliant, kind, diverse community of passionate and curious scientists, and it has been an

honor to call you my colleagues. To Dr. Yasutaka Okabe – thank you for teaching me to be meticulous in everything I do, no matter how trivial. To my classmate, Dr. Harding Luan, I am grateful for your friendship, your encouragement, and your unending curiosity. To Jaime Cullen, Dr. Ruth Franklin, Dr. Esther Borges Florsheim, and Dr. Naomi Philip – my scientific sisters – you are brilliant, strong, talented women scientists. I consider each of you to be a role model, and I am so lucky to call you my friends.

To the many scientists who believed in me before I believed in myself – Ms. Mary Kush, Dr. Bruce Walker, Dr. Richard Losick, Dr. Eric Rubin, and Dr. Amanda Martinot – thank you for your mentorship, your encouragement, your wisdom, and your generosity.

The studies presented here would not have been possible without the support of many important collaborators in- and outside the Medzhitov Lab. Thank you to Dr. William Khoury-Hanold, for being a friend and role model to me before I even joined the lab, and for your tireless efforts and sage advice at and beyond the bench. I am deeply indebted to Dr. Jaechul Lim and Dr. Scott Pope for much of the bioinformatics analysis presented here. To my collaborators at The Rockefeller University, Dr. Bernardo Sgarbi Rice and Dr. Daniel Mucida – thank you for welcoming me into your lab, and for your generosity and expertise in the imaging studies presented in this dissertation. My collaborators at the Broad Institute – Dr. Chris Smillie, Dr. Moshe Biton, and Dr. Aviv Regev – performed the single-cell epithelial sequencing analysis presented here, and are trailblazers in the field of intestinal biology. Thank you to Lauren Gonzalez, a Graduate Writing Fellow in the Poorvu Center for Teaching and Learning at Yale, for her enormously helpful comments on many

sections of this dissertation. Finally, I am grateful to the many members of the lab who have supported this project in ways big and small – John Shanabrough, Chuck Annicelli, Sophie Cronin, Cuiling Zhang, and Shuang Yu.

To the many friends I have made throughout my time at Yale – you have made graduate school one of the most meaningful experiences of my life. Thank you to Aileen Lee for being by my side since our interviews, and for the years of laughter over many, many glasses of wine. To my dear friend, Dr. Rachel Zwick – I feel so lucky to have met you and to have bonded over triathlon training, science communication, and the fascinating world of epithelial tissues. You are an exceptional scientist and a loving friend, and I feel grateful to have you in my life.

To my beautiful community of friends – Alyssa Yamamoto, Amanda Kersen, Daniel Pellerin, Daniel Selgrade, Kemi Ajisekola, Andrea Lynch – thank you for supporting me throughout this long journey through graduate school, and for the many therapeutic escapes to New York City.

To my vibrant, beautiful, Sullivan and Cumberbatch families – as Sasha likes to say, I won the family lottery. I am so fortunate to have come from a long line of strong, Black men and women, and to have been surrounded by love and laughter each day of my life.

To my brother, Armando Sullivan – you are my first and greatest friend. Your brilliance, compassion, creativity, and fearlessness inspire me every day. Thank you for always

listening without judgement, for being my companion on so many adventures, and for encouraging me to be the best version of myself.

Finally, to my loving parents, Karen and Rogelio Sullivan – words cannot express how grateful I am for the countless sacrifices you have made to make me the woman I am today. Thank you for teaching me that hard work is more important talent, to never back down from a challenge, to stay humble, practice gratitude and generosity, to be proud of who I am, to be unapologetically different, and to make my voice heard. This work is as much yours as it is mine.

PREVIEW

Dedication

I dedicate this dissertation to the activists and trailblazers, thought leaders and freedom fighters, and all others, past and present, working to bend the arc of the moral universe towards justice.

Your struggle is my inspiration.

PREVIEW

List of Figures

Figure 1.1: Digestive design reflects species ecology.	5
Figure 2.1: Food allergy as a biological food quality control system.....	27
Figure 2.2: Conditional value of food components	30
Figure 2.3: Food sensing in the GI tract	34
Figure 2.4: Food selection as a function of internal and external states.	38
Figure 2.5: Conditioned taste aversion versus allergic sensitization.	41
Figure 3.1. Carbohydrate availability drives expression of carbohydrate transcriptional program.	70
Figure 3.2: Diet alters composition of epithelial compartment.	72
Figure 3.3: Annotation of epithelial cell types by scRNAseq.	73
Figure 3.4: Epithelial transcriptional response to diet in germ-free mice.....	74
Figure 3.5: Role of epithelial sensors in transcriptional response to diet.	75
Figure 3.6: Diet supersedes circadian regulation of carbohydrate transcriptional program.	76
Figure 3.7: Cytokine receptor expression on small intestine epithelial cells.....	77
Figure 3.8: Inflammation regulates expression of carbohydrate transcriptional program.	78
Figure 4.1: $\gamma\delta$ T-cells are required for induction of carbohydrate transcriptional program.	89
Figure 4.2: Role of T-cells and ILCs in epithelial transcriptional response to diet.	91
Figure 4.3: $\gamma\delta$ T-cell response to diet.....	92
Figure 4.4: Distribution of $\gamma\delta$ T-cells along crypt-villus axis.	93
Figure 4.5: scRNAseq of $\gamma\delta$ T-cells.....	94
Figure 4.6: Transcriptional response of $\gamma\delta$ T-cells to diet.	95
Figure 4.7: Jagged2 regulates intestinal epithelial response to diet.....	97
Figure 4.8: IL-15 regulates intestinal epithelial response to diet.....	98
Figure 4.9: T-cell insulin receptor signaling regulates intestinal epithelial response to diet.	99
Figure 4.10: $\gamma\delta$ T-cells regulate carbohydrate transcriptional program through suppression of IL-22.	100
Figure 4.11: Th17 cells do not produce IL-22 in response to diet.	102
Figure 4.12: Tuft cells regulate carbohydrate transcriptional program.	103
Figure 5.1: Diet rapidly alters gut microbial community composition.....	109
Figure 5.2: Diet alters tissue localization of commensal microbiota.....	110
Figure 5.3: Colon IL-6 and gastrointestinal transit time following dietary manipulation of commensal microbiota.	111
Figure 5.4: Diet alters bacterial IgA coating.....	112
Figure 5.5: PXR and AhR are required for host response to dietary manipulation of commensal microbiota.	113
Figure 6.1: Principles of adaptability in the small intestine epithelium.	116

List of Abbreviations

ABC	ATP-binding cassette
AgRP	agouti-related peptide
AHR	aryl hydrocarbon
BTNL	butyrophilin-like
CBC	crypt base columnar cell
CCK	Cholecystokinin
cDC	classical dendritic cell
CGRP	calcitonin gene-related peptide
CNS	central nervous system
COX	cyclooxygenase
CS	conditional stimulus
CTA	conditioned taste aversion
DAPI	4',6-diamidino-2-phenylindole
DRG	dorsal root ganglion
EEC	enteroendocrine cell
EGF	epidermal growth factor
ELISA	enzyme-linked immunosorbent assay
EpCAM	Epithelial cell adhesion molecule
FABP	fatty acid binding protein
FQC	food quality control
GAP	goblet cell associated antigen passage
GI	gastrointestinal
GIP	gastric inhibitory peptide
GLP	glucagon like-peptide
GPCR	G protein-coupled receptor
HMO	human milk oligosaccharide
IEC	intestinal epithelial cell
IEL	intraepithelial lymphocyte
IFN	interferon
Ig	immunoglobulin
IGF	Insulin-like growth factor
IL	interleukin
ILC	innate lymphoid cell
IPA	ingenuity pathway analysis
ISC	intestinal stem cell
LP	lamina propria
LPS	lipopolysaccharide

LTP	lipid transport protein
M cell	microfold cell
MAIT	mucosal associated invariant T
MHC	major histocompatibility complex
MyD88	Myeloid differentiation primary response 88
NK	natural killer
NMU	neuromedin U
NOD	non-obese diabetic
NTS	nucleus tractus solitarius
OUT	operational taxonomic unit
PAF	platelet activating factor
PBN	parabrachial nucleus
Poly I:C	polyinosinic:polycytidylic acid
POMC	proopiomelanocortin
PR	pathogenesis related
PRR	pattern recognition receptor
PSM	plant secondary metabolite
PUL	polysaccharide utilization loci
PXR	pregnane X receptor
ROR	RAR-related orphan receptor
SCFA	short chain fatty acid
scRNAseq	single-cell RNA sequencing
SFB	segmented filamentous bacteria
SGLT	sodium glucose transport protein
TA	transit amplifying
TCR	T-cell receptor
Tfh	follicular T helper
TGF	transforming growth factor
TLR	toll like receptor
Treg	regulatory T-cell
TSLP	thymic stromal lymphopoietin
tSNE	t-dependent stochastic neighbor embedding
UCS	unconditional stimulus
UR	unconditioned response
VANM	vancomycin ampicillin neomycin metronidazole
ZT	Zeitgeber time

Chapter 1: Introduction

The digestive tract is an ancient structure conserved across metazoans that facilitates the procurement of nutrients from the environment. In direct contact with the outside world, digestive tissues are also a site of exposure to pathogens and toxins, necessitating multilayered systems of host defense. The design and organization of digestive systems are highly diverse, mirroring diverse species ecology and nutritional strategies. In mammals, the gastrointestinal (GI) tract consists of several specialized organs that each contributes a specific step in the digestive process. The largest of these is the small intestine, which carries out the final steps in nutrient procurement, and is composed principally of a single-layer of absorptive and secretory epithelial cells that self-renews every 4-5 days (1). Intimately coupled with the intestinal epithelium are the largest population of immune cells of any organ in the body, the enormous sensory capacity of the enteric nervous system, sometimes referred to as the “second brain,” and the trillions of commensal microbes whose constitutive colonization of the GI tract is a fundamental feature of mammalian physiology (2-4). The exquisite coordination of these diverse cell types balances the fortification of a barrier against potentially lethal environmental threats with the absorption of dietary nutrients that are essential for survival. This dissertation examines the cellular and molecular mechanisms that link nutrient uptake and host defense in the intestine.

Ecological physiology of the gastrointestinal tract

The logic underlying the organization and design features of digestive systems is best understood through the lens of evolutionary ecology. In (5), William H. Karasov and

colleagues propose three unifying principles for understanding the ecological physiology of these systems:

(1) *Variation in the nutritional value and chemical composition of foods drives diversification of digestive systems.*

Across species, the presence and number of enzymes and transporters for a given nutrient are positively correlated with the level of the corresponding nutrient in an animal's diet (5). For example, carnivores, whose diet consists primarily of protein and lipids, have lower rates of intestinal glucose uptake than other vertebrates, and changes in copy number of the epithelial glucose transporter SGLT1 mirror the relative abundance of carbohydrates across diets (5). Furthermore, copy number variation in amylase, which carries out enzymatic digestion of starch, is observed across primates – humans, whose diets are high in starch-rich storage polysaccharides, have more copies of salivary amylase than do chimpanzees or bonobos (5). Additional variation in the expression level of specific enzymes can be observed across populations within a given species. A familiar example is the preponderance of lactose intolerance across adult mammals, following the cessation of lactation and introduction of solid food, due to diminished expression of intestinal lactase upon weaning. In human populations historically associated with domestic ungulates (cows, sheep, and goats), however, polymorphisms in lactase regulatory regions confer an increased frequency of adult lactose tolerance (6).

In addition to variations in the number and expression level of digestive enzymes, animals also differ in the organization and morphology of their digestive systems in a manner that

reflects the nutritional composition of their respective diets (5). Herbivores, whose diets contain an abundance of structural carbohydrates refractory to digestion, generally have longer digestive tracts than carnivores of comparable body size (5). This length affords adequate time for the digestion of these refractory materials.

(2) Simplified models clarify the complex array of digestive forms observed across metazoans.

Digestive strategies can be summarized in three categories: (1) catalytic digestion, which relies on the activity of endogenous enzymes for nutrient harvesting; (2) phenotypic plasticity, in which digestive activity is adjusted to according to diet composition; (3) microbial fermentation, in which resident bacteria of the gut microbiota extend the enzymatic capacity of their host (5). Species differences in the relative utilization of each strategy accord with the chemical composition of different foods.

Penry and Jumars categorize digestive systems as belonging to one of three types of chemical reactors: batch reactors, such as the gastric cavity of hydra; plug flow reactors (PFRs) such as the tubular intestine of most vertebrates; and continuous flow stirred tank reactors (CSTRs), such as the rumen of cows (7). Each of these reactor types is optimized for different nutritional strategies. PFRs are best suited for digestion that involves catalytic activity of endogenous enzymes, while CSTRs maximize fermentation for those animals who rely heavily on the catalytic activity of microbial enzymes (5, 7).

Additional models help explain the relationship between different variable features of digestive systems. The efficiency of nutrient extraction, which confers positive fitness, is defined by Karasov and colleagues as follows (5):

$$\text{Extraction efficiency} \propto \frac{\text{reaction rate} \times \text{digesta retention time}}{\text{concentration of reactants} \times \text{reactor volume}}$$

This equation illustrates the relationship between nutrient extraction efficiency and the size of different digestive organs (e.g. reactor volume) versus diet (e.g. concentration of reactants), and formalizes the relationships between diverse digestive forms and diets across animals.

(3) *Digestive design accords with the “economy of nature.”*

Digestive organs are energetically costly to maintain – in vertebrates, the digestive tract and liver can account for up to 25 % of total energy expenditure (5). Principles of economic design therefore help explain variation in digestive features across species (5). Accordingly, the size and performance of a given digestive system should be matched to the intake and nutrient density of its corresponding foods (5). In conjunction with the two principles outlined above, the “economy of nature” dictates that individual digestive features are designed to efficiently process a limited number of foods in accordance with species ecology (5). These features include the size and complexity of the digestive system, the elaboration of specialized digestive organs, the relative reliance on microbial fermentation, and the expression and number of enzymes and transporters for the breakdown and absorption of individual nutrients. A critical point is that, for humans and other omnivores, each of these features is adaptable to the availability and selection of

different foods, in accordance with the principles defined above. The mechanisms underlying the adaptability of each of these features are the focus of this dissertation.

In summary, the design of digestive systems is dictated by species ecology, with animals who consume specialized diets having particular features of the GI tract exaggerated to meet their nutritional needs. For generalists, animals that consume a wide variety of food sources, digestive systems are flexible, and enable adaptability to the shifting consumption of different

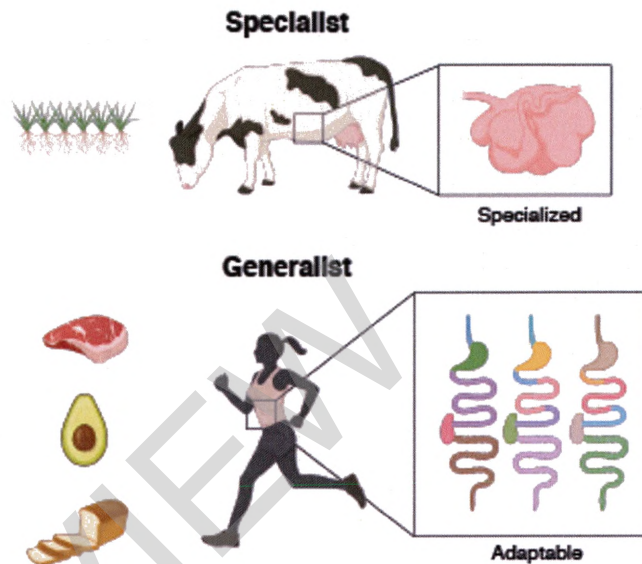


Figure 1.1: Digestive design reflects species ecology.

nutrients from day to day and over the lifespan of the organism (Figure 1.1). The cellular and molecular mechanisms that confer this adaptability are incompletely understood. How and whether the mechanisms that confer efficiency in nutrient uptake interact with systems of host defense, the other major function of the GI tract, are largely unknown. I explore each of these questions in subsequent chapters in this dissertation. In the remainder of this Chapter, I review the major epithelial and hematopoietic cell types that contribute to nutrient uptake and host defense, and briefly discuss links between diet, immunity, and commensal microbiota.

Intestinal epithelium

In mammals, the task of nutrient absorption is accomplished through the coordinated activity of multiple organs in the GI tract and can be summarized in three phases. In the cephalic phase, aroma, sight, smell, and taste of food trigger anticipatory responses along the length of the GI tract to prepare for the incoming food bolus (8-10). During the gastric phase, food is mechanically and chemically disrupted through the action of churning and gastric acid secretion in the stomach (8, 11). Finally, in the intestinal phase, the food bolus enters the duodenum where it is met with bile acids secreted from the gallbladder that aid in lipid emulsification, as well as pancreatic proteases, amylases, and lipases, which act on proteins, starch, and lipids, respectively (8). Following enzymatic digestion in the duodenum, macronutrient substrates are further digested by enzymes expressed on the brush border of absorptive enterocytes in the jejunum and proximal ileum, allowing for their final absorption via transporters expressed on the apical surface of absorptive epithelial cells called enterocytes (8, 12). Nutrients are subsequently secreted across the basolateral enterocyte membrane where they enter systemic metabolism (8). The small intestine epithelium therefore sits at the intersection of the external and internal environments, the site at which ingested nutrients are absorbed and distributed throughout the organism, and a principal line of defense against external threats.

The small intestine is organized into units called crypts, invaginations in the tissue that house intestinal stem cells at their base, and villi, protrusions into the lumen that are composed of differentiated mature epithelial cells (13). Crypts house the intestinal stem cell niche, which includes epithelial stem cells, Paneth cells, and mesenchymal cells.

Epithelial cells become more differentiated as they move up the crypt – villus axis, directed by signals that will be discussed later. Differentiated cells (with the exception of Paneth cells) migrate upwards towards the villus tip, and apoptotic cells are shed into the lumen, a process called anoikis, 3-5 days after their birth (13). It is likely that this lifespan may have exceptions for specialized secretory epithelial cells.

The small intestine epithelium is a highly dynamic tissue that self-renews every 4-5 days from a pool of constantly cycling epithelial stem cells called crypt base columnar (CBC) cells (13). These cells express the surface receptor Lgr5, and numerous genetic tools using this marker have enabled researchers to probe the biology of intestinal stem cells with precision (1). The rapid self-renewal of the intestinal epithelium is understood to enable its resilience to damage by environmental insults and the digestive process (13). In Chapter 6, I propose that in addition to protecting the tissue from environmental insults, rapid self-renewal allows for plasticity in the cellular composition of the epithelium itself, thereby enabling *adaptability* to the constantly shifting environment.

Intestinal epithelial cells (IECs) can be divided into two main lineages: absorptive and secretory. Absorptive cells include enterocytes and microfold (M) cells, and the secretory lineage includes enteroendocrine cells (EECs), goblet cells, Paneth cells, and tuft cells (13). The self-renewal and lineage specification of intestinal epithelial cells are controlled by key signaling pathways, most notably Wnt, Notch, EGF, and BMP. Wnt ligands are expressed in a gradient from the crypt, where they are most highly expressed, to the tip of the villus (1, 14). Wnt signaling through the receptor complex including Frizzled, Lpr5/6

on ISCs controls self-renewal of ISCs (13). BMPs exist in a reverse gradient to Wnt ligands, reaching their highest concentration at the villus tip, and promote differentiation over proliferation of intestinal stem cells (13). EGF signaling via ligands EGF and TGF α controls the proliferation rate of ISCs (13). Finally, Notch signaling by ligands DLL1 and DLL4 controls the fate choice between absorptive and secretory lineages (13). Notch signaling blocks the differentiation of secretory cells and maintains the ratio of absorptive to secretory cells in the epithelium (13).

Enterocytes

Approximately 80% of the intestinal epithelium is composed of absorptive enterocytes (13). These cells express brush border enzymes and nutrient transporters that carry out the digestion and uptake of dietary nutrients (8). Specifically, enterocytes express oligosaccharidases, peptidases, and fatty acid binding proteins that carry out the final steps in digestion of polysaccharides, proteins, and lipids, respectively (8). Importantly, digestion of lipids involves the formation of chylomicrons within enterocytes that are further secreted across the basolateral membrane, following which they enter the lymphatics (8). Monosaccharides, peptides, and amino acids are absorbed across the apical membrane of enterocytes by specialized transporters, and enter portal circulation following transport across the basolateral membrane (8). The degree to which brush border enzymes and transporters are expressed heterogeneously across enterocyte, and whether enterocytes can be specialized for the absorption of different nutrients, are currently unknown.

Microfold cells

Microfold (M) cells are a specialized subset of absorptive epithelial cells that are located on top of Peyer's Patches, secondary lymphoid structures distributed along the length of the small intestine (13). M cells transport luminal antigen to immune cells within the Peyer's Patches, which gives rise to oral tolerance (15). M cell development is driven by RANK ligand produced by stromal cells in the Peyer's Patch (13).

Paneth cells

Paneth cells are secretory epithelial cells that reside at the base of small intestine crypts. Along with underlying mesenchymal cells, Paneth cells constitute the niche for intestinal stem cells (13). Unlike other mature intestinal epithelial cells, Paneth cells migrate downward after differentiation, a process mediated by ephrinB2 and ephrinB3 (13). Within the base of the crypts, Paneth cells sit adjacent to CBCs in alternating units. Here, they produce Wnt ligands, EGF, and Notch signals that maintain the intestinal stem cell pool (13). In addition to their role in the maintenance of intestinal stem cells, Paneth cells secrete antimicrobial compounds including defensins, phospholipase-A2, lysozyme, and the antimicrobial lectins Reg3 β and Reg3 γ (16, 17). These compounds protect CBCs from microbial attack, and are also secreted into the lumen where they constitute an antimicrobial barrier, in conjunction with the mucus layer (18). Paneth cells have a longer lifespan than other mature epithelial cells, surviving for 1-2 months after their migration to the crypt base (13). Paneth cell differentiation depends on expression of the Wnt target gene Sox9, as well as MAPK signaling (13).

Goblet cells

Goblet cells are found at the highest frequency of all secretory epithelial cell types (13). Their differentiation depends on the transcription factor SPDEF, and hyperplasia can be driven by the type-2 immunity cytokines IL-4 and 13 (19). The principal role of goblet cell is secretion of mucins from secretory granules, the most abundant of which is MUC2 (20). Mucins are highly glycosylated proteins that form a gel-like matrix that constitute a physical barrier against microbes in the lumen (20). Microbial signals are required for proper development of the mucus barrier, and mucus glycans form a metabolic niche for specialized mucinophilic commensal organisms (21, 22). The small intestine contains a single mucus layer, while the more heavily colonized colon has a largely sterile, inner mucus layer, and an outer layer that is colonized by certain commensal microbes (23). In addition to their function in barrier defense through the secretion of mucus, goblet cells have been reported to play an important role in the uptake of luminal antigens and subsequent induction of oral tolerance through the activity of goblet cell associated antigen passages (GAPs) (24).

Tuft cells

Tuft cells are rare, isolated, chemosensory epithelial cells found at mucosal surfaces. In the small intestine, they constitute <0.4% of the epithelium (13). Named for the microtubule-rich cluster of microvilli that form a “tuft” on their apical membrane, they were first identified over 50 years ago, and only in recent years has their biology been defined in molecular detail (25). Tuft cells are now defined as secretory epithelial cells that express