

THE SCOVILLE SPLICE LIBRARY · VOLUME V

The Flavor Atlas

Forty-two territories. Eight meridians. *The whole map of taste.*

The master visual index of designed flavor — forty-two engineered organisms down the side, eight receptor axes across the top, and every intersection between them surveyed, scored, and drawn to one scale. The coffee-table reference for a world we are still finishing.

SCOVILLE SPLICE · GROWN BY OUR FAMILY. ENGINEERED FROM SCRATCH.

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Opening essay · The map and the territory

Long before anyone drew a coastline, people knew the coast by walking it. They knew which cove held fish, which headland took the wind, where the fresh water ran under the shingle — a whole geography carried in the body, exact and unwritten, impossible to hand to anyone who had not walked it too. Taste has lived like that for the entire history of our kind. Every cook our family has ever loved knew their own country by heart: the precise ripeness of a tomato on the third hot day, the moment a clove of garlic turns from sharp to round in the oil, the way a chili's warmth arrives, blooms, crests, and goes. A deep and reliable knowledge, and one that died with the knower every single time — because there was never a way to write it down.

An atlas is the technology that ends that kind of silence. It is not a picture of the world; it is a promise about the world — that the thing in front of you and the thing on the page are held in a fixed, knowable proportion, so that a distance measured on paper is a distance you can trust on the ground. Give a place two numbers and you have given it an address. You can send someone there who has never been. You can return to it exactly. You can, if you are patient and a little audacious, decide to build a road to it before it exists.



The founders in the research greenhouse at dawn — the walk where the question that became this atlas was first asked aloud.

The Iyengar Flavor Index gave taste its first coordinates. Eight axes, one for each of the receptor pathways through which a plant actually speaks to the body — heat through TRPV1, sweetness through the TAS1R2·TAS1R3 pair, umami through mGluR1, and five more — and on each axis one honest number: not how much of a compound a food contains, but how *loudly* that compound speaks to the nerve. The formula underneath is almost plain enough to embarrass:

> **$IFI = 1{,}000 \times EC_{50}(\text{reference}) \div EC_{50}(\text{candidate})$**

EC_{50} is the concentration at which a stimulus drives its receptor to half of its full response — the physical, unsentimental measure of loudness. Invert it against a fixed reference, scale the ratio by a

thousand so the everyday numbers are whole and friendly, and loudness becomes a coordinate. A chili, a tomato, and a cup of tea can at last be read against one another on the same sheet, in the same units, without a single word of poetry having to carry the weight it was never built to carry.

This book is the sheet. Forty-two organisms we have tuned, drawn down the left margin; eight axes ruled across the top; and in the cells between them, every place where a living plant meets a human receptor — **three hundred and thirty-six intersections** (forty-two times eight), each one a question we can now ask precisely and, more and more often, answer. The axes are the meridians. The receptors are the legend. The IFI is the scale bar that holds the whole page to one proportion, so that nothing on it can lie about its size. And at the far margin, past the surveyed country, is the terra incognita that every honest atlas carries at its edge: the **sixty-four** organisms we have charted on paper and not yet walked.

A word on what separates an atlas from a catalog, because the difference is the whole reason this particular book exists. A catalog is a list of things you can buy; it answers *what is for sale*, and when the stock changes it is obsolete. An atlas answers a deeper and more durable question — *where things stand in relation to one another* — and that relational knowledge does not expire when the inventory does. The forty catalogs of this company sell the constructs; this volume maps the country they belong to. It is organized, as any atlas is, into three readings of one survey: the index at the back of this book, which lets you find any organism, axis, cultivar, compound, or intersection by name; the master cross-reference that threads this volume to every other in the library, so that *kokumi* looked up here points you to the garlic monograph, the savory-depth intersection, and the broth in the vegetarian kitchen all at once; and the living web of entity pages where each coordinate — one umami, one tomato, one SS-0096 — resolves to a single canonical place the whole library points toward. One survey, read three ways. That triple structure is why a map of three hundred and thirty-six cells can stay coherent across sixty-four books: nothing is defined twice, and everything agrees.

We want to say plainly, here at the front, what kind of book this is and is not. It is a reference — the master index, the leave-behind, the volume you keep on the table and open to settle an argument. It is not a manifesto and not a memoir. The warmth in it is the warmth of people who love the living thing they study; the rigor in it is our way of respecting you enough to show our work. Those two are not in tension. They never were. A map drawn with love and a map drawn to scale are the same map, if the cartographer is any good — and we have tried, across every one of these pages, to be good.

There is one more thing an atlas quietly insists on, and it runs under every chapter here without ever being the subject until the very end: that the country is worth the care of mapping it at all. We grow these organisms to carry the most flavor they honestly can, and in the same gesture, by the same logic of the same pathways, to carry the most nourishment they honestly can — because to us those have

never been two projects. You do not have to believe that to use this atlas. The coordinates are true regardless. But it is why we drew it, and we would rather you knew.

Turn the page. The survey comes first — the instruments, the projection, the meridians. Then the territories, one family at a time. Then the places where the meridians cross, which is where the design actually lives. Then the edge of the known world, which is the most honest and the most exciting part of any map ever made.



PART I OF IV

The Projection

IFI · EC_{50} · ESM2 · genome-scale flux balance · the eight meridians · how to read a plate

Chapter 1 · The Graticule — *the number that holds the sheet to scale.*

Every map is a lie you have agreed to tell carefully. The earth is a sphere; a page is flat; something has to give, and the cartographer's whole art is choosing *what* gives so that the thing you need to measure stays true. A projection is that choice made explicit — a rule for turning the round world into a flat grid of meridians and parallels you can lay a ruler across. The Iyengar Flavor Index is the projection of this atlas, and the graticule — the ruled grid of lines every reading is plotted against — is the single equation we keep returning to, because everything downstream inherits its discipline.

Start with the honest problem. A tomato warm from the vine is a conversation of several hundred volatile and non-volatile compounds, and your tongue does not count molecules. It reports *loudness*: how hard each compound leans on the receptor it fits. Two foods can hold the very same concentration of a sweetener and taste a world apart in sweetness, because the molecules differ in how tightly they seat into the TAS1R2·TAS1R3 pocket and how efficiently that seating opens the downstream signal. Concentration is an inventory. Perception is a transaction. The Index measures the transaction.

The instrument for that is the dose–response curve. Expose the receptor — in a cell line, in a tissue preparation, in a validated panel — to a rising ladder of concentrations and record the response at each step. The points fall on a sigmoid, flat at the bottom, steep through the middle, flattening again at saturation, and the one number that summarizes the whole curve is **EC_{50}**: the concentration that produces half of the maximum response. A small EC_{50} means the receptor answers at a whisper — the compound is *loud*. A large EC_{50} means you must shout — the compound is *quiet*. Loudness and EC_{50} are inverses, and that inversion is the hinge of the entire scale.



The sequencer bench where a coordinate begins — every reading in this atlas starts as a dose–response curve, not a number someone liked.

So we invert it, against a fixed reference, and scale by a thousand:

$$\mathbf{IFI(candidate) = 1{,}000 \times EC_{50}(reference) \div EC_{50}(candidate)}$$

Read it slowly. If a candidate has exactly the reference's EC_{50}, the ratio is one and the score is **1,000** — the pin at the center of the graticule, the equivalent of the prime meridian running through zero. If the candidate is twice as loud (half the EC_{50}), the score is **2,000**. Half as loud, **500**. The scale is linear in loudness and anchored to a physical reference, which is what lets a heat reading and a sweetness reading sit on the same sheet without either one bullying the other. The thousand is cosmetic — it keeps the everyday numbers whole — but the ratio is the physics.

A worked reading, so the abstraction has a body. Take IFI-H, the heat meridian, whose receptor is TRPV1 and whose reference is a native wild-type capsaicin response.

CANDIDATE	EC_{50} (RELATIVE TO REFERENCE)	LOUDNESS RATIO	IFI-H
Reference wild type	1.00	1.00	1,000
Shishito, field-grown	25.0	0.04	~40
Blaze · SS-0091	0.38	2.63	2,630
Firestorm · SS-0094	0.287	3.49	3,490
Phoenix · SS-0096	0.238	4.20	4,200

The shishito and Phoenix are both peppers, both read on the same axis against the same reference, and the atlas can hold them two lines apart without distortion: one at a sunlit 40, one at 4,200, a hundredfold of loudness compressed onto a ruler you can read at a glance. That is the whole point of a projection — to make incommensurable things commensurable without pretending they are the same size.

It is worth seeing where EC_{50} actually comes from, because the number is not read off a single measurement but fitted to a shape. The dose–response curve is well described by the **Hill equation**, which relates the receptor's fractional response to the stimulus concentration:

$$\text{Response} = R_{max} \cdot [L]^n \div (EC_{50}^n + [L]^n)$$

Here [L] is the concentration of the ligand, R_max the saturated response, and **n** the Hill coefficient — the steepness of the curve, a measure of how cooperatively the receptor's subunits act. When [L] equals EC_{50} the two terms in the denominator are equal and the response is exactly half of R_max, which is the definition we started from; what the full equation adds is that EC_{50} is the midpoint of a *fitted sigmoid*, estimated from the whole ladder of concentrations with its own confidence interval, not guessed from one dose. A steep curve (high n) means a sensation that switches on sharply over a narrow range — heat behaves this way, which is why the step from pleasant to overwhelming can feel like a cliff — while a shallow curve means a sensation that builds gently, which is how sweetness tends to arrive. The Index reports the midpoint; the steepness is a second fact we keep in the lab notebook, because it governs how a flavor *feels* even when two foods share an EC_{50}.

One design choice in the scale deserves defending, because it runs against the grain of how perception is usually modeled. Perceived taste intensity does not rise linearly with concentration; it follows a **compressive power law** — Stevens' law, $\psi = k \cdot S^a$, with exponents

that for most tastes sit below one, so that doubling a compound's concentration raises its felt intensity by less than double. We could have built the Index on perceived intensity and let it compress. We did not. The IFI is linear in *receptor loudness* — in the inverse of EC_{50} — precisely because we want a measure the perceptual compression has not already folded into itself. A designer needs the untransformed quantity, the physical loudness at the receptor, because that is the lever the biology actually moves; the compression that turns loudness into sensation happens downstream, in the nerve and the mind, and it is the same for everyone's tongue. Measure the lever, not the felt result, and the number stays a tool you can design against.

Each meridian is pinned to its own reference, chosen to be stable, well-characterized, and physiologically honest, and it is useful to see them gathered:

AXIS	RECEPTOR	REFERENCE STIMULUS	READS
IFI-H	TRPV1	native wild-type capsaicin response	heat
IFI-S	TAS1R2·R3	sucrose	sweetness
IFI-U	mGluR1 · TAS1R1·R3	monosodium L-glutamate	savory depth
IFI-B	TAS2R38	a calibrated bitter ligand, scored as attenuation	bitterness silenced
IFI-K	CaSR	glutathione (a γ-glutamyl peptide)	richness
IFI-C	TRPM8	(−)-menthol	cooling
IFI-P	TRPA1	allyl isothiocyanate	pungency
IFI-A	salivary PRPs	a defined tannin, by precipitation	astringency

The heat axis carries a second scale most readers already know — the **Scoville Heat Unit** — and it is worth saying how the two relate, because the atlas uses both. The modern SHU is not the old taste-dilution panel but a chemical measurement: high-performance liquid chromatography quantifies the capsaicinoids in parts per million, and that figure times roughly sixteen gives the SHU. The IFI-H is the *receptor* reading of the same fruit — how loudly those capsaicinoids speak to TRPV1 — which is why the two track each other but are not identical; a fruit can carry its heat in a blend of capsaicin and dihydrocapsaicin that shifts the perceived shape of the burn without

moving the SHU much at all. We report SHU where tradition expects it and IFI-H where design requires it, and we never let one masquerade as the other.

Two disciplines keep the graticule honest, and we hold them hard. The first is **the fixed reference**. A relative scale is only as trustworthy as the thing it is relative to, so each axis is pinned to one reference compound and response, measured under one protocol, and that reference does not drift to flatter a result. The second is **per-axis normalization for the scorecard**: when we draw the eight-pointed plate you will meet in Chapter 4, every axis is scaled to a common ceiling of **5,000**, so that the *shape* of a flavor — which axes it leans on and by how much — reads instantly even across axes whose raw dynamic ranges differ. The radar shows proportion; the number beside it keeps the absolute truth. You need both, the way a map needs both a shape and a scale bar.

There is a temptation, with a scale this clean, to mistake it for the thing itself. It is not. IFI-H 4,200 is not the pleasure of heat any more than 44°N is the smell of a particular morning on a particular hill. The number is the address; the experience is the place; and the reason an address is worth having is that it lets you return, lets you send someone, lets you decide to build. We did not draw the graticule to replace the walk. We drew it because you cannot design a country you cannot locate — and design, not description, is what this atlas is finally for.

Chapter 2 · The Survey — *how a coastline becomes a coordinate.*

A graticule is only a promise until someone goes out and fixes the points. In cartography that work is the survey: the slow, instrument-heavy business of turning a felt coastline into a measured one, headland by headland, until the map earns the right to be trusted. Our survey is molecular, and it runs in silico before it ever runs in soil, because the space we are mapping is too large to walk. A single enzyme of three hundred residues has twenty possibilities at each position — more variants than there are atoms in a great many things we like to compare it to. You cannot grow your way across a space like that. You have to *read* your way across it first.

The reading instrument is a protein language model. We use **ESM2**, a 650-million-parameter transformer trained on tens of millions of natural protein sequences until it had internalized, statistically, what a plausible, foldable, functional protein looks like — the grammar of life's own sentences. Shown the sequence of a target enzyme, it will score every possible single-residue substitution by how much that edit is predicted to help or hurt two things at once: **catalytic efficiency** (does the chemistry get faster?) and **fold stability** (does the protein still hold its shape long enough to do the chemistry?). The product of those two — a better catalyst that also survives — is the quantity we optimize, because a brilliant enzyme that misfolds is no enzyme at all.

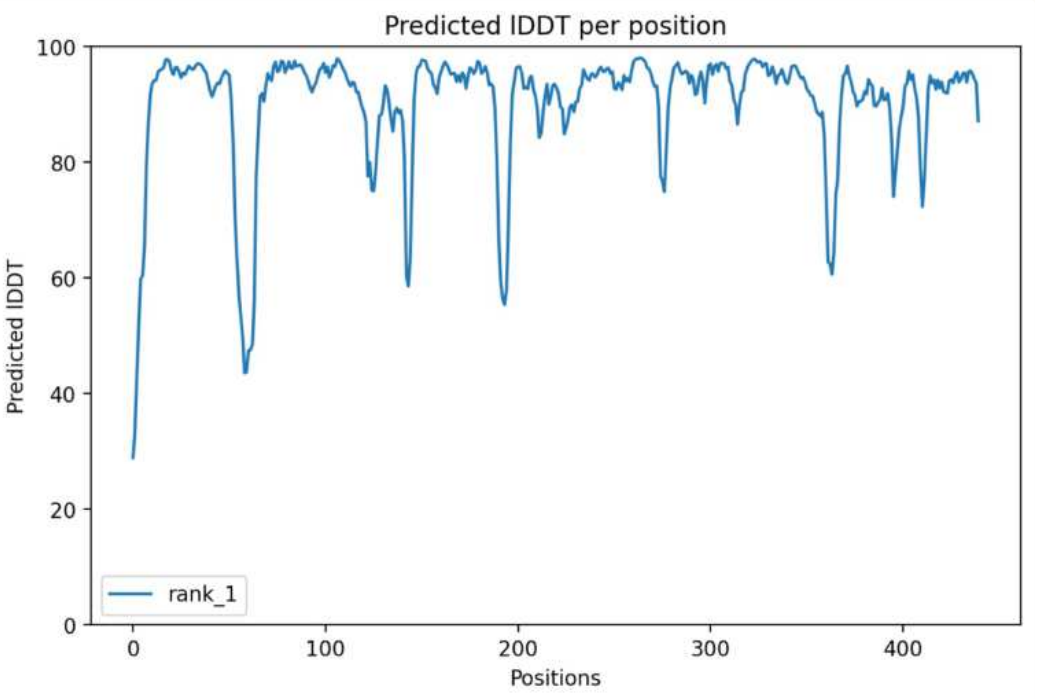


FIG. 2.1 — the Pun1/AT3 acyltransferase coloured by pLDDT model confidence. The binding domain and the active-site cleft resolve as high-confidence; the flexible loops, honestly, do not — and the map says so.

The model proposes; it does not get to decide. Each promising variant is folded — we predict its three-dimensional structure and read two confidence surfaces off the result. The first is **pLDDT**, a per-residue confidence score that tells us how sure the structure is of each position; the active site has to land in the high-confidence band or the prediction isn't worth acting on. The second is the **predicted aligned error**, or PAE — a full matrix of how confident the

model is about the relative position of every residue against every other, which is where you catch a domain that folds beautifully on its own but floats uncertainly against the rest of the protein. A clean diagonal with tight off-diagonal blocks means the parts that must hold together are predicted to hold together. It is, quite literally, a confidence map read like any other map — by its grid.

Then the question changes from *can this enzyme be better?* to *would a better enzyme even matter?* — and that is a systems question, not a protein question. A cell is a web of coupled reactions sharing a finite budget of carbon, energy, and reducing power. Speed up one step and the limit may simply move upstream to whatever now can't keep up. To find the step that actually governs output, we build a **genome-scale metabolic model** of the host and run **flux-balance analysis**: encode every known reaction as a constraint, set the objective to maximize the flavor compound, and let linear programming find the distribution of flux that the stoichiometry allows. The model returns the flux control analysis — and in the pepper our model predicts that metabolic control sits upstream in the phenylpropanoid pathway, at **4CL** (4-coumarate-CoA ligase) and **HCT/CCoAOMT**, not at the terminal Pun1/AT3 step. Pun1 is the final capsaicin synthase; it labels the product, it does not govern the rate.

Only after a variant has passed all three gates — language model, structure, flux — does it earn a place in the soil. We write it in with **CRISPR**, precisely, at the native locus, and then we measure what we actually got, because the survey is not finished until the ground agrees with the page. For the pepper, the pipeline converged on a **double variant** in the Pun1/AT3 acyltransferase — two substitutions in the shipped construct, never before combined by any breeder, because no breeder could have searched the space that found them. A third edit, C175S, was modelled as a structural annotation and is not in the shipped construct:

EDIT	EFFECT	ΔΔG (KCAL·MOL⁻¹)	STATUS
S39L	binding affinity ↑ at the N-terminal lobe	−2.1	shipped
L345G	steric relief in the active-site cleft	−1.8	shipped
C175S	prevents a disulfide-misfold pathway	−0.9	structural annotation only

A negative ΔΔG is a stabilizing edit — the protein sits lower in its energy well, folds more reliably, lasts longer at the bench. The two shipped substitutions, S39L and L345G, improve binding and stability at the final capsaicin-assembly step; our model predicts peak output of approximately **2.95 million SHU**, and together with the broader design program they target a batch-to-batch coefficient of variation of **≤7%**, against **42%** in the wild type. That second number is the one formulators circle. A loud flavor you cannot reproduce is a rumor. A loud flavor with a tight CV is an ingredient — a coordinate you can return to, which is the only kind worth putting on a map.

It is worth being precise about how a language model *scores* a mutation, because the mechanism is not magic and its limits matter. ESM2 is trained by masking residues in natural sequences and learning to predict what belongs in the gap; after training, it will assign every amino acid at every position a probability given the surrounding sequence. The effect of a substitution is then read as a **log-likelihood ratio** — the log of the probability the model assigns the mutant residue, minus the log it assigns the wild-type residue — a single number that says whether the edit moves the protein toward or away from what evolution has found workable. This is *zero-shot* variant prediction: the model has never seen our enzyme, only the grammar of proteins in general, and it generalizes from that grammar to a sequence it was never shown. We fold the likelihood signal together with an explicit **ΔΔG** estimate of fold stability, and the product is the score we rank by. The honesty of the method is in what it does *not* claim: the model proposes plausibility, not certainty, which is exactly why every proposal still has to survive the structure gate and the flux gate and, finally, the soil.

The flux question can be written as plainly as the IFI itself. A metabolic network of m metabolites and n reactions is a stoichiometric matrix $\mathbf{S}$; a distribution of reaction rates is a vector $\mathbf{v}$. At steady state nothing accumulates, so $\mathbf{S}\cdot\mathbf{v} = \mathbf{0}$, and each reaction is bounded by what thermodynamics and enzyme capacity allow, $lb \le v \le ub$. Flux-balance analysis then solves a linear program — **maximize $\mathbf{c}^{\mathsf{T}}\mathbf{v}$** subject to those constraints, where $\mathbf{c}$ selects the flavor compound as the objective — and returns the flux distribution the stoichiometry permits at maximum output. Run it, and the rate-limiting step is not a matter of opinion; it is the constraint that, when relaxed, lets the objective rise. For the pepper, our model predicts that flux control sits at the upstream phenylpropanoid steps — 4CL and HCT/CCoAOMT — which supply the vanilloid precursors to the terminal branch. Pun1/AT3 is the acyltransferase that assembles capsaicin at the final step, and improving its binding and stability through protein engineering raises efficiency at that step; but the ceiling on overall output is set by the upstream pathway gates.

The write itself is the least mysterious part and the most exacting. We edit at the native locus rather than inserting a foreign cassette, because a plant that carries only precise changes to its own genes is a cleaner thing biologically and, as Chapter 16 will note, a different thing in the eyes of the world's regulators. Depending on the edit, that means a targeted double-strand break repaired against a supplied template, or a **base editor** that converts one letter to another with no break at all, or a prime edit for the small insertions and deletions the base editors cannot reach. The guide is designed for specificity, the off-target space is searched before anything is cut, and then — the part no model can do for us — the plant is grown, and measured, and either agrees with the page or sends us back to it.

MODULE	FUNCTION	ORGANISM-SPECIFIC?
1	Target selection by flux-balance analysis	no
2	Sequence design by protein language model	no
3	Structure prediction and confidence (pLDDT, PAE)	no
4	Construct assembly and guide design	no
5	Analytics — dose–response, EC_{50}, the IFI reading	no
6	Delivery and transformation	yes
7	Terminal-enzyme pathway engineering	yes

Hold on to the shape of this pipeline, because the rest of the atlas depends on it generalizing. Of the platform's seven modules, five — target selection by flux, sequence design by language model, structure confidence, construct assembly, and the analytics that produce an IFI reading — know nothing about peppers. They are organism-agnostic. Only the last steps, the terminal enzymes that make a *particular* molecule, are species-specific. That is the technical reason forty-two territories could be surveyed with one set of instruments, and why the frontier at the edge of this book is a schedule rather than a fantasy.

Chapter 3 · The Eight Meridians — *the lines every flavor is read against.*

A map needs its lines before it needs its places. The meridians of this atlas are the eight axes of the Index, and each one corresponds to a real receptor or receptor-class through which a molecule reaches the nervous system — not a flavor word we liked, but a protein the body actually keeps on the surface of the tongue and the palate for exactly this purpose. To know the meridians is to know, mechanistically, every direction in which a flavor can be loud. Here is the full ruling of the grid.

CODE	AXIS	RECEPTOR	WHAT THE RECEPTOR READS	ACCENT
IFI-H	Heat	TRPV1	capsaicinoids; the chemistry of warmth	#B0442F
IFI-S	Sweetness	TAS1R2 · TAS1R3	sugars and sweet proteins, sugar-free	#3E7D4F
IFI-U	Umami	mGluR1 · TAS1R1·TAS1R3	free glutamate and 5′-nucleotides	#6B4E9E
IFI-B	Zero-Bitter	TAS2R38	the *silencing* of bitter ligands	#3A6B8C
IFI-K	Kokumi	CaSR	γ-glutamyl peptides; richness, continuity	#6E7A3A
IFI-C	Cool-Burn	TRPM8 · TRPV1	menthol and thermal modulation	#2F7E8C
IFI-P	Pungency	TRPA1	electrophiles; the sharp, nasal channel	#C06A3A
IFI-A	Astringency	salivary PRPs	tannins; the tactile dry finish	#8C4A6B

Walk them one at a time, because each meridian runs by its own law.

IFI-H, Heat — TRPV1. Capsaicin binds the transient receptor potential vanilloid-1 channel on the trigeminal nerve endings, the same channel that opens above 43°C and under acid. The molecule adds no heat; it lowers the channel's thermal threshold, so the body

reports a fire that is not physically there. This is the loudest-ranging meridian in the surveyed world, from a shishito near 40 to Phoenix at 4,200.

IFI-S, Sweetness — TAS1R2·TAS1R3. A class C GPCR heterodimer with a Venus-flytrap domain that closes on sugars; sweet *proteins* like brazzein and thaumatin dock differently, against the outside of the clamp, which is why a protein a thousand times the size of glucose can be far sweeter by weight. The engineering here is sweetness decoupled from sugar — steviol glycosides, mogrosides, the sweet proteins — loudness without the caloric load.

IFI-U, Umami — mGluR1 and the TAS1R1·TAS1R3 pair. Free L-glutamate is the ligand; 5′-ribonucleotides (inosinate, guanylate) are its synergists, and the synergy is not additive but multiplicative — a nucleotide locks the flytrap's closed conformation so glutamate binds harder, which is why a pinch of dried shiitake deepens a tomato broth far past what either brings alone.

IFI-B, Zero-Bitter — TAS2R38. The one meridian that measures a *subtraction*. Where the others score how loudly a thing speaks, IFI-B scores how thoroughly a bitter signal has been *quieted* — attenuation across the 20–65% band. A high IFI-B is a near-silent TAS2R38: the goitrin of a Brassica, the chlorogenic lactones of a dark roast, the iso-acids of hops, all turned down without the sugar or fat usually conscripted to mask them.

IFI-K, Kokumi — CaSR. The invisible meridian. γ-Glutamyl peptides — glutathione and its kin — are positive modulators of the calcium-sensing receptor, and they carry no taste of their own. What they do is lend *mouthfulness*: richness, continuity, the sense that a flavor has a middle and not just an attack and a finish. You never taste kokumi; you taste its absence, as thinness, and its presence, as a broth that seems to have been cooked longer than it was.

IFI-C, Cool-Burn — TRPM8. Menthol's receptor, the cold channel, opening below about 26°C and under menthol, eucalyptol, icilin. Cooling without cold — the thermal illusion run in the opposite direction from heat. We draw it as the only meridian that runs toward winter.

IFI-P, Pungency — TRPA1. The sharp, upward channel: the wasabi receptor, an ankyrin-rich sensor that electrophilic molecules open by covalently modifying cysteines near its N-terminus. Allyl isothiocyanate from mustard, allicin from garlic, cinnamaldehyde from cinnamon — pungency is a chemical reaction *with the channel*, not a mere fit, which is why it feels like an event rather than a taste. The IFI-P axis is anchored to a stated convention: AITC at a reference constant of **2.1 µM**, defined in the same spirit as the Scoville scale's dilution threshold — a fixed, agreed point that sets IFI-P = 1,000, not a measured literature value.

IFI-A, Astringency — salivary PRPs. Strictly, not a taste at all but a touch. Tannins bind and precipitate the proline-rich proteins that lubricate the mouth; lose the lubrication and you feel drag, pucker,

the clean architecture of a good tea or a structured wine. We map it as a meridian because the Index measures what the body reports, and the body reports this clearly.

The eight meridians are not read by one kind of machinery, and the differences in machinery are worth knowing, because they govern the *tempo* of a flavor as much as its loudness. Three of the axes — sweetness, umami, and kokumi — run through **class C G-protein-coupled receptors**, the large clamp-shaped proteins with a Venus-flytrap domain; these are catalytic amplifiers, slower to fire and slower to fade, which is why sweetness and savor bloom and linger rather than spike. Bitterness runs through the **class A** TAS2R family, a different GPCR architecture with twenty-five distinct human receptors tuned to different bitter ligands. Three more axes — heat, cool, and pungency — run through **TRP ion channels**, which are not amplifiers but gates: they open and let current flood directly across the membrane, which is why heat and pungency arrive *fast*, as events, and why they can overwhelm the slower GPCR sensations if a flavor is not balanced. And astringency runs through none of these — it is a mechanical, tactile signal from the loss of salivary lubrication, the one meridian read by touch rather than chemistry. A plate's silhouette is partly a map of these tempos: the TRP arms arrive first, the GPCR arms last, and a flavor you can *read as you eat it* is one whose designer respected the order.

The zero-bitter meridian deserves one more line of arithmetic, because it is the only axis that scores a subtraction and the inversion confuses people. For the seven positive axes, loudness is 1,000 × EC_{50}(reference) ÷ EC_{50}(candidate) — more loudness, higher number. For IFI-B we measure **percent attenuation** of a calibrated bitter response and map it onto the same 0–5,000 frame, so that a high IFI-B is a *low* bitter signal — the near-silencing of TAS2R38. The Index's working band for engineered attenuation is 20–65%; an unengineered bitter food reads low on IFI-B not because it is quiet but because its bitterness is loud. It is the one place in the atlas where a tall arm means an absence, and we flag it everywhere it appears, because a reader who forgets will read every coffee and cacao plate exactly backwards.

Two composite readings ride on top of the eight. **IFI-F, Full-Spectrum**, is the measure of a single organism speaking on *all eight* at once — the rarest coordinate in the atlas, carried by the line of 300 full-spectrum products and the nanoparticle-delivery work that lets eight signals arrive in proportion; it is the subject of this book's capital city. **IFI-M, Multi-axis**, is the engineering of deliberate combinations short of the full eight — the **M2** dual-axis library of **8,400** constructs and the **M3** triple-axis library of **2,800**, eleven thousand two hundred constructs whose entire purpose is to make two or three meridians sing together in one plant. The meridians are where flavor is read. The composites are where it is composed — but we are getting ahead of the survey. First, learn to read a single plate.

Chapter 4 · The Legend — *how to read a single plate.*

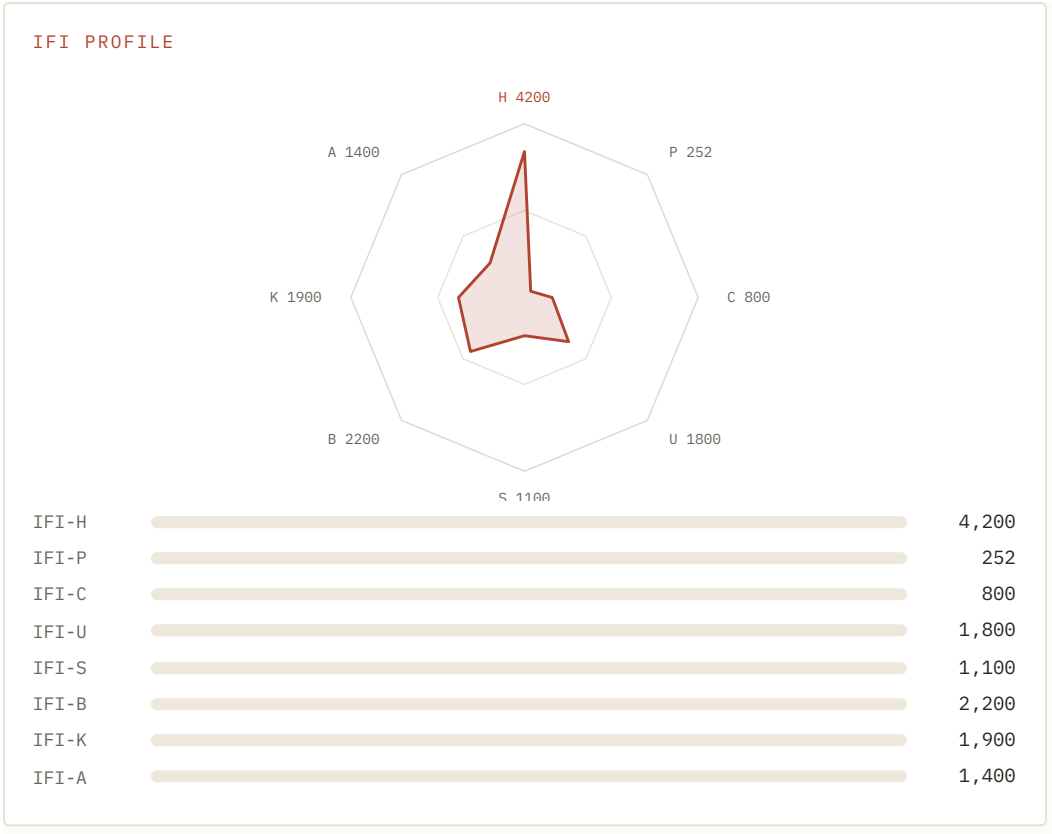
Open any atlas and the first page that matters is the legend — the small keyed box that tells you what every mark means, so that the thousand pages after it can be silent and still understood. The legend of *this* atlas is a single recurring object: the eight-axis plate. Every territory, every intersection, every flagship in this book is drawn as one, and once you can read it, you can read the whole volume at a glance. So let us read one slowly, together, before you have to do it alone three hundred times.

The plate has two parts. The first is the **radar** — eight spokes from a common center, one per meridian, in the fixed clockwise order **H, P, C, U, S, B, K, A**, each scaled to the common ceiling of 5,000 so that the *shape* carries meaning. A reading pulled far out on a spoke is loud on that axis; a reading tucked near the center is quiet. Join the eight points and the enclosed figure is the flavor's silhouette — its fingerprint, the thing you learn to recognize across a room. A lopsided star with one long arm is a specialist; a broad, filled octagon is a generalist; and a nearly perfect eight-pointed bloom is the rarest thing in the book. The second part is the **readout**, the lab-notebook block of the eight numbers themselves, because a silhouette tells you the shape and only the number tells you the size. You read the shape first and confirm it with the number, the way you read a coastline first and then check the scale bar.

Here is the one plate worth memorizing — the full-spectrum profile of **Phoenix, SS-0096**, the only surveyed organism that registers on all eight meridians at once, and the reference silhouette against which every narrower flavor in this atlas is implicitly compared:



FIG. 4.1 — Phoenix (SS-0096) on the controlled-chamber stage. The first cultivar engineered to read on all eight axes; the plate below is its exact surveyed profile.



Read it as we do. The **H** arm is enormous — 4,200, nearly the ceiling — so the eye goes there first: this is, before anything else, a heat object. But follow the figure around and it never collapses to the center the way a pure chili would. **B** at 2,200 says the bitterness that a fruit this loud would ordinarily carry has been deliberately quieted. **K** at 1,900 and **U** at 1,800 give it a savory floor, a continuity under the fire. **A** at 1,400 lends a structured, drying finish; **P** at 252 a sharp top note; **S** at 1,100 a thread of sweetness to keep the heat from reading as mere assault; and even **C**, the cool meridian, is awake at 800, a faint menthol counter-current running against the burn. No single number is the story. The *filled octagon* is the story — a flavor with no silent direction, which is precisely why it earns the composite reading IFI-F and a chapter of its own later in this book.

The radar is constructed, not drawn by feel, and the construction is worth one paragraph because it is what makes two plates comparable. Each of the eight readings is divided by the common ceiling of **5,000** and plotted as a fraction of the way out its spoke, so a reading of 2,500 lands halfway, a reading of 1,000 — the reference pin — lands at one-fifth, and the whole figure is a normalized silhouette you can lay over any other at the same scale. Beneath the radar runs the second signature object, the **heat bar**: a single horizontal rule for IFI-H alone, carrying the SHU where tradition wants it, because heat is the one axis a general audience already reads in its own units and we honor that. Radar for the shape of the whole flavor; heat bar for the one axis everyone came for. Together they are the grammar of every scored page in this library.

Once you can read one plate you can classify any plate, and three silhouettes cover almost everything in this atlas. A **specialist** is a plate with one long arm and the rest near the floor — the restored tomato, the pure mint, the black mustard; a flavor that does one thing with conviction, and the most useful kind in a working kitchen, because you can place it precisely. A **generalist** is a broad, filled figure leaning on four or five arms at moderate length — the complete-broth plates, the structured wines; a flavor with body and balance rather than a single loud claim. And the **full-spectrum** plate,

the near-perfect bloom on all eight, is the rarest of all; in the entire surveyed world there is exactly one, and it is the capital. Learn to name the silhouette before you read the numbers, the way you learn to name a coastline's shape before you measure it, and the atlas opens to you at a glance.

One reading skill is worth practicing deliberately: the **overlay**. Because every plate is normalized to the same ceiling, you can mentally superimpose two and read the *difference* — where one flavor is louder, where the other is, where they agree. Overlay the restored tomato on the supermarket tomato and the whole violet umami arm is the gap the supply chain opened; overlay a swicy intersection on a plain chili and the green sweetness arm is exactly what the intersection added. Reading by overlay is how a designer uses this book — not to admire a single plate, but to see the vector between where a flavor is and where they mean to take it. That vector is the design, drawn.

Now the one convention you must hold while you read every other plate in Parts II and III, stated plainly so nothing is smuggled. This is an atlas of territories, and a territory is larger than any single point. Each regional plate is read **at the loudest surveyed cultivar in that territory, on all eight meridians**, rounded to the atlas's working precision. Two anchors are pinned and exact: the **reference wild type sits at 1,000** on its own native axis by construction of the formula, and where a cultivar has a surveyed value in the shared Index — Phoenix's full profile above, the restored tomato's umami at 2,600, every flagship's heat — that value is reported as surveyed, not rounded toward a prettier number. An axis a plant does not speak reads in the low hundreds, *quieter than the reference*, because silence on a meridian is a real and measurable fact. The plates are rendered readings of real primary-axis assignments, not invented SKUs; they tell you truthfully which directions a territory is loud in, and roughly how loud, which is exactly what a visual index exists to do. When you want a single point surveyed to the last digit, this atlas gives you one — the capital — and tells you it is the one.

One last note on the eight colors, because they are load-bearing and not decoration. Each meridian owns a hue, fixed across the whole library: heat's brick red, sweetness's leaf green, umami's violet, zero-bitter's slate blue, kokumi's olive, cool's teal, pungency's rust, astringency's plum. A plate you have seen a hundred times becomes legible pre-verbally — you know a violet-heavy plate is a savory thing before you have read a single label. That is the legend doing its quiet work. Close it now. The territories begin.



PART II OF IV

The Territories

forty-two organisms · nine plant families · the fungal kingdom · the surveyed country, drawn family by family

Chapter 5 · The Nightshade Heartland — *where the whole method was born.*

Every atlas has a home region — the country the cartographers knew first and best, drawn in the most loving detail because it is where they learned to draw. Ours is the Solanaceae, the nightshade family, and it is no accident. The pepper is where capsaicin lives, and capsaicin is where the whole platform cut its teeth; the tomato is where we first proved the method would carry a flavor *back* into a plant that had lost it. The heartland is small on the map and vast in what it taught us. Four surveyed organisms sit here, and together they hold more engineered constructs than any other territory in the book.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Habanero	3,190	F / M	Hard
Tomato	2,040	S / U / F / M	Easy
Pepper	1,060	all eight	Native
Potato	80	B	Easy



FIG. 5.1 — The tomato, restored. IFI-U lifted from a supermarket 300 to a surveyed 2,600 through the plant's own GAD / GDH1 glutamate route — the flavor the long-haul truck took, grown back in.

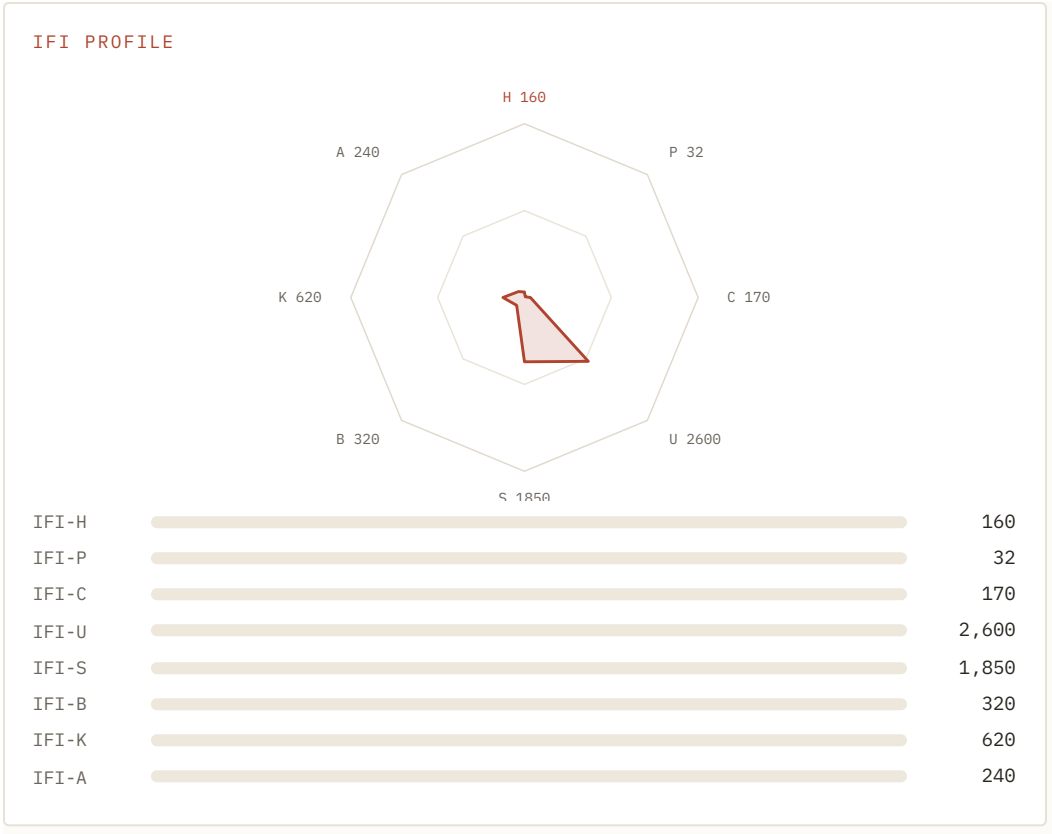
The pepper is the native speaker — the only organism in the atlas that can register on all eight meridians without a gene borrowed from anywhere else, because *Capsicum* evolved the full terminal capsaicinoid machinery and we have learned to turn each part of it up and down at will. The heat meridian runs through here from a sunlit shishito to the superhot flagships, and the whole of Part III's capital is a pepper. We draw it at the center of the heartland the way old maps drew the capital larger than the kingdom around it.

The span of that one meridian is worth laying out as a ladder, because it is the widest single axis in the atlas and the easiest to feel your way along. These are landmarks on the heat line — the wild reference types the world already knows, climbing to the surveyed summit of our own capital:

LANDMARK	APPROX. SHU	NOTE
Shishito	100–1,000	the sunlit low end (IFI-H ~40)
Jalapeño	4,000–8,000	the everyday warmth
Serrano	10,000–25,000	bright, clean heat
Cayenne	30,000–50,000	the sauce workhorse
Habanero	150,000–350,000	fruit-and-fire, the family's hot edge
Ghost (Bhut Jolokia)	~1,000,000	the old threshold of "superhot"
Phoenix · SS-0096	**~2.95M (predicted)**	our designed flagship

Read down it and you cross roughly five orders of magnitude of capsaicinoid content on a single axis — the Scoville scale is linear in that content, but the span from shishito to capital is so vast that any honest plot of it wants a logarithmic axis, the way one scale bar cannot serve a map of both a village and a continent. The heartland holds both ends of that ladder and most of what lies between, which is why we drew the whole atlas outward from here.

The tomato is the family's quiet masterpiece, and the clearest single argument for why an atlas of *designed* flavor is worth the paper. A vine-ripe tomato in late summer reads around **IFI-U 2,600** — a deep, round, almost brothy savoriness built from free glutamate the fruit accumulates as it ripens through its own **GAD** and **GDH1** enzymes, the native glutamate-handling route that every tomato already owns. The supermarket tomato, picked green for the truck and gassed to color, reads nearer **300**. Roughly ninety-three percent of the savory loudness is simply absent — not bred out on purpose, but lost to a supply chain that selected for everything except the thing you actually wanted to taste. We did not add a foreign gene to fix that. We restored the plant's own pathway to its own best expression, and the umami came home. Here is the heartland's representative plate, read at the restored tomato:



Notice the silhouette: a tall violet-and-green arm on the U and S meridians, everything else near the quiet floor. This is a specialist's plate, the opposite of the capital's filled octagon, and it is beautiful for the opposite reason — because a tomato that tastes overwhelmingly, almost shockingly, *like a tomato should* is a more useful thing in a kitchen than a tomato that tries to be eight flavors at once. The restored sweetness at 1,850 is the other half of the trick; ripe tomato flavor is a precise braid of glutamate savor and a low, clean sweetness, and restoring one without the other reads as flat. The atlas shows you the braid.

The biology underneath that braid is worth drawing, because it explains why the tomato is rated *Easy* while the pepper that shares its family is rated *Native* and nothing else comes close. Free glutamate accumulates in the tomato late in ripening, as the fruit's **GABA shunt** reverses its priorities: through the green stages the plant runs glutamate down the shunt into GABA via glutamate decarboxylase, and as the fruit turns and softens that flux falls and free glutamate rises, the savory pool filling just as the sugars and the color arrive. It is a native, regulated program — the plant already knows how to make itself delicious — and restoring it is a matter of returning the ripening regulation to its best expression rather than building a pathway from nothing. The pepper is the harder, stranger cousin: its heat lives not in the flesh but in the **placental septum**, the pale pith that holds the seeds, where specialized epidermal cells express Pun1 and secrete capsaicinoids into blister-like vacuoles. Bite the wall of a pepper and you get fruit; scrape the septum and you get fire. The atlas's loudest meridian is manufactured in the most hidden tissue of the fruit, which is a fact we never quite got over.

The two smaller members fill out the family's range. The habanero carries the family's heaviest construct load — **3,190** — and most of it is multi-axis work, the F and M territory where a single *C. chinense* fruit is pushed to speak on several meridians at once without losing

the fruity, apricot top note that makes a habanero a habanero and not merely a heat delivery device. The potato sits at the family's humble edge with a modest eighty constructs, almost all of them on the zero-bitter meridian — the attenuation of the glycoalkaloids and the dull after-bitterness that a storage tuber accumulates, so that a potato tastes cleanly of itself. It is the least glamorous plate in the heartland and one of the most quietly useful, because the floor of a great many meals is a potato, and a potato with its bitterness turned down is a better floor.

The potato's bitterness has a specific chemistry, and it is one the whole family shares in its own way: the **glycoalkaloids**, chiefly α-solanine and α-chaconine, steroidal alkaloids the plant makes to defend its tubers, concentrated just under the skin and in any patch that has greened in the light. They read bitter to TAS2R receptors, and they are the reason an old or light-struck potato tastes sharp and faintly numbing. The zero-bitter work on the potato is a careful, low attenuation — turning the glycoalkaloid bitterness down toward the clean, earthy sweetness of a good new potato — and it is careful precisely because these are defense compounds; the engineering tunes the *perception* and the balance toward the edible range rather than stripping the plant of its chemistry wholesale. It is the heartland's quietest example of a principle the whole atlas runs on: that turning a flavor down is as much design as turning one up, and often the more useful of the two.

What the heartland teaches, and teaches first, is that *restoration* and *amplification* are the same instrument pointed in two directions. The pepper is amplification — taking a plant that already shouts and teaching it to shout in eight directions. The tomato is restoration — taking a plant that has been made to whisper and giving it back its own voice. Both are the same pathway logic, the same survey, the same CRISPR-written edits at native loci. The family that gave us the loudest flavor on the map also gave us the gentlest argument for the whole enterprise: that much of what we call *designing* flavor is really just refusing to accept its loss.

Chapter 6 · The Mustard Reach — *the sharp country.*

North and a little east of the heartland, on our conceptual map, lies the largest single territory in the surveyed world by sheer number of distinct organisms: the Brassicaceae, the mustard and cabbage family, nine crucifers that between them own the pungency meridian and share a second, quieter mandate on zero-bitter. This is the sharp country — the land of the clean nasal burn that rises rather than sits, the flavor of a good mustard clearing the sinuses, of wasabi, of horseradish, of raw radish, of watercress. It is also, not coincidentally, the family where the engineering is hardest, because the chemistry here is a reaction that only happens when the plant is wounded.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Black Mustard	2,790	P / M	Hard
Broccoli	380	B / M	Moderate
Broccoli-Kale	280	B	Hard
White Mustard	200	P	Hard
Watercress	120	P	Hard
Cabbage	40	B	Moderate
Kale	40	B	Moderate
Radish	40	B	Hard
Rapeseed	40	B	Hard



FIG. 6.1 — Black mustard, the territory's loudest voice on the pungency meridian. The sharpness is not stored; it is manufactured in the instant of damage.

Here is the mechanism that defines the whole reach, and it is one of the most elegant in the plant kingdom. A Brassica stores its sharpness as two separated, inert components: a **glucosinolate** — in black mustard, *sinigrin* — held in one cellular compartment, and the enzyme **myrosinase**, a thioglucosidase, held in another. Intact, the plant tastes of almost nothing threatening. But bite it, crush it, grate it, and the compartments break; myrosinase meets sinigrin and cleaves it, and the unstable product rearranges into **allyl isothiocyanate** — AITC, the pungent principle. The sharpness is not a stored flavor. It is a *defense reaction*, triggered by the very act of

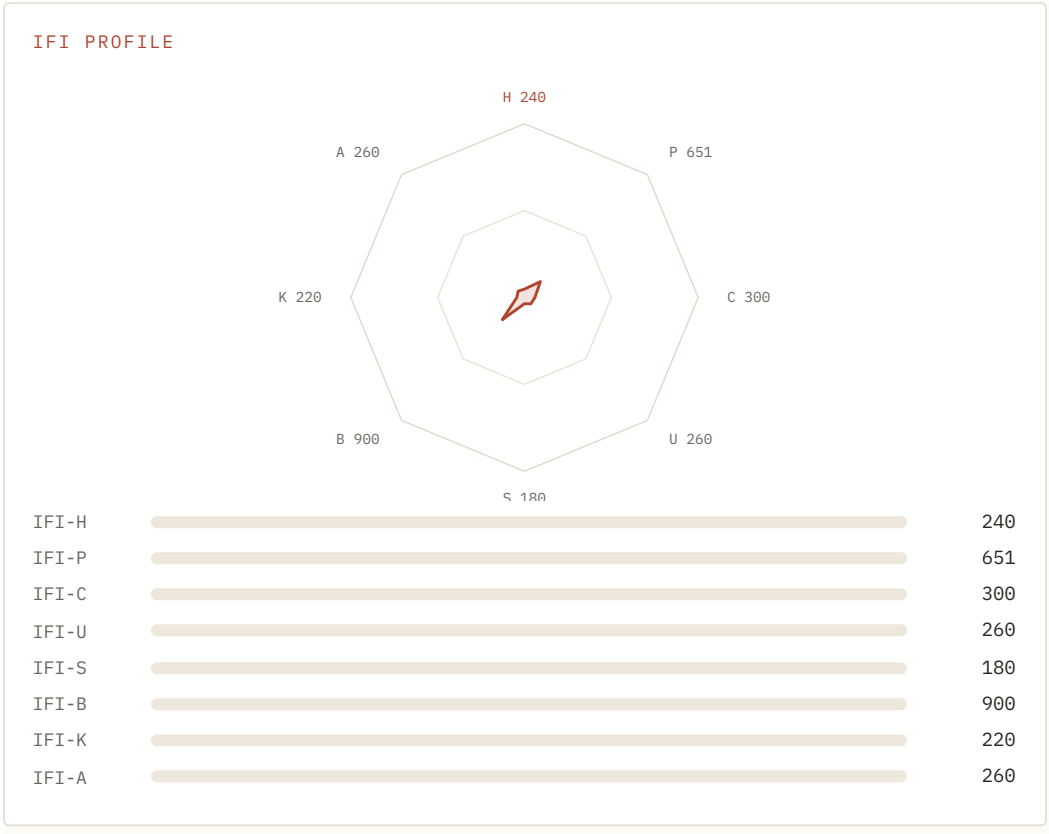
eating, manufactured fresh in your mouth from two harmless halves. This is why a whole radish is mild and a grated one is fierce; you are not releasing the pungency, you are *making* it.

The family runs this one trick with a whole vocabulary of glucosinolates, and which one a plant stores decides the character of its sharpness — the high nasal spike of mustard, the broad burn of horseradish, the green heat of watercress, the gentle bite of a radish:

GLUCOSINOLATE	ISOTHIOCYANATE PRODUCT	CARRIED BY	CHARACTER
Sinigrin	allyl isothiocyanate (AITC)	black mustard, horseradish	sharp, nasal, high
Sinalbin	p-hydroxybenzyl ITC	white mustard	milder, slower, tongue-held
Glucoraphanin	sulforaphane	broccoli	faint, nutty, barely pungent
Progoitrin	goitrin (not an ITC)	rapeseed, cabbage	bitter, sulfurous — the off-note

Two of those rows are the family's two projects in miniature. Sinigrin's AITC is the sharpness the mustards amplify; progoitrin's goitrin is the bitterness the vegetables attenuate. And one row — glucoraphanin — is the family's quiet aside, because its product sulforaphane is barely pungent at all, which is why broccoli can be bred toward the clean green sweetness people actually want without losing what makes it a crucifer.

The kinetics of the reaction matter as much as its chemistry. Myrosinase works in an instant once the compartments break, but its rate and the stability of the unstable intermediate between cleavage and the final isothiocyanate set how *fast* and how *hot* the pungency blooms — which is why freshly grated horseradish is volcanic and the same horseradish ten minutes later is flat, the reaction having run to completion and the volatile AITC having simply left. Part of the mustard engineering is tuning that tempo: a reaction that blooms at the right moment and holds rather than flashing and dying. AITC is a TRPA1 ligand, and it opens that channel the aggressive way — not by fitting a pocket but by covalently modifying cysteine residues near the channel's N-terminus, a genuine chemical bond rather than a handshake. That covalent mechanism is why pungency feels like an *event*: sudden, upward, nasal, cresting faster than heat and clearing faster too. On the atlas, black mustard's **2,790** constructs push this meridian harder than anywhere else in the surveyed world, tuning both the glucosinolate reservoir and the myrosinase kinetics so that the reaction runs hot and clean. The representative plate of the reach:



A single rust-colored spike on the P meridian, taller even than the tomato's umami arm — the most specialized silhouette we have met so far. But look at the modest lift on B, the zero-bitter axis, because it points at the family's second, gentler project. The crucifers carry glucosinolates that TAS2R38 reads as bitter, and *goitrin* in particular, the compound responsible for the sulfurous bitterness that turns so many people against broccoli and kale and cabbage. The vegetable crucifers — broccoli at 380 constructs, the broccoli-kale cross at 280, cabbage and kale and radish and rapeseed at the family's quiet edge — are engineered in the opposite direction from the mustards: not to amplify the sharp reaction but to *attenuate* the bitter one, turning down goitrin and the harsher glucosinolates by the Index's 20–65% band so that a crucifer tastes green and sweet and faintly nutty rather than sulfurous.

A note on where this pungency goes, because it explains the family's whole sensory character. Allyl isothiocyanate is small and volatile, which means it does not stay on the tongue — it rises, as a gas, up the back of the throat and into the nasal cavity, where it reaches TRPA1 endings the tongue's heat never touches. That retronasal route is why mustard and horseradish "clear the sinuses," why the burn is felt behind the eyes rather than on the lips, and why it crests and vanishes in seconds as the volatile simply leaves: pungency is the one sharp sensation delivered mostly by air. It is also why the family's most famous member is so often an impostor. True wasabi, from *Wasabia japonica*, is scarce and perishable, its myrosinase reaction fading within minutes of grating; most of what the world eats as "wasabi" is dyed horseradish standing in for it, carrying the same sinigrin-derived AITC with a coarser edge. Watercress runs the same chemistry toward a greener, gentler product — phenethyl isothiocyanate from gluconasturtiin, the peppery lift of the leaf. One family, one wound-triggered reaction, tuned from the volcanic to the merely bright.

There is a nourishment note here that we will make once and let lie, because the crucifers are the plants it belongs to most honestly. The glucosinolates that read as bitter are the same class of compounds

the plant makes to defend itself, and the project of turning down the *bitterness* is a careful one — attenuating the perception at the receptor, tuning the balance of compounds, so that a kale a child will actually eat is still a kale worth eating. We draw that balance as two arms on one plate, the loud P of the mustards and the restored B of the vegetables, because they are the same family solving the same chemistry from opposite ends. The sharp country is, under the sharpness, the family that most rewards being made easy to love.

Chapter 7 · The Cooling Range — *the only axis that runs cold.*

Of the eight meridians, seven run toward heat, sweetness, savor, sharpness — toward *more*. One runs the other way. IFI-C, the cool-burn, is the only axis in the atlas pointed at winter, and the territory that owns it is a range of aromatic plants spread across two families: the Lamiaceae mints and a scatter of cool-breathing trees and shrubs. This is the country of menthol, of the breath that feels cold going in though nothing has changed temperature, of the eucalyptus note at the back of a clean mouth. It is some of the hardest engineering in the book, because the signature compound sits at the end of a long, branching monoterpene pathway where one wrong turn makes an off-flavor instead.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Peppermint	2,360	C / M	Hard
Lavender	160	C	Hard
Thyme	120	P	Hard
Spearmint	80	C	Hard
Eucalyptus	80	C	Hard
Oregano	40	P	Hard
Camphor	40	C	Hard
Cinnamon	40	P	Hard



FIG. 7.1 — Peppermint, the range's loudest cool voice and the home of the five-to-six-step menthol pathway, where a single misrouted intermediate becomes an off-note instead of a crisp finish.

The cool itself is a receptor trick as clean as heat's. Menthol binds **TRPM8**, the cold-and-menthol channel, which the body normally opens below about 26°C to report cold. Menthol opens it chemically, with no drop in temperature, so the nerve sends *cold* and the mind, trusting its instruments, feels it. Where capsaicin lowers TRPV1's threshold to fake heat, menthol lowers TRPM8's threshold to fake cold — the same illusion, run in reverse, on a different channel. The two can even coexist on one plate, which is the whole basis of the numbing-cool intersections in Part III.

TRPM8 is a more subtle instrument than TRPV1, and the subtlety is the reason this range is both precise and treacherous to engineer. The channel integrates three inputs at once — temperature, membrane voltage, and chemical ligand — so that menthol does not simply "turn it on" but *shifts its activation curve*, lowering the temperature at which it fires until body temperature itself reads as cool. This is why a strong menthol can make a room-temperature mouth feel genuinely cold and why the cool outlasts the menthol's presence: the channel's sensitivity has been moved, and it takes time to return. It is also why different cooling molecules feel different. Menthol is sharp and fast; **icilin**, a synthetic super-agonist, is far more potent but needs intracellular calcium to act, giving it a slower, deeper cool; and the designed cooling agents the flavor industry reaches for when it wants cool without mint flavor — the WS-series carboxamides — are simply ligands that move the same curve with no monoterpene smell attached. The atlas maps all of them on one meridian because the channel does not care what opened it; it only reports cold.

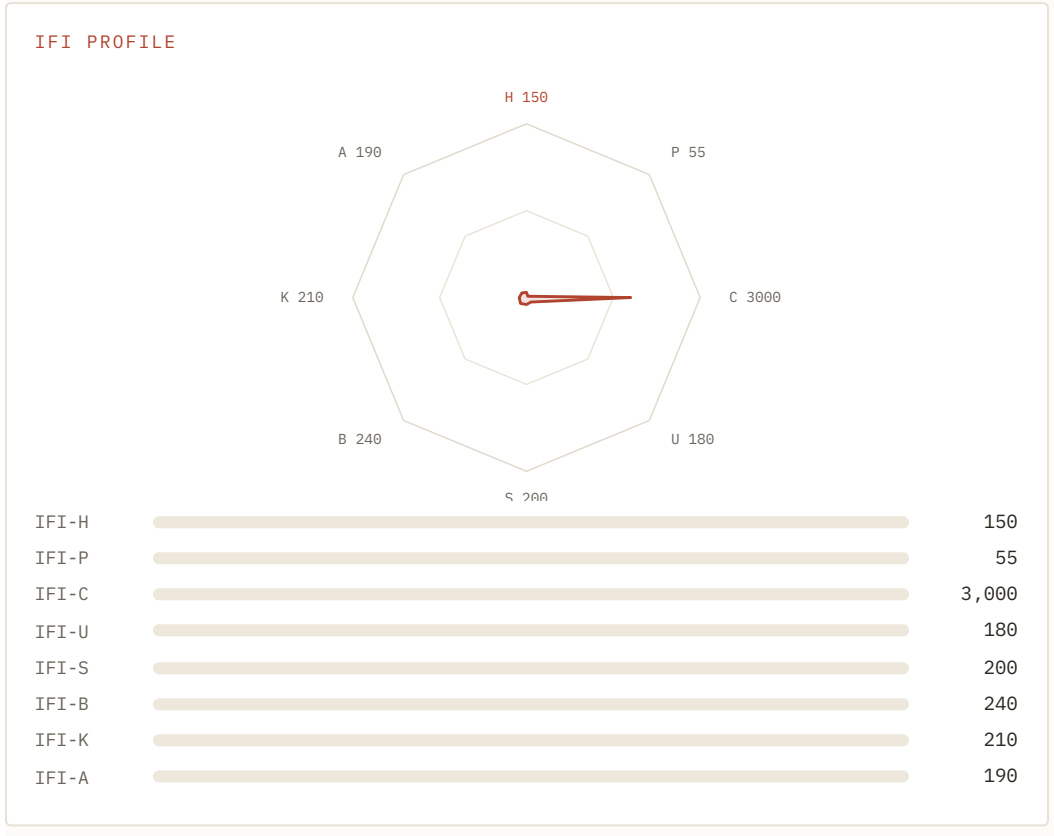
The clean cool is a chemistry problem of *which molecule*, and the range's neighbors each answer it differently. Spearmint's cool comes not from menthol but from **carvone**, and carvone is a lesson in how much stereochemistry matters to the tongue: (R)-(−)-carvone is the unmistakable smell of spearmint, while its mirror image (S)-(+)-carvone is the smell of caraway and dill — the same atoms, the same formula, assembled left-handed instead of right, and the nose reads them as two unrelated plants. A cool you can trust is a chirality you have controlled. Eucalyptus and camphor run on the bicyclic monoterpenes **eucalyptol** (1,8-cineole) and camphor itself, which open TRPM8 and, in camphor's case, the warm channel TRPV3 as well — the molecular reason camphor reads as cool-then-warm, a contradiction the atlas draws as a short teal arm with a faint red shadow.

Making menthol well is the hard part, and it is worth drawing the pathway because it shows why this range is rated Hard across almost every row. Peppermint builds (−)-menthol from a simple terpene precursor through a route of five to six enzymes, each a committed step, each with a branch point that can spill into an off-flavor if the flux is wrong:

STEP	ENZYME	PRODUCT
1	(−)-limonene synthase	`(−)-limonene`
2	(−)-limonene-3-hydroxylase (CYP71D)	`(−)-trans-isopiperitenol`
3	isopiperitenol dehydrogenase	`(−)-isopiperitenone`
4	isopiperitenone reductase	`(+)-cis-isopulegone`
5	(+)-pulegone reductase	`(−)-menthone`
6	menthone reductase (MMR)	`(−)-menthol`

The villain of this pathway is **menthofuran**, a branch product off pulegone that smells musty and bitter and ruins the clean finish; a peppermint that accumulates it tastes stale no matter how much menthol it also makes. So the engineering here is less about raw amplification than about *flux discipline* — using the flux-balance model from Chapter 2 to steer carbon down the clean steps and

starve the branch, so that the 2,360 constructs of peppermint buy a crisp, high, unmuddied cool rather than merely a strong one. The representative plate:



One tall teal arm on C, a faint rust lift on P from the trace of sharpness that good mint always carries, and otherwise the quiet floor — a specialist as pure as the mustard, pointed the opposite direction on the compass. Around these poles — peppermint's menthol, spearmint's carvone, the cineole of eucalyptus — the range spreads into its softest and sharpest neighbors. Lavender brings **linalool**, barely cool and mostly floral, the quietest voice in the range. And thyme and oregano and cinnamon lean off the cool meridian entirely toward pungency — thymol and carvacrol and cinnamaldehyde, the warm aromatic sharpness that makes them read as spice rather than mint, which is why we draw them at the border between this range and the aromatic coast of Chapter 12. Thymol and carvacrol are isomers, the same atoms arranged two ways, and both are mild TRPA1 and TRPV3 agonists — which is the molecular reason a good oregano carries a faint warmth under its herbal top, a warmth the atlas records as a short rust arm the plant's reputation as a cooling herb would never lead you to expect.

The territory's usefulness runs well past mint, and it is worth naming because it is where "cool without cold" earns its keep: a confection that reads refreshing at room temperature, a beverage that finishes clean, a lozenge whose relief is a channel trick and not an ice cube. Every one of those is the same TRPM8 shift, tuned to a loudness and a tempo, and the reason the atlas maps the cool as a meridian with a number rather than a mood is that a formulator reaching for any of them needs to ask for a *quantity* of cool — this much, arriving this fast, holding this long — and until the Index there was no unit in which to ask.

The cooling range is the clearest proof that the Index measures *sensation*, not chemistry in the abstract. Nothing here is cold. Every plant in the range is the same temperature as the plate it sits on. The cool is entirely a story the receptor tells — and the fact that we can

tune its loudness to the unit, starve its off-flavor branch, and place it to within a few hundred points on a meridian is the whole argument of this atlas compressed into one sprig of mint.

Chapter 8 · The Allium Lowlands — *the savory floor under every cuisine.*

Some territories are loud. This one is foundational, which is different and rarer. The alliums — garlic and onion, and their shallot and leek kin off the edge of the surveyed list — are the plants almost every savory dish on earth is built on top of, the first thing into the pan in cuisine after cuisine, and they earn that universality by owning two meridians at once in a way no other territory quite does: kokumi, the invisible richness, and pungency, the sharp top. The allium lowlands are where a meal gets its floor and its edge from the same bulb.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Garlic	560	K / P	Moderate
Onion	40	K	Moderate



FIG. 8.1 — Garlic in cross-section. The sharpness and the richness are stored apart and made at the knife; the clove whole is mild, the clove crushed is a different plant.

Garlic runs the same wound-triggered trick as the mustards, with a different cast. The clove stores **alliin** — S-allyl-L-cysteine sulfoxide — inert and nearly odorless, alongside the enzyme **alliinase** kept safely apart. Crush the clove and the two meet; alliinase cleaves alliin and the products condense into **allicin**, the diallyl thiosulfinate that is garlic's pungent, pricking sharpness. Allicin is a TRPA1 ligand, like mustard's AITC, and like AITC it is *manufactured at the moment of damage* — which is why whole roasted garlic is sweet and mellow (the enzyme denatured by heat before it could act) and raw minced

garlic is fierce (the reaction run to completion on the board). The atlas captures both: the P meridian is the raw, cut garlic, high and sharp.

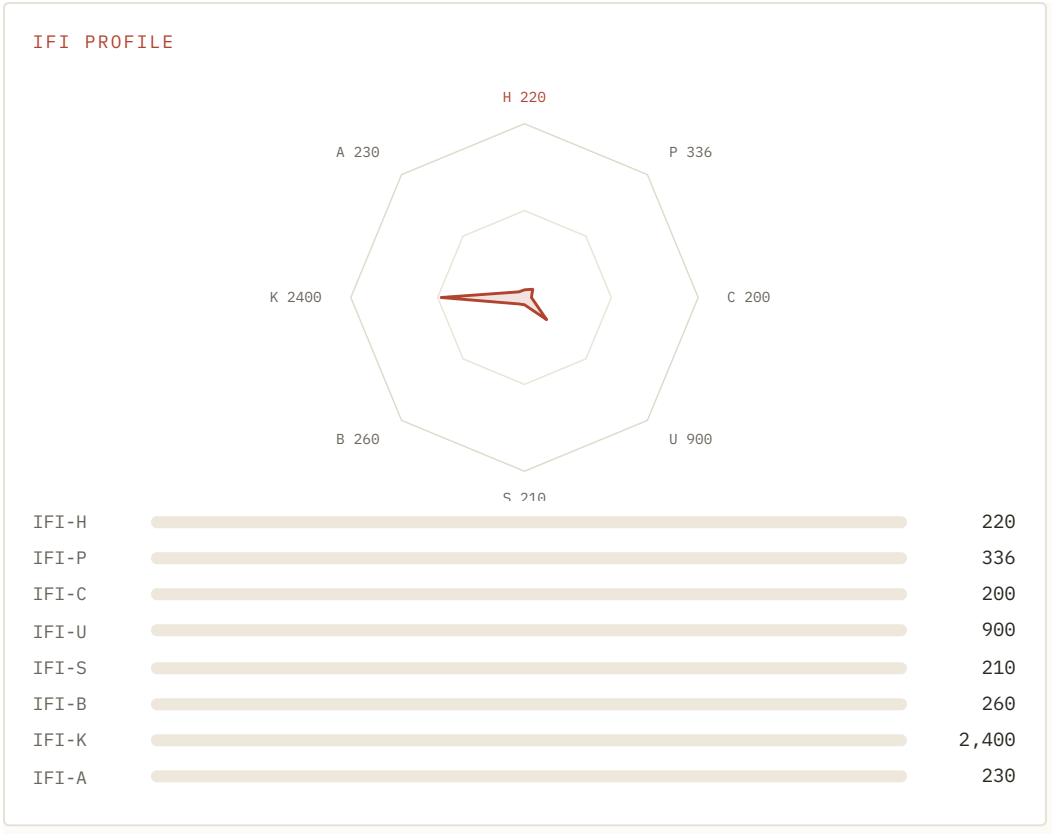
But the deeper allium story, and the harder engineering, is on the kokumi meridian — the invisible axis, the one you taste only as the difference between a thin broth and a complete one. Garlic and onion accumulate **γ-glutamyl peptides**, chiefly γ-glutamyl-S-allyl-cysteine and its relatives, and these are the plant kingdom's great natural activators of **CaSR**, the calcium-sensing receptor that reads richness. γ-Glutamyl peptides carry no flavor of their own. What they do is make everything *else* on the palate read as rounder, longer, more continuous — they fill the middle of a flavor, which is exactly what a long-cooked stock does and exactly what a thin, rushed one lacks. This is why aged garlic and slow-sweated onion taste "deeper" than their raw selves: aging and gentle cooking *convert and concentrate* the γ-glutamyl peptides.

The mechanism at the receptor is worth drawing, because kokumi is the meridian people find hardest to believe in. CaSR, the calcium-sensing receptor, is a class C GPCR whose day job is monitoring blood calcium; on the tongue it reads γ-glutamyl peptides as **positive allosteric modulators** — they do not activate it alone so much as make it more responsive to everything else, which is the molecular definition of "enhances without tasting of itself." The archetypal kokumi peptides are small and specific, and the atlas keeps a short roster of them:

PEPTIDE	STRUCTURE	FOUND IN
Glutathione	γ-Glu-Cys-Gly	yeast, aged garlic, meat
γ-Glu-Val-Gly	γ-Glu-Val-Gly	fermented sauces, aged cheese
γ-Glu-S-allyl-Cys	γ-Glu-S-allyl-cysteine	garlic, especially aged
γ-Glu-Cys	γ-Glu-Cys	onion, allium bulbs

What they share is the γ-glutamyl bond — a peptide linkage through glutamate's *side-chain* carboxyl rather than its backbone — and the enzyme that builds and remodels them is **γ-glutamyl transpeptidase**, which runs slowly in the stored or aging bulb. That is the molecular clock behind "deeper with time": aging is transpeptidase quietly assembling kokumi peptides the fresh clove had not yet made. The allium engineering accelerates and directs that clock, so a bulb carries its complete, rounded richness without months in the dark.

The representative plate of the lowlands, read at the kokumi-forward, aged profile:



An olive arm on K, a rust arm on P, a modest violet lift on U — a two-armed silhouette, richness and sharpness together, with a savory thread between them. That is the allium signature, and once you can see it you will find it faintly present under the plate of almost every cuisine in the kitchen shelves of this library, because the allium is the floor they are all standing on.

Onion carries only forty constructs to garlic's five hundred and sixty, and most of them are kokumi work, because onion's pungency travels a different and more complicated road. Cut an onion and alliinase acts on *isoalliin*, but a second enzyme — **lachrymatory factor synthase** — diverts the product into **propanethial S-oxide**, the volatile that reaches your eyes and makes them water. The tear is a branch of the pungency pathway, and part of the onion engineering is simply steering flux away from that branch so the sweetness and richness come forward without the assault — a sweeter onion that does not make the cook cry, which is a small kindness the flux model happens to be very good at delivering.

Allicin is only the first product of a cascade, and the cascade is why alliums taste so different cooked than raw. Allicin is unstable; left to itself it rearranges into **ajoene**, **diallyl disulfide** and **trisulfide**, and a family of polysulfides, each with its own smell and its own slower, rounder character — the warm, almost sweet note of long-cooked garlic rather than the prickling sharpness of raw. Heat changes everything upstream of this, because the whole reaction depends on alliinase, and alliinase is a protein that denatures above roughly 60°C. Add garlic to hot oil whole and the enzyme dies before it can act, so little allicin ever forms and the clove turns sweet and nutty; crush it and let it stand before heating and the reaction runs to completion first, so the dish carries the full organosulfur cascade. The cook who "lets the garlic rest after chopping" is, without knowing it, running a timed enzyme reaction — and the atlas's work is to make that timing a dial rather than a folk rule. The rest of the family plays variations on the same two instruments: the leek and the shallot and the chive each balance the pungency and the kokumi

differently, the shallot leaning sweet and round, the chive keeping a bright raw lift, all of them the same chemistry tuned to a gentler setting than the garlic clove.

The allium lowlands are the territory that best explains why kokumi earns a meridian at all. It is the only axis you cannot point to on a single ingredient and name — nobody says "this tastes of kokumi" the way they say "this is sweet." You know it only by its work: the broth that seems to have simmered longer than it did, the sauce with a middle, the roast garlic that makes a whole dish feel *finished*. The atlas gives that invisible thing a number and an address, and in doing so makes it something a cook can ask for on purpose instead of stumbling into. That is the lowlands' gift — not a loud flavor, but the floor every loud flavor needs to stand on.

Chapter 9 · The Tannin Archipelago — *the islands of the dry finish.*

Not every territory is a continent. Some are archipelagos — a scatter of islands that share a climate without sharing a landmass, grouped on the map not by family but by what they do. The tannin archipelago is the atlas's clearest example: six organisms from six different plant families, united only by their command of the astringency meridian, the tactile dry-finish axis that is not a taste at all but a touch. Grape and tea and pomegranate and blueberry and raspberry and sorghum are no kin to one another, but they all speak the same language to the same salivary proteins, and so we draw them as one chain of islands under one flag.

ORGANISM	FAMILY	CONSTRUCTS	PRIMARY MERIDIANS
Grape	Vitaceae	1,610	B / A / M
Tea	Theaceae	280	U / B / A
Blueberry	Ericaceae	120	A
Pomegranate	Lythraceae	120	A
Sorghum	Poaceae	120	A
Raspberry	Rosaceae	40	A



FIG. 9.1 — Grape in cross-section. The tannin that structures a wine is built in the seed and skin by the flavonoid pathway; the atlas tunes it by the branch that chooses catechin over anthocyanin.

The mechanism first, because astringency is the most misunderstood meridian on the map. Tannins are large polyphenols — **condensed tannins** (proanthocyanidins, chains of catechin and epicatechin) and **hydrolyzable tannins** (gallo- and ellagitannins). They have a strong affinity for proteins, and the mouth is full of one kind in particular: the **proline-rich proteins** of saliva, which exist largely to lubricate. When tannins meet PRPs they bind, hydrogen-bond and hydrophobically stack, and *precipitate* — the lubricating film collapses, and the surfaces of the mouth drag against one another. What you feel as astringency is that loss of lubrication:

pucker, grip, drying, the clean architectural finish of a structured tea or a serious red wine. It is mechanical, not gustatory; the tongue's taste cells are barely involved. The Index maps it anyway, because the body reports it unmistakably, and because it is one of the great structural elements of flavor — the thing that gives a drink a *shape* and an *end*.

Astringency is not even a single sensation but a small family of them, which is why the meridian carries so much information in one number. Sensory panels separate the *puckering* of an unripe fruit from the *drying* of a strong tea, the *graininess* of a young red from the velvet grip of a mature one, and the difference comes down to tannin size and structure: small, reactive tannins strip the saliva fast and feel harsh and grainy; large, well-organized ones bind more gently and feel smooth and long. The engineering therefore works on *how* a tannin precipitates the proline-rich proteins, not just how much — a structural tuning that lets a grape or a tea hold a serious, architectural finish without the green harshness that tannin usually drags behind it.

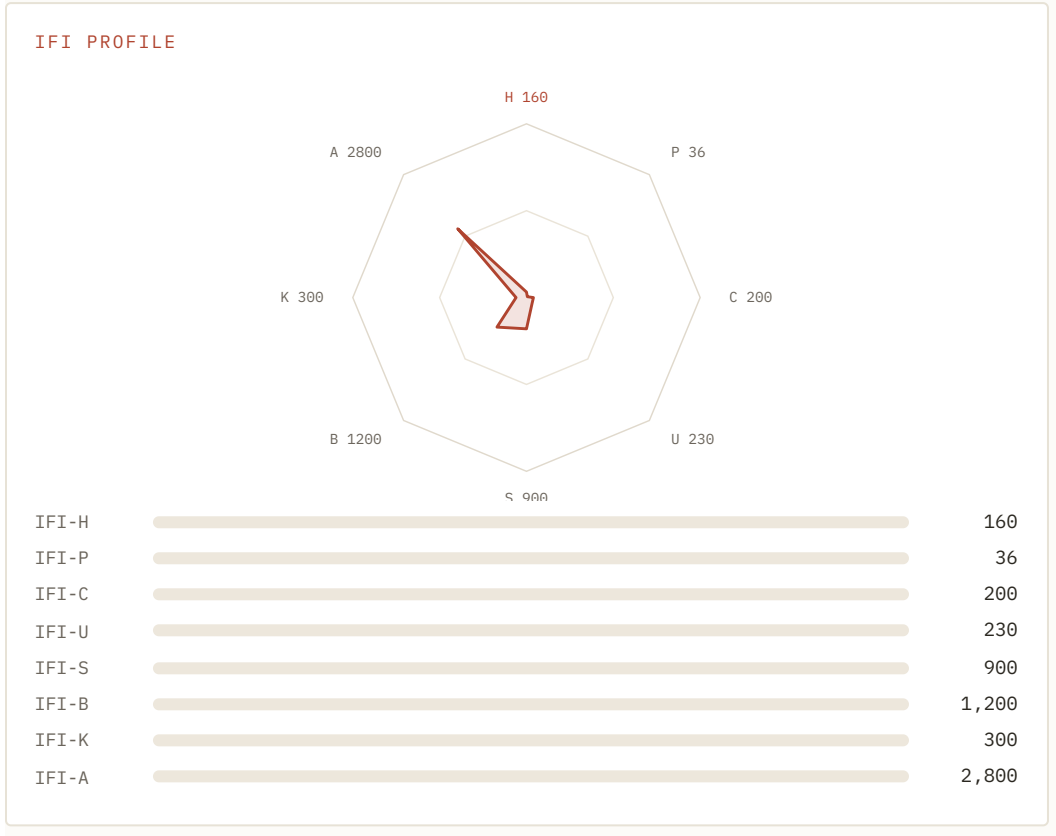
Grape is the archipelago's largest island by far, **1,610** constructs, and the richest single case study in the book for *directed* tannin. The flavonoid pathway in the grape berry reaches a branch point at the leucoanthocyanidins, and two enzymes compete for the substrate: **LAR** (leucoanthocyanidin reductase) makes catechin, and **ANR** (anthocyanidin reductase) makes epicatechin from the anthocyanidins. The ratio and the degree of polymerization of what comes off that branch set whether a wine's tannin is soft and round or hard and green, whether it grips on the front or the finish, whether it will integrate in two years or ten.

The branch sits at the end of a long, universal flavonoid road, and seeing the whole of it shows where the grape's structure is actually decided:

STEP	ENZYME	PRODUCT
1	chalcone synthase (CHS)	`naringenin chalcone`
2	chalcone isomerase (CHI)	`flavanones`
3	flavanone 3-hydroxylase (F3H)	`dihydroflavonols`
4	dihydroflavonol reductase (DFR)	`leucoanthocyanidins`
5a	leucoanthocyanidin reductase (LAR)	`catechin`
5b	anthocyanidin synthase + ANR	`epicatechin`
6	polymerization	`proanthocyanidins (condensed tannin)`

The whole sequence is governed by a transcriptional switch — the MYB–bHLH–WD40 complex, with grape's own **VvMYBPA1** and **VvMYBPA2** regulators turning the proanthocyanidin branch up or down — so an edit at the regulator can retune the entire downstream profile at once. And the quantity that most governs mouthfeel is the **mean degree of polymerization**: short proanthocyanidin chains (a mean DP of two or three) read soft and supple, long chains (a mean DP approaching ten and beyond) read firm and gripping and age-worthy. Tune the branch — up-regulate the reductase route, control

the chain length — and you are, quite literally, engineering the *structure* of the finish rather than merely its amount. The representative plate, read at a structured grape:



A tall plum arm on A, a slate-blue arm on B — astringency and attenuated bitterness together, the signature of a grape engineered for structure *and* drinkability — with a low green thread of sweetness underneath. This is a specialist plate with a second voice, and the second voice is the point: a tannin you can read to the unit is only useful if you can also manage the bitterness that so often rides with it, which is why grape's primary meridians are *both* A and B.

The smaller islands each tune the same touch to a different purpose. Tea carries **280** constructs and uniquely among the archipelago speaks three meridians — U, B, and A — because tea leaf holds **L-theanine**, an umami-adjacent amino acid that gives a fine green tea its savory roundness, braided in the same leaf with the astringency of its catechins, chiefly **EGCG** (epigallocatechin gallate). Green tea and black tea are the same leaf stopped at different points of one enzymatic reaction: leave the plucked leaf to wither and bruise and its own **polyphenol oxidase** goes to work, polymerizing the colorless catechins into the orange **theaflavins** and red **thearubigins** of black tea, which is why black tea is darker, rounder, and less sharply astringent than green — the oxidation has traded the young catechin bite for a softer, redder grip. The engineering therefore has two handles: the catechin and theanine the leaf grows, and the oxidation the processor runs, and a tea's final place on the astringency and umami meridians is set by both together. Pomegranate runs on **punicalagins**, the big ellagitannins that give the juice its serious, almost wine-like structure. Blueberry braids astringency into its anthocyanins. Sorghum — the one grain in the archipelago — carries condensed tannins in its seed coat that have long made it a difficult grain to love, and the engineering there is the gentlest of

attenuations, a drying edge turned down so the grain reads clean. Raspberry, at the quiet edge, tunes a bright, low astringency into fruit.

The archipelago is the atlas's best lesson in reading the map by *behavior* rather than by lineage. Nothing botanical connects a grape to a grain of sorghum. But a map of flavor is a map of what the body feels, and the body feels all six of these as the same clean drag at the end of a swallow. Group the world by its receptors and you discover kinships no botanist would draw — islands in a chain, flying one flag, each tuning the dry finish to its own light.

Chapter 10 · The Sweet Latitudes — *sweetness without the sugar.*

There is a band of the map we think of as the sweet latitudes — a small, warm, intensely useful territory of plants that have independently solved the same problem: how to be powerfully sweet without being sugar. These are the organisms that speak loudest on IFI-S through molecules that the sweet receptor reads as intensely sweet but the body does not meter as caloric load, and they are among the most quietly consequential plants in the whole atlas, because the thing they enable — sweetness decoupled from sugar — is one of the few flavor problems that is also, honestly and without any health claim needing to be made, a problem of how we feed ourselves.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Stevia	910	S / F / M	Moderate
Sugarcane	200	S	Frontier
Monk Fruit	80	S	Hard



FIG. 10.1 — Stevia, the territory's largest voice. Its sweetness lives in steviol glycosides built by a chain of UGT glycosyltransferases — and the cleanest of them carry no bitter tail.

The receptor is the same **TAS1R2·TAS1R3** heterodimer we met on the meridians, and the sweet latitudes exploit a quirk of its architecture. Sugars bind inside the Venus-flytrap domain, and there is a ceiling to how sweet a sugar can be. But the dimer has *other* binding surfaces, and molecules that engage them can be hundreds of times sweeter than sucrose by weight — which means a vanishingly small mass can produce a loud IFI-S. The sweet proteins exploit this most dramatically of all: by the **wedge model**, a protein like thaumatin is too large to enter the flytrap and instead docks against its outer surface, stabilizing the closed, active conformation from the outside,

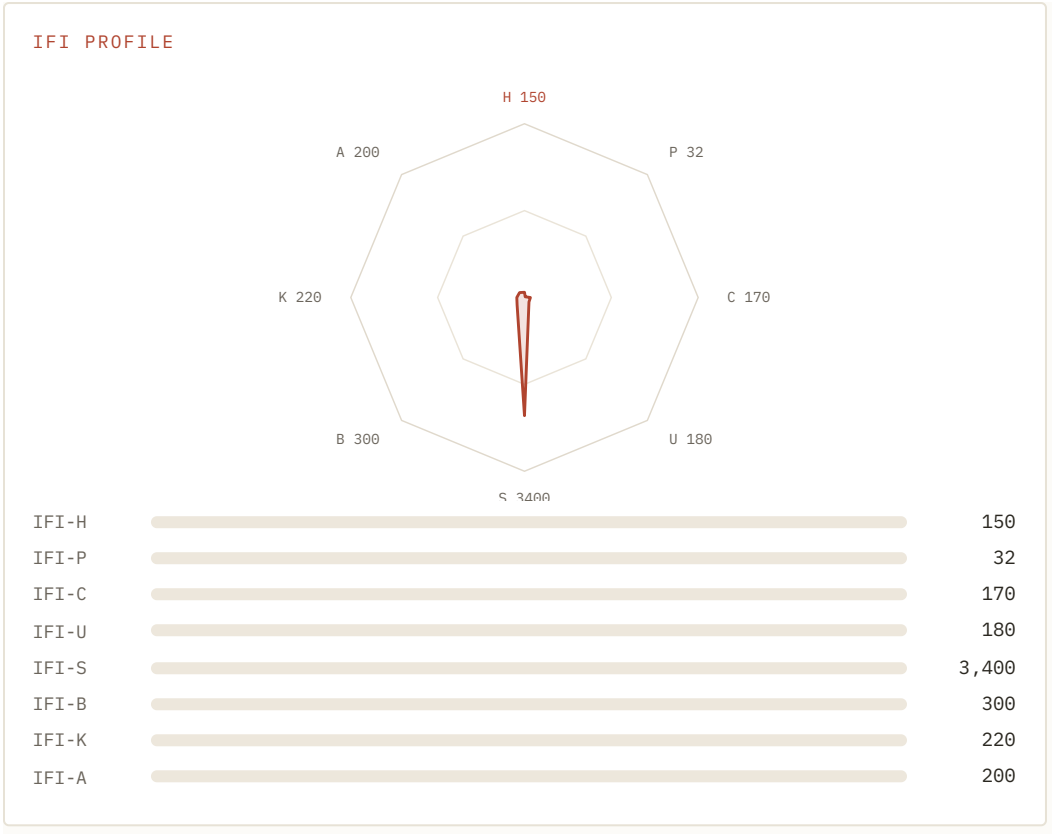
which is how a molecule thousands of times the mass of glucose can be thousands of times sweeter by weight. The potencies are worth seeing side by side, because they are the reason this small territory matters so much:

SWEETENER	SOURCE	SWEETNESS VS SUCROSE (BY WEIGHT)
Sucrose	cane, beet	1×
Stevioside	stevia	~200–300×
Rebaudioside A	stevia	~300–400×
Mogroside V	monk fruit	~250×
Brazzein	*Pentadiplandra* berry	~500–2,000×
Thaumatin	katemfe fruit	~2,000–3,000×

Stevia's sweetness lives in **steviol glycosides**, and the pathway is a lovely one to draw because it shows where the *quality* of a sweetness is decided:

STEP	ENZYME	PRODUCT
1	copalyl diphosphate synthase (CPS)	*ent*-copalyl diphosphate
2	kaurene synthase (KS)	*ent*-kaurene
3	kaurene oxidase (KO)	*ent*-kaurenoic acid
4	kaurenoic acid hydroxylase (KAH)	steviol
5	UGT glycosyltransferases (76G1, 85C2, 74G1…)	stevioside → rebaudiosides A, D, M

The last step is where sweetness is won or lost. The early steviol glycosides — stevioside, rebaudioside A — are intensely sweet but carry a bitter, licorice-like tail, and the tail has a known address: they activate the bitter receptors **TAS2R4** and **TAS2R14** even as they activate the sweet dimer, so a single molecule speaks sweetness and bitterness at once, and the tongue hears both. This is the off-note that has dogged stevia products for years, and it is why a sweetness can read "clean" or "cheap" at the same potency. The later, more fully glycosylated glycosides — **rebaudioside D** and especially **rebaudioside M** — are cleaner, rounder, far less bitter, because the extra sugar groups reshape the molecule so it still fills the sweet flytrap but no longer fits the bitter pocket. The whole art of a great stevia is spoken in two meridians: lift S, and in the same edit *lower* the bitter activation, which on a plate reads as a tall green arm beside a deliberately short slate one. So the engineering of stevia is not "make more sweetness" but "steer the UGT steps toward Reb M and away from the bitter early glycosides" — a flux problem again, a branch to be chosen, exactly the kind of thing the platform's survey was built to solve. Stevia's **910** constructs, its F and M meridians, reflect that it is also a multi-axis workhorse, a sweetness that must be shaped as much as amplified. The representative plate:



A single green spire on S, the cleanest specialist plate in the book, with a deliberately *low* B reading — because the whole art of stevia is a sweetness with no bitter shadow, and the atlas shows the shadow's absence as a short slate arm where a cruder stevia would show a tall one.

Monk fruit tells the same story in a different molecule. Its sweetness is carried by **mogrosides** — cucurbitane triterpenoid glycosides, built from cucurbitadienol through a chain of oxidations and UGT glycosylations — and **mogroside V**, the most-glycosylated form, is the clean, round, intensely sweet principle, perhaps two hundred times the sweetness of sucrose by weight with little of stevia's herbal edge. The engineering again lives in the glycosylation: steer toward mogroside V and away from the less-sweet, less-clean intermediates. Monk fruit's eighty constructs are a concentrated bet on that one branch.

Sugarcane sits at the territory's frontier edge, marked *Frontier* for difficulty, and it is the interesting outlier — because sugarcane's sweetness *is* sugar, sucrose in abundance, the straightforward kind. What makes it a frontier organism is the ambition of doing something subtler than simply making more of it: tuning the plant's sucrose metabolism and the balance of accompanying compounds so that the sweetness reads clean and bright rather than flat, and doing it in a grass genome that is large, polyploid, and famously stubborn. The levers are the enzymes of sugar handling — **sucrose-phosphate synthase**, which builds sucrose in the leaf, and the **invertases**, which split it in the stem and govern how much is stored sweet versus burned for growth — and the balance among them, together with the source-to-sink flux from leaf to cane, decides not just how much sugar a stalk holds but how *clean* that sweetness reads against the grassy, mineral background compounds that a raw cane also carries. It is the one sweet latitude where the molecule is old and the engineering is new — where the question is not what to make but how to make the familiar thing taste like the best version of itself.

We will make the nourishment note here once, plainly, and then let the coordinates speak. A sweetness the tongue reads as loud and the body does not meter as sugar is, simply, a useful thing to be able to design — not a cure for anything, not a claim about anyone's health, just a tool that lets a food be sweet with a lighter load. The sweet latitudes are a small territory. They may turn out to be among the most important on the map, and we drew them with that quiet possibility in mind.

Chapter 11 · The Umami Kingdom — *the depth that is not a plant at all.*

Here the map does something it does nowhere else: it crosses out of the plant kingdom entirely. Four of the five organisms in the umami territory are not plants — they are fungi and yeasts, a separate kingdom of life with its own biology, its own enzymes, its own relationship to the savory molecule the whole territory is built on. We draw it as the umami *kingdom* rather than a continent to mark that border honestly. The savory depth that anchors cuisines from Japan to Italy comes, more often than not, from an organism that is no more a plant than you are — and the atlas, which maps by sensation and not by taxonomy, folds them in without apology.

ORGANISM	KINGDOM	CONSTRUCTS	PRIMARY MERIDIANS
Soybean	Plant (Fabaceae)	360	U / K
Yeast	Fungi	240	U / K
Koji Mold	Fungi	80	U
Shiitake	Fungi	80	U
Mushroom	Fungi	40	U



FIG. 11.1 — Shiitake, whose savor runs on guanylate rather than glutamate — the nucleotide that multiplies umami rather than merely adding to it.

The receptor story here is the richest on the map, because umami is the one meridian built on *synergy*. The primary ligand is free **L-glutamate**, read by **mGluR1** and the **TAS1R1·TAS1R3** pair. On its own, glutamate is savory but finite. The magic is in the **5′-ribonucleotides** — **inosinate** (IMP) and **guanylate** (GMP) — which are not very savory alone but which bind the receptor's flytrap domain and stabilize its closed, glutamate-bound conformation. The result is not additive but *multiplicative*: glutamate plus a nucleotide can read many times louder than the sum of the two apart. This is the single

most important fact in savory cooking, and most cooks know it only as folklore — kombu (glutamate) with bonito (inosinate) in a dashi; tomato (glutamate) with mushroom (guanylate) in a ragù; the pairing that makes a broth bloom. The atlas gives the folklore its mechanism and its number.

The synergy can be written, and writing it shows why it is not a figure of speech. If a glutamate concentration alone would give an umami intensity U_0, adding a 5′-nucleotide at concentration [N] raises it to roughly

$$U = U_0 \cdot (1 + \beta \cdot [N])$$

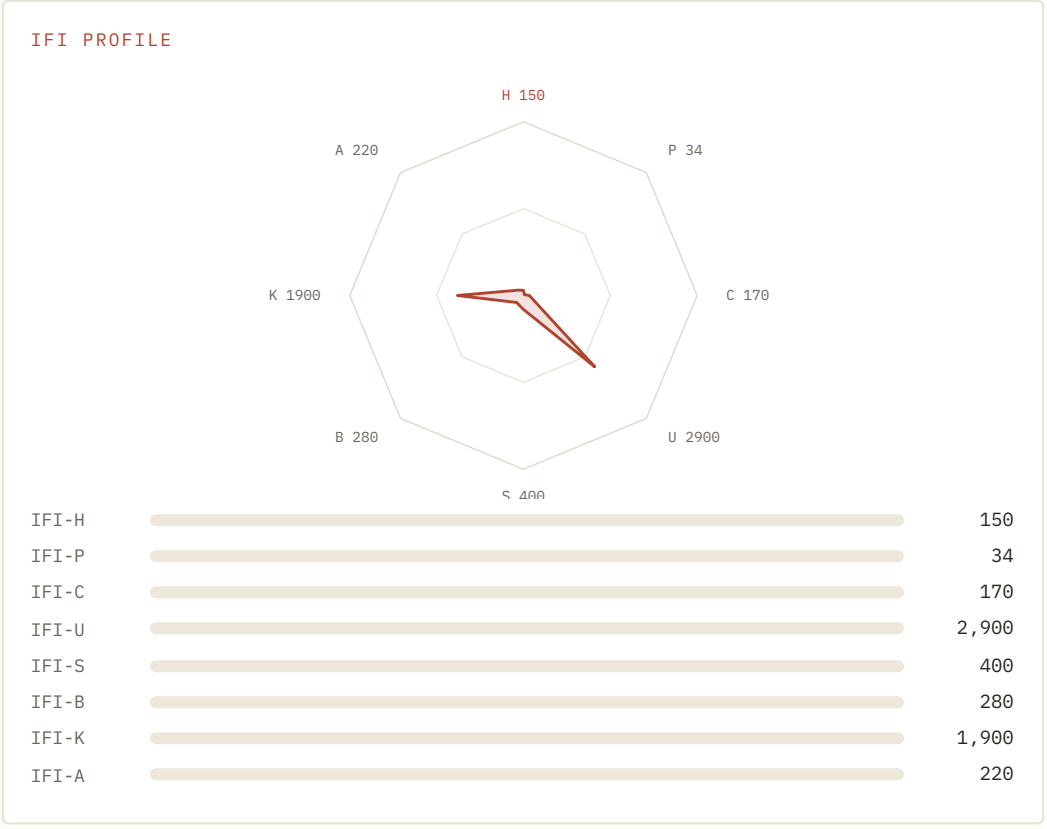
where β is large — the nucleotide multiplies rather than adds, and at the right ratio the combined intensity can reach something on the order of eight times what the glutamate gave alone. The molecular reason is allosteric: the nucleotide binds a site on the outside of the receptor's flytrap domain and stabilizes the *closed*, glutamate-bound conformation, so glutamate lets go more slowly and the receptor stays lit. Two quiet molecules make one loud sensation because one of them is holding the door. The engineering of this kingdom is therefore never about a single compound; it is about building *both* halves of the multiplication in one organism, or in one dish, which is exactly what the savory-depth intersection of Chapter 14 formalizes.

The territory divides its labor by which half of the equation each organism carries, and the raw glutamate and nucleotide loads are worth seeing:

ORGANISM	PRINCIPAL SAVORY MOLECULE	NOTE
Koji / soy ferment	free L-glutamate (protease-released)	the glutamate engine
Soybean	glutamate + γ-glutamyl peptides	glutamate and a kokumi voice
Shiitake	guanylate (GMP)	the multiplying nucleotide
Yeast	glutamate + inosinate + guanylate	both halves in one
Button mushroom	glutamate, modest	the everyday savor

The kingdom divides its labor along exactly that synergy. Soybean — the one true plant in the territory — is a glutamate powerhouse, **360** constructs, and the historical foundation of fermented savor across East Asia; it brings the glutamate half of the equation and, through its γ-glutamyl peptides, a second voice on kokumi. **Koji mold** (*Aspergillus oryzae*) is the great enzymatic engine: it floods a substrate with proteases that cleave storage proteins into free glutamate, which is why koji is the organism behind soy sauce, miso, and sake, the fungus that *manufactures* umami from otherwise bland protein. Its arsenal is specific and worth naming — a suite of acid, neutral, and alkaline proteases that dismantle protein at different pH along a ferment's life, plus **glutaminase**, which converts the glutamine freed by those proteases into the glutamate the receptor actually reads. A soybean is a locked box of storage protein; koji is

the key, and East Asia built a thousand years of savory cooking on that one fungal trick, long before anyone could name mGluR1 or draw the synergy equation. What the atlas adds is not the flavor — the flavor is ancestral — but the *measure*: a way to say how loud a koji ferment's umami runs, and to tune the enzyme balance toward it on purpose rather than by the patient trial of generations. **Shiitake** is the guanylate specialist — its savor is GMP-driven, the multiplying nucleotide — which is precisely why a few grams of dried shiitake deepens a glutamate-rich broth out of all proportion to its mass. **Yeast** brings both glutamate and nucleotides in one organism, the basis of yeast extract's loud, complete savor. And the button mushroom at the quiet edge tunes a gentle, everyday glutamate. The representative plate, read at a glutamate-and-nucleotide-rich profile:



A tall violet arm on U and a substantial olive arm on K — umami and kokumi together, the territory's signature braid, the savory depth and the mouthfulness that make it feel *complete* rather than merely savory. This is the plate that the savory kitchen is forever chasing, and the reason the U×K intersection has its own famous cell in Chapter 14.

The engineering challenge across the kingdom is rated Hard or Frontier almost everywhere, and the reason is biological strangeness. Fungi are not plants; the organism-agnostic modules of

the platform's survey still transfer — the language model reads a fungal protein as readily as a plant one, the flux model handles fungal metabolism — but the delivery, the regulation, and the metabolic context are foreign, and foreign ground is always slower to map. That we can survey a mold and a soybean to the same meridian with the same instruments is a quiet vindication of the whole method: the Index measures what the receptor reads, and the receptor does not care what kingdom its dinner came from.

There is a reverence we feel for this territory that we will admit to, because it is vegetarian-first cooking's deepest well. The savory satisfaction that so many people believe lives only in meat lives, mechanistically, in *glutamate and nucleotides* — and those are made in abundance by a bean and a mushroom and a mold. The umami kingdom is the proof, drawn to scale, that depth is not the property of flesh but of a molecule, and that the molecule grows in the ground and on the fallen log as readily as anywhere. We map it with particular care, because it is the territory that most quietly expands what a plant-forward plate can be.

Chapter 12 · The Bitter Coast & the Aromatic Spices — *the edge we learned to soften.*

The last of the surveyed territories is really two neighbors we draw together because they share a coastline: the bitter coast, where coffee and hops and orange live under the zero-bitter meridian, and the aromatic spices just inland — ginger, cinnamon, vanilla — the warm, pungent, deeply scented plants that round out the map's edge. It is the most various territory in the book, a borderland rather than a heartland, and it holds two of the atlas's most beloved and most *engineered-against* flavors: the bitterness of coffee, and the roundness of vanilla.

ORGANISM	CONSTRUCTS	PRIMARY MERIDIANS	DIFFICULTY
Ginger	120	P	Moderate
Orange	120	B / C	Hard
Hops	80	B	Moderate
Coffee	40	B	Hard
Cinnamon	40	P	Hard
Vanilla	40	K	Hard



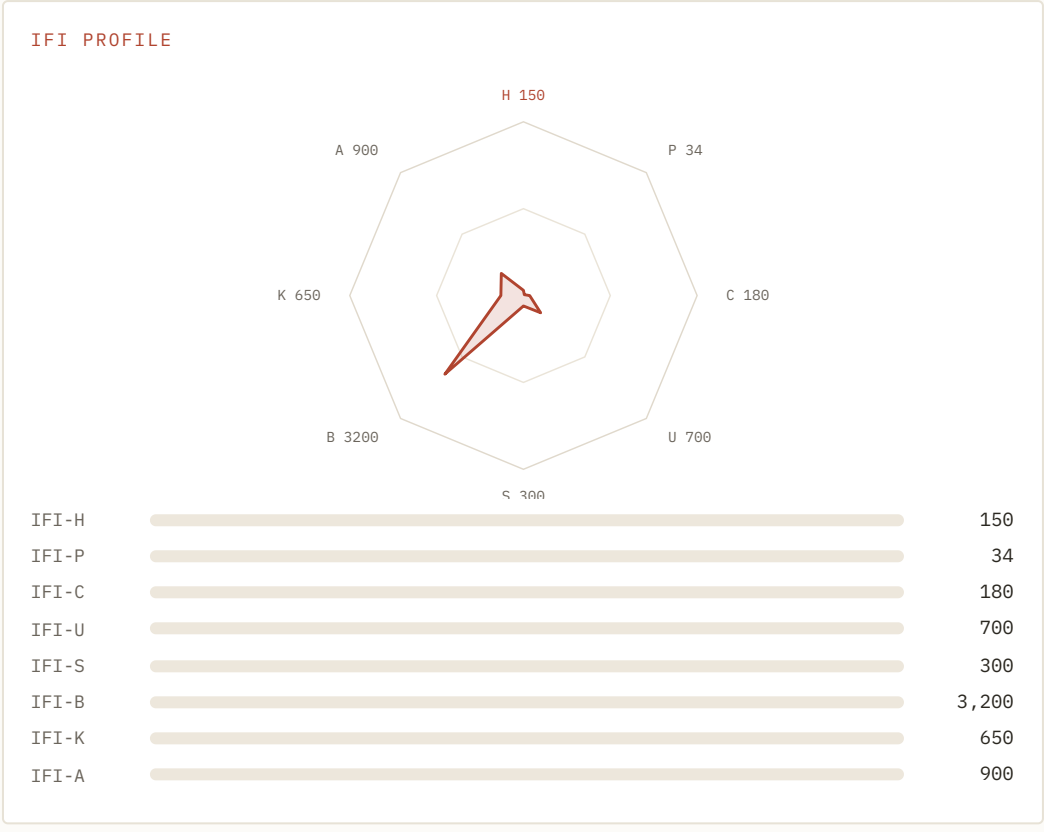
FIG. 12.1 — Coffee in cross-section. Bitterness here is not one molecule but a committee — caffeine, chlorogenic-acid lactones, and the phenylindanes that roasting itself creates.

Coffee is the coast's hardest and most instructive case, because its bitterness is a committee, not a culprit. Caffeine accounts for perhaps a sixth of the perceived bitterness — real but minor. The larger drivers are the **chlorogenic acid lactones** and, above all, the **phenylindanes** that form when chlorogenic acids degrade under the heat of a dark roast. That last fact is the trap: the darker you roast for body and depth, the more phenylindane bitterness you manufacture, so the very process that makes coffee taste of coffee

also makes it bitter. The committee is worth itemizing, because the zero-bitter engineering has to know which member it is turning down:

BITTER COMPOUND	ORIGIN	RECEPTORS ENGAGED
Caffeine	native to the bean	TAS2R7, 10, 14, 43, 46
Chlorogenic acids	native, abundant in green bean	several TAS2R
Chlorogenic-acid lactones	formed in light-to-medium roast	several TAS2R
Phenylindanes	formed in dark roast from CGA degradation	TAS2R, harsh and lingering

The receptor side is a committee too. Humans carry about **twenty-five** TAS2R bitter receptors — a far larger family than the single sweet or umami dimer — because bitterness evolved as a broad alarm for the thousands of structurally unrelated toxins a foraging animal might meet, and breadth mattered more than precision. That is why bitterness is so hard to mask and so easy to over-trigger: one food can light up a dozen of the twenty-five at once. Attenuating it at the receptor is nearly hopeless; attenuating it at the *source*, by tuning down the synthesis of the specific bitter compounds, is the only clean route, which is exactly what the atlas's zero-bitter work does. Only forty constructs sit on coffee in the surveyed library, because it is a hard, slow genome to work — but the aim of every one of them is the zero-bitter meridian: attenuating the bitter committee at the bean, by the Index's 20–65% band, so that a coffee can carry the body of a dark roast without the harsh edge that drives so many drinkers to drown it in sugar and cream. The representative plate, read at an attenuated-bitter coffee:



Read that B arm carefully, because it is the atlas's clearest example of the inverted meridian from Chapter 3. IFI-B 3,200 does not mean *more bitter*. It means bitterness strongly *silenced* — a near-quiet TAS2R38 where a wild coffee would scream. The modest A and U and K readings are coffee's real body — the astringency, the trace savor, the roundness — finally audible because the bitterness that

used to drown them has been turned down. This is subtraction as design, the only meridian where a tall arm is an absence, and coffee is its masterpiece.

Hops runs the same project in beer: its bitterness comes from **humulone**, an alpha-acid that isomerizes to **isohumulone** during the boil, and the engineering tunes that bitterness to the brewer's intent rather than eliminating it — a bitterness made *precise*. Orange sits at the coast's corner with a dual mandate, B and C: the naringin-and-limonin bitterness of citrus pith turned down, and a faint cool-bright lift from the peel oils, which is why we draw it reaching toward the cooling range.

Inland, the aromatic spices tune the pungency and kokumi meridians to warmth rather than sharpness. **Ginger** carries gingerol and its cooked form shogaol — TRPA1 and TRPV1 ligands both, which is why ginger reads as *warm pungency*, a heat-adjacent sharpness rather than the cold-nasal spike of mustard. Ginger is in fact three spices in one root, depending on what you do to it: fresh, its pungency is **6-gingerol**, bright and lemony; dry it, and gingerol dehydrates to **6-shogaol**, markedly hotter, which is why powdered ginger bites harder than fresh; cook it gently and gingerol converts toward **zingerone**, sweeter and far milder, the warm note of a ginger cake rather than the slap of the raw rhizome. One rhizome, three preparations, three different readings on the pungency meridian — a reminder that in this territory the *kitchen* is part of the pathway, and the atlas maps the molecule the cook actually delivers, not merely the one the plant grew. **Cinnamon** runs on **cinnamaldehyde**, a clean TRPA1 electrophile, the warm sweet-sharp of the whole baking tradition. And **vanilla** — the territory's quiet aristocrat — is the one aromatic spice whose meridian is kokumi:

Vanilla deserves its own close reading, because it is the most complex and most counterfeited flavor in the surveyed world. Its signature molecule, **vanillin**, is a single phenolic aldehyde made from ferulic acid by vanillin synthase — simple enough that the global market runs mostly on a synthetic copy of it. But real vanilla is not vanillin; it is vanillin braided with two hundred-odd minor compounds and, crucially, a **kokumi** roundness — a CaSR-active mouthfeel that gives true vanilla a body and continuity the synthetic single-molecule version utterly lacks. That is why vanilla's primary meridian in this atlas is K, not S or P: the thing that makes real vanilla *real* is not its smell but its *mouthfulness*, the invisible richness it shares, improbably, with aged garlic and long-simmered broth. Forty constructs chase that roundness — the hardest and most beautiful target on the coast, because it is the one where the molecule everyone can name is the least important part of the flavor.

The bitter coast and the aromatic spices close the surveyed world on a fitting note: a borderland where the work is as much *subtraction* as amplification, where the point is sometimes to turn a flavor down until its quieter companions can finally be heard. Coffee without its harsh edge. Citrus without its pithy bite. Vanilla restored to its full round body. The edge of the map is where we learned that designing flavor is not always making it louder — sometimes it is making it *kind*.



PART III OF IV

The Intersections

where meridians cross · M2 dual · M3 triple · the famous cells · the full-spectrum capital

Chapter 13 · Where Meridians Cross — *how two numbers make a third taste.*

The territories are the easy part of any atlas — the places you can walk to and name. The hard, interesting, *designed* part is always the intersections, where two meridians cross and a coordinate exists that no single territory can reach alone. A pepper is loud on heat; a stevia is loud on sweetness; but *sweet heat* — the intersection, the cell at row-pepper column-sweet — is not simply a pepper and a stevia in the same bowl. It is a single organism, or a single formulation, engineered to speak on both meridians at once, and getting there requires understanding something the territory chapters could politely ignore: that the axes are not independent. They interfere. They compete. They borrow from the same metabolic budget and signal through receptors that sometimes share hardware. The intersections are where the atlas stops being a description of the world and becomes a plan for building new country in it.

Begin with the combinatorics, because the number is staggering and it is the reason this book can keep growing forever. Forty-two organisms by eight meridians is three hundred and thirty-six single cells — but flavor does not live in single cells. It lives in *combinations*. Two axes chosen from eight is twenty-eight distinct pairings; three axes is fifty-six triplets; and that is before you multiply by which organism carries them. The platform treats this explicitly as a library problem, the same way it treats single constructs:

LIBRARY	AXES COMBINED	CONSTRUCTS
M2 (dual-axis)	any 2 of 8	8,400
M3 (triple-axis)	any 3 of 8	2,800

Eleven thousand two hundred constructs whose entire purpose is to make two or three meridians sing together in one plant — a larger engineered effort than any single territory in Part II. That is how seriously the intersections are taken, and it is why the famous cells of the next chapter are not thought experiments but surveyed coordinates.

The arithmetic of combination is also, not incidentally, the arithmetic of this whole library. Two meridians chosen from eight is "eight choose two," C(8,2) = **28** distinct pairs; three from eight is C(8,3) = **56** distinct triplets; and the full count of non-empty axis combinations is $2^8 - 1 = 255$ before a single organism is named. Multiply by forty-two surveyed organisms and the map holds more addressable coordinates than anyone will visit in a lifetime — which is precisely why a program of sixty-four books does not exhaust it,

and why we can keep minting a new volume simply by naming a cell nobody has walked to yet. The intersections are not a finite list. They are a generative grammar, and the atlas is its first dictionary.

Before the engineering, the perception, because perception decides which cells are worth building at all. Some axis pairs flatter each other and some fight, and a designer keeps the interaction map in mind the way a navigator keeps the prevailing winds:

PAIR	INTERACTION	RESULT
Sweetness × Heat	sweet suppresses heat perception	rounded, pleasurable burn (swicy)
Sweetness × Bitter	sweet suppresses bitter perception	bitterness unveiled as flavor
Umami × Kokumi	kokumi lengthens umami	the complete-broth depth
Umami × salt (trace)	salt amplifies umami	savor brought forward
Astringency × Sweet	astringency can flatten sweet	balance, or a muddied read if overdone
Heat × Cool	co-activation, not cancellation	the numbing málà buzz

Read that table and you have the perceptual board of the whole design game — the reason swicy and savory-depth and bitter-sweet are easy to love and the reason málà is hard to balance. The intersections that became famous are the ones where this board said *yes*.

The engineering difficulty of an intersection comes down to three kinds of interaction, and it is worth naming them because they govern which cells are easy and which are nearly impossible. The first is **metabolic competition**. Two flavor molecules built from overlapping precursors draw on the same pool of carbon and reducing power; amplify both and you may starve one to feed the other. The flux-balance model from Chapter 2 is the only honest way to see this coming — you set a dual objective, maximize both compounds at once, and the model tells you whether the stoichiometry even permits it or whether you are asking the plant for more than its budget allows. Some intersections are easy because their pathways are independent; some are hard because they fight over the same intermediate; and you cannot tell which from tasting, only from modeling.

The second interaction is **perceptual**, and it runs at the receptor, not in the plant. Some axis pairs *enhance* each other — sweetness suppresses the perception of bitterness and of heat, which is the entire basis of sweet-heat and of bitter-sweet balance; a trace of salt amplifies umami; kokumi lengthens everything. Other pairs *mask* each other — strong astringency can flatten the read of sweetness; heat can overrun a delicate cool. The intersection designer is therefore working on two boards at once: the metabolic board, where molecules compete for carbon, and the perceptual board, where sensations compete for attention. A great intersection is one where both boards align — where the molecules can be made together *and* the sensations flatter each other.

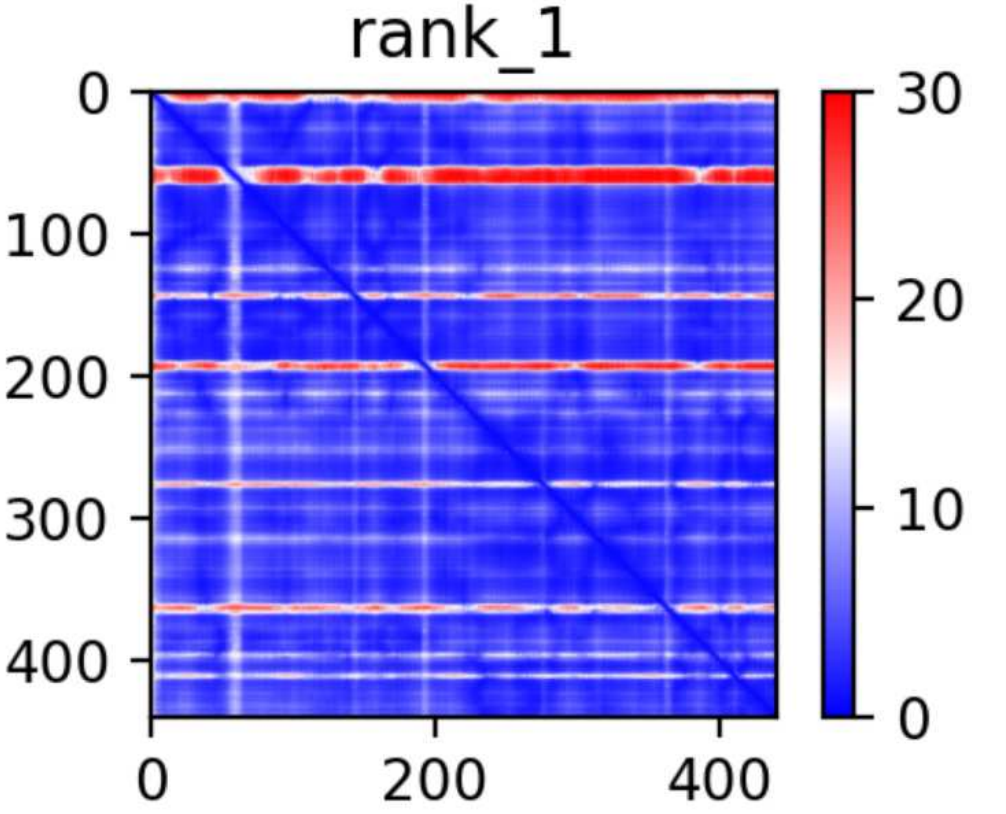


FIG. 13.1 — the predicted-aligned-error matrix of the Pun1/AT3 model, read like any other grid. The diagonal is the territory; the off-diagonal blocks are the intersections — where parts must hold together for the whole to stand.

The third interaction is **competitive inhibition at the molecular level**, the subtlest of the three. When two engineered enzymes draw on a shared substrate, or when a regulatory protein governs two branches at once, turning up one output can *inhibit* the machinery of the other in ways a simple pathway diagram hides. The kinetics make it concrete: an enzyme's rate follows Michaelis–Menten, v = V_max·[S] ÷ (K_m + [S]), and a competitive inhibitor — here, often the *other* pathway's intermediate — raises the apparent K_m by a factor of (1 + [I]/K_i), so the shared enzyme needs more substrate to run at the same speed. Flood the branch you want and you may starve the branch you also want, not through any grand regulation but through two molecules quietly contesting one active site. The inhibition constant K_i is therefore a number the intersection designer watches as closely as any EC_{50}, because it decides whether two meridians can be loud *at the same instant* or only in turns. This is where the structural survey earns its place — the language model and the folded structures let us ask, before we build, whether two edits made for two different meridians will interfere in the same active site or the same regulatory network. The PAE matrix above is a literal picture of that question for a single enzyme: the bright off-diagonal blocks are the regions whose relative positions must stay confident for the protein to work, and reading them is reading, in advance, which combinations the molecule will tolerate.

What all three interactions mean, taken together, is that an intersection is a genuinely *new* coordinate, not a sum of old ones. IFI-H 2,200 beside IFI-S 2,400 in the same plant is a different thing from either read alone, because the sweetness is actively suppressing the perception of the heat even as both register on their meridians — the number says loud-heat-and-loud-sweet, and the tongue says *pleasantly warm candy*, and both are true, because the Index measures the receptor and the pleasure lives downstream of

it. This is the deepest lesson of the intersections, and the reason the atlas needs both the plate's numbers and the plate's shape: the coordinate tells you what was built; only the whole silhouette, read with the perceptual rules in mind, tells you what it will taste like. The crossing of two meridians is where measurement and design finally become the same act — and the famous cells are where that act has produced the places worth a pilgrimage.

Chapter 14 · The Famous Cells — *the intersections worth a pilgrimage.*

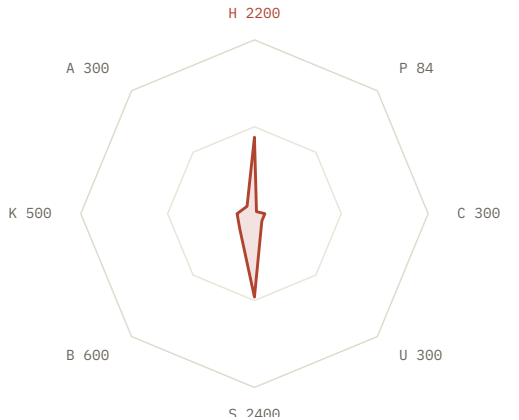
Every atlas has its celebrated places — the cells of the grid that have become destinations in their own right, that people seek out by name. The flavor map has these too: four intersections so useful, so commercially alive, so perfectly matched between the metabolic board and the perceptual board, that each has effectively become its own small territory. We survey them here as scorecards, read as *composition targets* — the coordinate the intersection is designed toward — because an intersection is a plan as much as a place, and a plan is best drawn as the plate it aims to produce.



FIG. 14.1 — a research tray of multi-axis candidates. Most intersections fail on the metabolic board or the perceptual one; the famous cells are the few where both aligned.

Swicy — IFI-H × IFI-S. The dominant intersection of the age, and the easiest to love: heat and sweetness in one plant, the chili-chocolate and hot-honey and Asian sweet-heat axis. It works so well because the perceptual board is kind to it — sweetness genuinely *suppresses* the perception of capsaicin heat at the receptor level, so a sweet-hot flavor reads as rounded and pleasurable rather than punishing, the burn arriving wrapped rather than bare. The composition target:

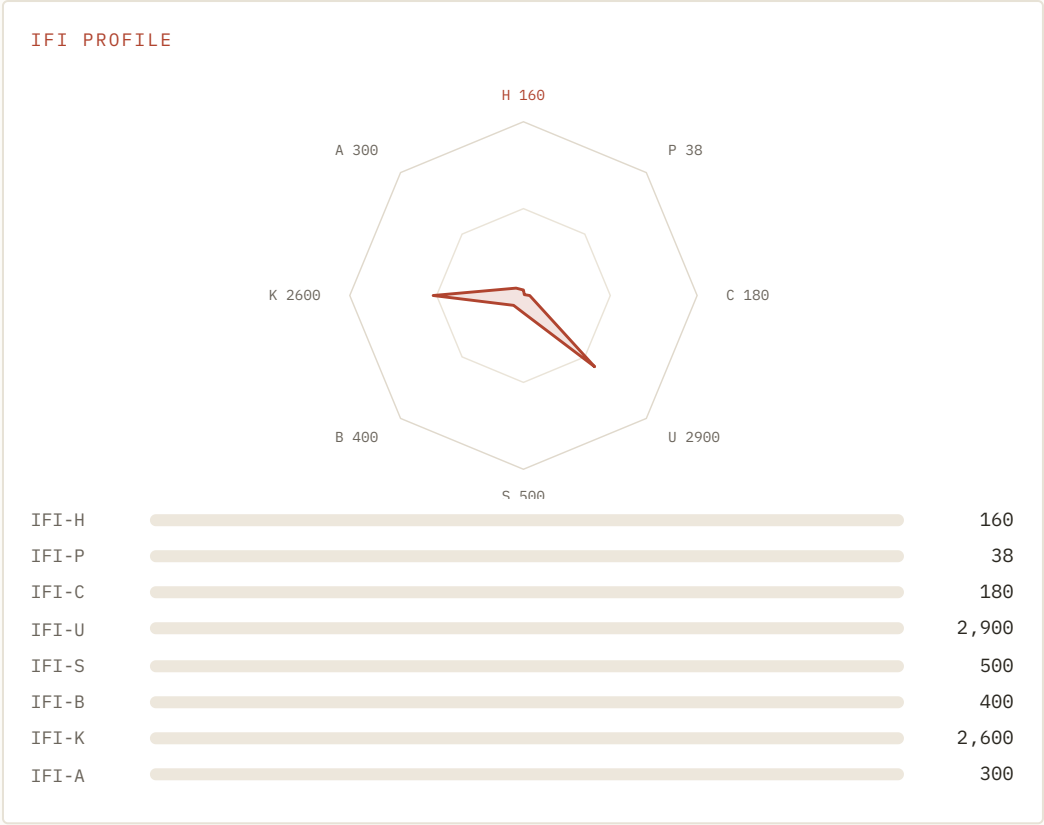
IFI PROFILE



IFI-H	2,200
IFI-P	84
IFI-C	300
IFI-U	300
IFI-S	2,400
IFI-B	600
IFI-K	500
IFI-A	300

Two balanced arms, brick-red and leaf-green, nearly equal — a plate you could not reach from any single territory, and the reason the sweet-heat frontier (the strawberry, the melon, the apple of Part IV) is the most commercially watched country on the whole map.

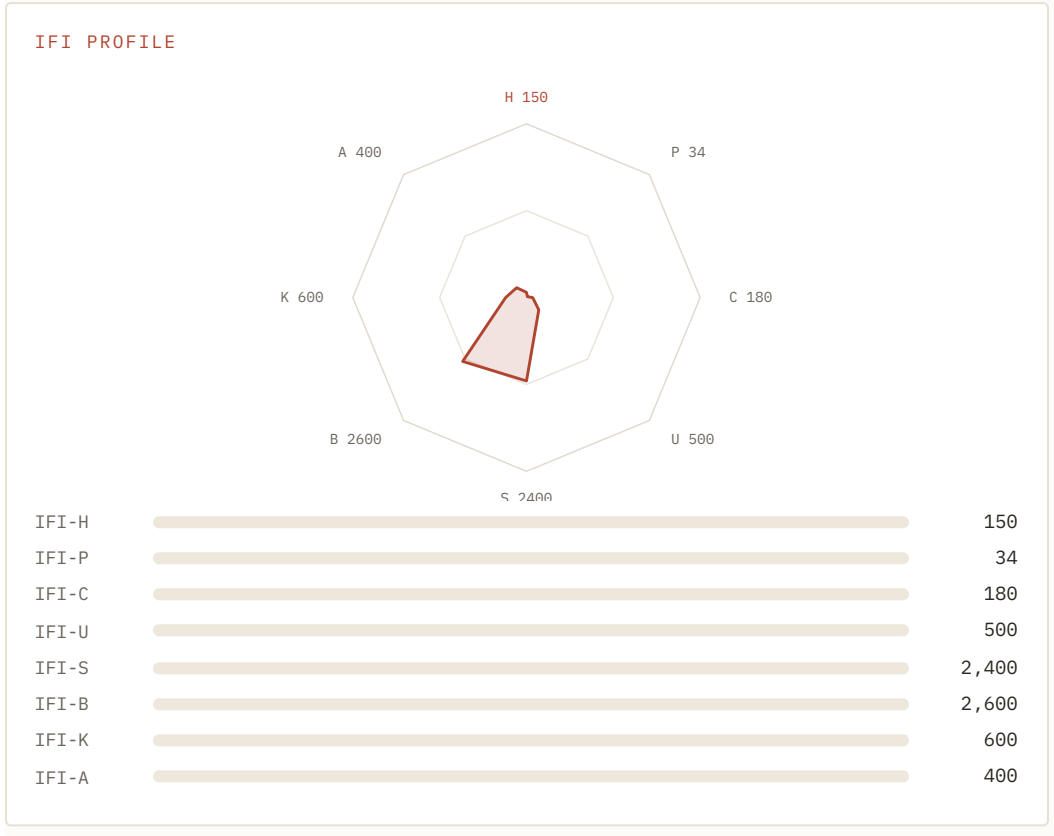
Savory Depth — IFI-U × IFI-K. The most-requested intersection in the professional kitchen, and the quiet opposite of swicy's showmanship: umami and kokumi together, savory loudness *and* mouthfulness, the complete-broth coordinate. The two are metabolically friendly — glutamate and γ-glutamyl peptides are built on compatible routes — and perceptually they are made for each other, because kokumi's whole function is to lengthen and round whatever it accompanies, and what it accompanies best is umami. This is the coordinate every stock, every sauce, every plant-based savory product is reaching for:



Violet and olive, tall and close — the filled, satisfying lower-left of the plate that reads, on the tongue, as *finished*. No showpiece arm; just depth and continuity, the flavor of something cooked with care and time, reached by design.

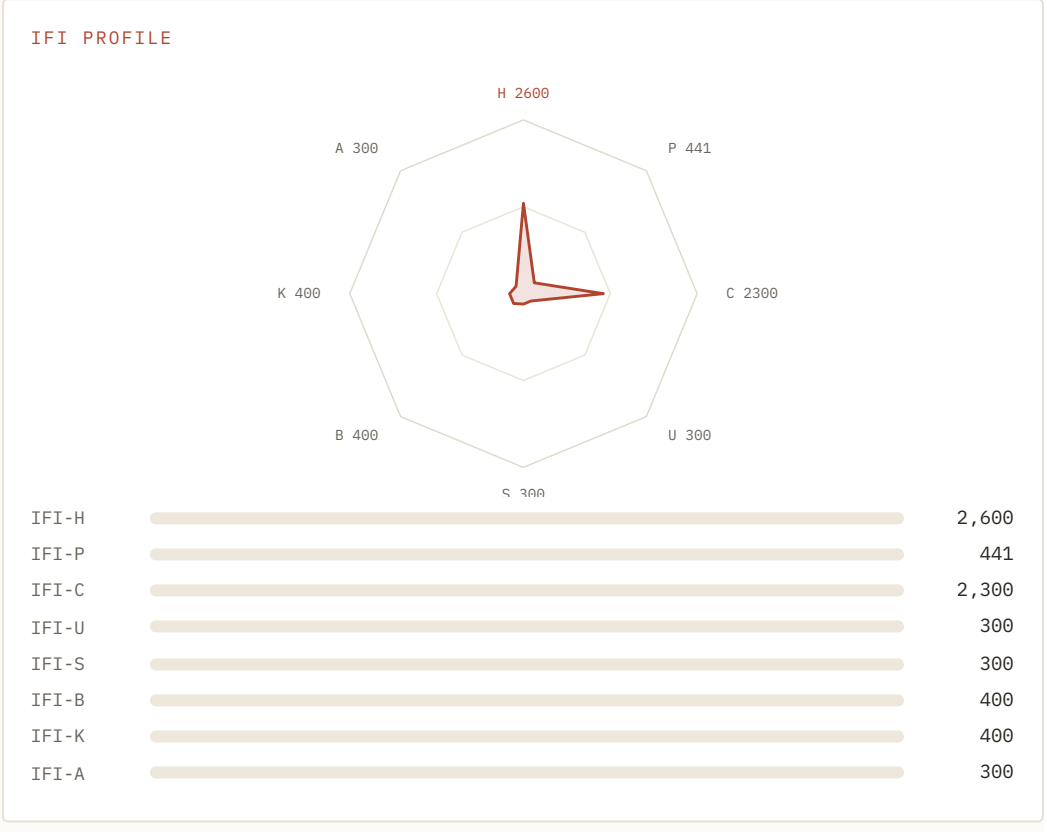
Bitter-Sweet Balance — IFI-B × IFI-S. The reformulator's intersection: attenuate the bitterness and lift the sweetness at once, the coordinate behind a dark chocolate that keeps its complexity without the harsh edge, a coffee that needs no sugar, a nutrition product that tastes like a treat. It leans entirely on the perceptual

board — sweetness suppresses bitterness perception and attenuation removes it at the source, a double subtraction of the harsh that lets the good flavors through:



The slate-blue B arm and the green S arm together — remember that a tall B is a *quieted* bitterness — so this plate reads as sweetness unveiled, the sugar made audible by the removal of the bitter that used to shout over it.

Mála — IFI-H × IFI-C × IFI-P. The one triple-axis famous cell, and the most sophisticated coordinate in the book: the numbing-hot-sharp intersection of Sichuan cooking, heat and cool and pungency braided into the sensation the tradition calls *málà* — the tingling, buzzing, hot-and-cold-at-once mouthfeel that no single meridian can produce. It is hard precisely because it fights on both boards: three pathways to feed, and three sensations that must balance rather than one drowning the others. When it lands, it is unlike anything a single territory can reach:



Three arms — brick-red heat, teal cool, rust pungency — standing nearly equal, the only three-armed plate among the famous cells, and the clearest proof that the intersections are a genuinely new territory. You cannot walk to málà from the heartland or the cooling range. You can only build it, at the crossing of three meridians, with the whole survey behind you.

Gathered, the four famous cells show how the libraries sort themselves — three dual-axis coordinates out of the M2 library, one triple out of M3, in rising order of how hard the two boards were to reconcile:

CELL	AXES	LIBRARY	PERCEPTUAL BOARD	DIFFICULTY
Swicy	H × S	M2	sweet suppresses heat — kind	moderate
Savory Depth	U × K	M2	kokumi lengthens umami — kind	moderate
Bitter-Sweet	B × S	M2	double subtraction of harsh — kind	moderate
Málà	H × C × P	M3	three sensations to balance — hard	hard

The pattern is not an accident. The dual-axis cells that became commercial — sweet-heat in every hot-sauce aisle, savory-depth in every plant-based product, bitter-sweet in every better-for-you reformulation — are the ones where the perceptual board did half the work for free, where two sensations happened to flatter each other at the receptor so the designer only had to solve the metabolic board. Málà is the outlier and the aspiration: a triple where nothing is free, where all three sensations must be held in balance and all three pathways fed at once, and where success is correspondingly rare and correspondingly prized. The famous cells are a ranking, in other words, of how much the world wanted a coordinate against how hard it was to reach — and the frontier of Part IV is mostly the project of making the hard, wanted cells into whole crops.

Just off the famous four lie the next destinations, named and surveyed but not yet crowded. **Cool-Sweet** (C × S) is the confectioner's cell — a mint that is sweet without sugar, the coordinate behind a cooling candy or a clean-finishing gum. **Heat-Umami** (H × U) is the savory-heat of a great chili oil, where the burn sits on a brothy floor rather than on nothing, a coordinate the Sichuan and Korean kitchens have always reached for by hand. **Astringent-Sweet** (A × S) is the structure-and-fruit of a fine dessert wine or a serious dark berry, tannin given something sweet to grip. **Kokumi-Bitter** (K × B) is the reformulator's quiet favorite, richness laid under an attenuated bitterness to make a dark chocolate or a coffee taste *complete* rather than merely less harsh. None of these is exotic; each is a coordinate the libraries already hold, waiting for the demand that turns a surveyed cell into a built one.

These four are the celebrated cells, but they are only the four most traveled. The M2 and M3 libraries hold thousands of coordinates between them, most unvisited, each a potential destination the moment someone names it and the metabolic and perceptual boards both say yes. An atlas of intersections is never finished, because the grid keeps offering cells. The famous ones are simply the places enough of us have wanted to go that a road got built — and the next famous cell is already somewhere in the libraries, waiting for its name.

Chapter 15 · The Capital — *one fruit at every coordinate at once.*

Every atlas has a capital — the one place where everything the map describes comes together in a single location, the city that is the whole country in miniature. The capital of the flavor atlas is a pepper called **Phoenix**, SKU **SS-0096**, and it is the only surveyed organism in the entire book that registers on all eight meridians at once. It is the full-spectrum coordinate, the IFI-F reading made flesh, the proof-of-everything fruit — and it earns the capital's place not because it is the loudest on any single axis, though its heat is nearly off the chart, but because it is the only point on the map with *no silent direction*.



FIG. 15.1 — Phoenix (SS-0096), the capital of the atlas. Not the loudest coordinate on any one meridian, but the only one that reads on all eight.

To understand the capital you have to climb to it, and the climb is a ladder of ten flagship cultivars — the design tier of superhots, all *Capsicum chinense*, each one adding computational design scope and, more importantly, *activated meridians*, until the last reaches all eight. This is the single most important table in the book, because it is the atlas's whole thesis compressed into ten rows: that flavor can be designed, deliberately, one predicted coordinate at a time.

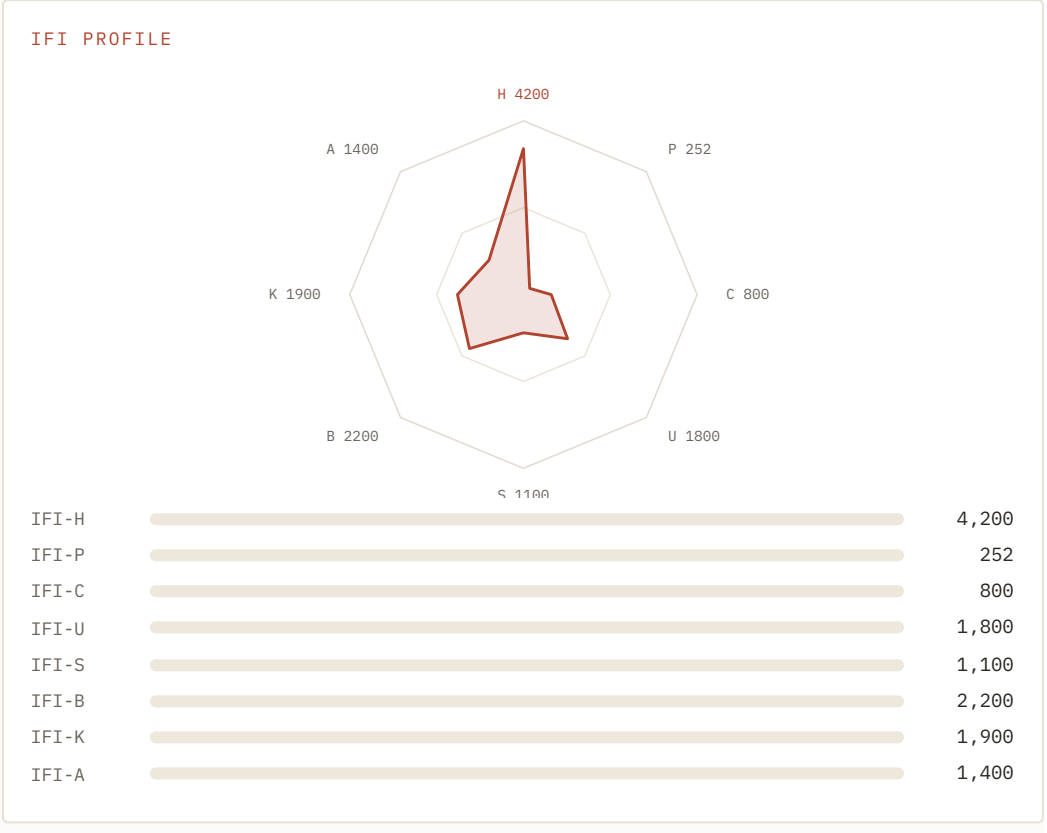
CULTIVAR	SKU	PREDICTED SHU	IFI-H	MERIDIANS
Ember	SS-0087	866K	1,570	2/8
Cinder	SS-0088	1.05M	2,290	3/8
Kindle	SS-0089	1.25M	2,000	3/8
Flare	SS-0090	1.48M	—	4/8
Blaze	SS-0091	1.72M	2,630	4/8
Wildfire	SS-0092	1.96M	2,930	5/8
Scorch	SS-0093	2.21M	3,220	5/8
Firestorm	SS-0094	2.47M	3,490	6/8
Solara	SS-0095	2.72M	3,980	6/8
Phoenix	**SS-0096**	**2.95M**	**4,200**	**8/8**

Read down the right column and watch the capital assemble itself. The early cultivars are specialists — two meridians, three — loud on heat and little else. Then the climb begins adding directions: a fourth meridian at Blaze, a fifth at Wildfire, a sixth at Solara, and finally all

eight at Phoenix The predicted SHU climbs steadily, from 866K to approximately **2.95 million** at the summit, but the SHU is almost the less interesting number. Any breeding program, given enough generations, can chase raw heat. What no breeding program ever did was chase *breadth* — a single fruit speaking on every axis of taste at once — because you cannot select for a phenotype you have no way to measure, and until the Index there was no way to measure a fruit's position on eight meridians simultaneously. The capital is a thing the map made possible. It could not have existed before its own coordinates did.

Read the climb as an assembly rather than a race, because that is what it was. Each rung is a module added: the early cultivars push IFI-H alone, tuning the capsaicinoid branch harder; then the work turns from loudness to *breadth*, and each new rung switches on a meridian the fruit did not speak before — a zero-bitter module to quiet the harshness a fruit this concentrated would carry, a kokumi and umami module to lay a savory floor under the fire, an astringency module for a structured finish, a pungency and a cool module for the top notes, a thread of sweetness to keep the heat from reading as assault. The SHU climbs steadily up the left of the ladder because the heat module keeps being refined; the meridian count climbs up the right because breadth modules keep being added; and only at the final rung do all eight stand lit at once, at which point the fruit crosses from a multi-axis reading, IFI-M, into the full-spectrum reading, IFI-F, that no cultivar below it earns. The capital is the point where the M-series work becomes F-series work — the exact place on the map where *several meridians* becomes *all of them*.

Here, once more and for the last time, is the capital's computed profile — the reference silhouette of the whole book:



And here is how it was built, because the capital is also the clearest single demonstration of the survey from Chapter 2. Every added meridian is a pathway tuned; every tuning is an edit found by the language model, confirmed by the flux model, written by CRISPR.

The heat itself — the 4,200 that anchors the whole plate — rests on a double variant in the Pun1/AT3 acyltransferase, the two shipped substitutions the entire pipeline converged on:

EDIT	EFFECT	ΔΔG (KCAL·MOL⁻¹)	STATUS
S39L	binding affinity ↑ at the N-terminal lobe	−2.1	shipped
L345G	steric relief in the active-site cleft	−1.8	shipped
C175S	prevents a disulfide-misfold pathway	−0.9	structural annotation only

The double variant S39L+L345G, never before combined, positions the capsaicinoid branch to reach its full potential — our model predicts peak output of approximately **2.95 million SHU** at a designed batch-to-batch CV of **≤7%**, against the wild type's **42%** — and that CV is the detail that makes the capital a real place rather than a lucky harvest. A full-spectrum design you could grow once and never again would be a curiosity. A full-spectrum design with a seven-percent coefficient of variation target is a *coordinate* — reproducible, returnable, buildable-upon — which is the only kind of place worth making a capital.

The predicted heat figure emerges from computational modelling: our model tracks the designed capsaicinoid profile — primarily capsaicin and dihydrocapsaicin — and applies the standard conversion factor that physical HPLC measurement would use. The *ratio* between those two principal capsaicinoids matters as much as their sum, because capsaicin and dihydrocapsaicin have slightly different time courses on TRPV1 — capsaicin's burn arrives and fades a little faster, dihydrocapsaicin's sits longer and lower — so the designed blend sets not just how hot the fruit is but the *shape* of its heat across a bite. The capital's figure is a computational prediction; the design is specified to that target because precision gives you something returnable to, which is the only kind of coordinate worth building a capital around.

There is one more thing the capital teaches, and it is about delivery as much as design. Eight meridians in one fruit is a formulation problem as well as a biological one: the eight loud signals have to reach the tongue in the right order and the right proportion, or the heat simply buries the other seven. Part of the full-spectrum work is therefore the nanoparticle delivery that lets each axis arrive on its own schedule — the heat wrapped so it blooms rather than detonates, the quieter meridians protected so they are not lost under the fire. The principle is encapsulation: the loudest, fastest signals are enclosed in lipid or polymer carriers whose release is *timed*, so that a hydrophobic capsaicinoid does not flood the palate in the first instant but unspools across the whole bite, while the slower GPCR sensations — the umami floor, the kokumi roundness — are given the clear early moments they need to register before the fire arrives. It is the same logic a great cook uses when layering a dish so no one element buries the rest, run at the scale of a single fruit and a single mouthful. Delivery is where the biology of eight loud pathways becomes the *experience* of eight legible ones; without it, a full-spectrum fruit would measure as eight and taste as one. The result

is a fruit you can actually *read* as you eat it: the sharp top note, the savory floor, the drying finish, the faint cool counter-current, all of it legible beneath a heat that would, undelivered, have drowned the lot. The capital is not only the point where every meridian meets. It is the point where we learned to make all eight of them *heard at once* — which is, in the end, what the whole atlas was drawn to make possible.



PART IV OF IV

Terra Incognita

sixty-four concepts · five tiers · the phenylpropanoid road · the edge of the known world

Chapter 16 · The Unmapped Lands — *sixty-four coordinates, charted on paper.*

Every honest atlas tells the truth about its own edges. Where the survey stops, the old cartographers wrote *terra incognita* and sometimes drew a sea serpent — a mark of honesty, not ignorance, a way of saying *here the map ends and the world does not*. This atlas has such an edge, and it is the most exciting territory in the book precisely because it is the one we have charted on paper and not yet walked. Forty-two organisms are surveyed. **Sixty-four more** are mapped as concepts — named, sequenced where possible, their pathways sketched, their difficulty estimated, their coordinates predicted — and arranged into five tiers by how far they lie from the known coast.

The reason the frontier is a schedule and not a fantasy is the single most important biochemical fact in the whole library, and it belongs here at the edge where it does its work. The pathway that builds capsaicin begins with a road that runs through *every vascular plant on earth*: the **phenylpropanoid branch**, five enzymes deep —

STEP	ENZYME	ROLE
1	PAL (phenylalanine ammonia-lyase)	enters the pathway from phenylalanine
2	C4H (cinnamate 4-hydroxylase)	hydroxylates the ring
3	4CL (4-coumarate-CoA ligase)	activates as a CoA thioester
4	HCT (hydroxycinnamoyl transferase)	transfers to the shikimate route
5	COMT (caffeic acid O-methyltransferase)	methylates toward the vanilloid

— and only *then* branches into the four terminal enzymes that are pepper-specific: **pAMT**, which aminates to vanillylamine; **Pun1/CS**, the acyltransferase that condenses it into capsaicin; and **KAS** and **BCAT**, which build the branched-chain fatty acid the other half of the molecule needs. The phenylpropanoid road is already paved in every plant you could name. Only the last four turns are pepper's own. This is why five of the platform's seven modules transfer unchanged to any sequenced organism: the hard, universal chemistry is shared, and the frontier is a matter of building four terminal turns onto a road that already reaches the edge of every genome in the world. Here is the charted frontier, tier by tier:

TIER	TERRITORY	GENES	HORIZON	FLAGSHIP CONCEPTS
T1	Solanaceae Core	4–5	18–24 mo	Volcanic Tomato · Dark Matter Eggplant · Laboratory Tobacco
T2	Extended Nightshades	5–7	24–36 mo	Seismic Potato · Celestial Ground Cherry · Acid Tomatillo · Floral Petunia
T3	Cross-Family	7–10	36–48 mo	Sweet-Heat Strawberry · Contradiction Cucumber · Solar Melon · Forbidden Apple · Espionage Lettuce
T4	Frontier Synthetic	10–12	48–72 mo	Deep-Earth Carrot · Nuclear Cabbage · Wildfire Broccoli · Storm Corn · Dynasty Rice



FIG. 16.1 — Strawberry, the surveyed face of the sweet-heat frontier. The T3 concepts — Warm Kiss, Sugar Burn, Candied Fang, Devil's Dessert — are the swicy intersection grown into a fruit that has never carried heat before.

Read the tiers as rings of distance from the known coast. **T1**, the Solanaceae core, is the near shore — tomato, eggplant, tobacco, all family of the heartland, all reachable in four or five genes because they are close kin to the pepper and share much of its machinery already. The Volcanic Tomato concept series (Ember, Magma, Pyroclast, Caldera, Krakatoa) is heat written into the atlas's gentlest territory, a tomato that burns — eighteen to twenty-four months of work, the frontier's low-hanging fruit in the most literal sense. **T2** pushes into the extended nightshades, five to seven genes, two to three years: a Seismic Potato, an Acid Tomatillo, a Floral Petunia, each a nightshade just far enough from the pepper to require more terminal engineering.

T3 is where the frontier gets genuinely hard and genuinely thrilling, because it crosses *out* of the nightshades into other families entirely — seven to ten genes, three to four years. The Sweet-Heat Strawberry (Warm Kiss, Sugar Burn, Candied Fang, Devil's Dessert) is the swicy intersection from Chapter 14 grown into a berry that has never in its evolutionary history made a capsaicinoid — the famous cell made into a crop. The Contradiction Cucumber, the Solar Melon, the Forbidden Apple, the Espionage Lettuce: each is a cross-family build, a case where the universal phenylpropanoid road has to be fitted with pepper's four terminal turns in a genome that has never carried them. **T4**, the far shore, is the fully synthetic frontier — ten to twelve genes, four to six years — where the ambition is largest and

the sea serpents are drawn biggest: a Storm Corn, a Dynasty Rice, a Wildfire Broccoli, a Nuclear Cabbage, flavors engineered into the staple grains and brassicas that feed the world.

What makes the far tiers hard is not any single gene but the **stacking** of them. Each terminal enzyme added to a foreign genome must be expressed in the right tissue, at the right time, in the right amount, without starving the host's own metabolism or triggering the plant's defenses — and the difficulty compounds, because ten genes that each work alone can still fail together if two compete for a precursor or a third's product inhibits a fourth. This is why the horizons lengthen tier by tier even though the instruments do not change: the survey of Chapter 2 scales to any single enzyme, but a ten-gene stack is a flux problem of a different order, solved by the same flux-balance logic run across a far larger network. The grasses of T4 — corn, rice, sorghum's kin — are harder still for a reason that has nothing to do with flavor: their genomes are large, often polyploid, and historically stubborn to transform, so the delivery module, the one organism-specific step, becomes the rate limiter the far shore is really waiting on.

A word on the compliance landscape, because an atlas that charts a frontier owes the reader honesty about the laws at its edge, and this is where they bind. The platform edits at native loci — precise changes to a plant's own genes, most often with no foreign DNA left in the final organism — and that distinction matters enormously, because the world's regulators treat a plant carrying only edits to its own genome very differently from one carrying a transgene from another species. The frameworks are a genuine patchwork and they are still moving: some jurisdictions have carved out gene-edited crops with no novel foreign DNA from the heaviest transgenic rules, others fold any edited organism into a full novel-food or GMO review, and the line between "precision-bred" and "genetically modified" is being drawn and redrawn in real time across the major markets. We make no claim here about any specific crop's status in any specific place — that is a question for regulators and the moment, not for a reference volume — and we say only that the path from a charted T3 concept to a crop in a field runs through that review as surely as through the lab. Our posture toward it is the one the whole atlas takes: build at native loci, document everything, publish the science openly under the twenty-one papers, and let the work be auditable rather than asking anyone to take a frontier on faith.

We draw this frontier with real estimates — gene counts, month horizons, named concepts — rather than vague promise, because that is the discipline the whole atlas is built on. A frontier charted with numbers is a plan; a frontier charted with adjectives is a daydream, and we have tried very hard, across every page of this book, to make nothing a daydream that could be made a plan. The sixty-four concepts are not yet walked. But they are *charted* — their coordinates predicted, their pathways sketched, their difficulty honestly tiered — and the distance from a good chart to a walked coast is exactly the distance this company exists to close. The edge of the map is not where the world ends. It is where the next volume begins.

Chapter 17 · Reading the Whole Map — *what an atlas is for.*

We have come to the last page of the survey, and it is the place to step back from the individual coordinates and ask what the whole map is for — because an atlas is finally not a collection of places but an argument about how to see. Close the book for a moment in your mind and picture the whole sheet at once: forty-two territories down the side, eight meridians across the top, three hundred and thirty-six surveyed intersections, a capital that reads on every axis, and a charted frontier of sixty-four at the edge. What is it an argument *for*?

First, for honesty about size. The reason every number in this atlas is anchored to a physical EC_{50} and scaled to one reference is that a map whose scale drifts is worse than no map at all — it will send you confidently to the wrong place. So we hold the whole library to one locked set of figures, and we will state them here plainly, because an atlas that cannot keep its own numbers straight has no business asking you to trust its coordinates:

QUANTITY	LOCKED FIGURE
Engineered constructs	~19,000
Live / purchasable today	1,000
Total SKUs	78,800
Host organisms surveyed	42
Sensory meridians	8
Batch coefficient of variation	≤7%
Patents filed	3
Peer-reviewed papers (Zenodo, CC BY 4.0)	21

Those twenty-one papers, released openly under a Creative Commons license, are the part of this we are proudest of in the plain professional sense — because a coordinate that cannot be checked is a rumor, and we would rather hand the world a map it can audit than a marvel it has to take on faith. The three patents protect the instruments; the open papers give away the readings. We think that is the right division, and it is the one this atlas is built on.

The locked figures also carry a quieter discipline, the one that keeps sixty-four books from contradicting one another. A number that drifts across a library — nineteen thousand constructs here, a different count there, a thousand "live" on one page and something else on the next — reads as sloppiness even when every individual figure was once true, because a reader cannot tell an honest

revision from a careless one. So the whole library resolves every count against a single source: the figures in the table above are the figures in every other volume, in every web entity page, in every catalog, pulled from one place and changed in one place. An atlas is a promise about proportion, and the promise has to hold between the pages as strictly as within them. A map whose own legend disagreed with itself would be no map at all — and across sixteen thousand pages, consistency is not a nicety but the whole claim to trust.



FIG. 17.1 — the greenhouse at dusk. The computing was one pair of hands; the country it mapped belongs to the family that grew it.

Second, the map is an argument for a particular relationship between wonder and rigor — the one that runs under every chapter here and that we will name now that the survey is done. We began this book by saying that a map drawn with love and a map drawn to scale are the same map if the cartographer is any good. We meant it as the whole method. The reverence is not decoration on the science and the science is not a cage around the reverence; they are two readings of one thing. When we write that a tomato's umami was 2,600 and the truck took ninety-three percent of it, the number is the love — it is how much we cared to measure what was lost. When we write that Phoenix is designed to read on all eight meridians, the wonder is the rigor — it is a thing that could only be known by being computed and placed on the Index, a marvel that is *made of* its own precision. An atlas is where those two stop being opposites.

Third, the map is a *living* document, and an honest atlas says so. The country it charts is growing — forty-two territories today, sixty-four more charted at the edge, new intersections named as fast as anyone wants to walk to them — which means this volume is a snapshot of a survey that never stops, and every coordinate in it is a hypothesis held open to re-measurement. This is where the ≤7% coefficient of variation does its quietest and most important work: a map is only re-surveyable if its benchmarks hold still between editions, and a flavor that drifts batch to batch cannot anchor a coordinate any more than a shoreline that moves can anchor a chart. The tight CV is what lets a reading taken this year still mean the same thing next year — what makes the atlas a document that can be *revised* rather than merely *replaced*. We expect to redraw it. We expect the frontier to move inward as T1 and T2 are walked and surveyed, the terra incognita to shrink, new famous cells to join the

four, and some number here and there to be corrected by a better measurement — and we regard all of that not as the atlas failing but as the atlas doing exactly what a living map is for. A map that could never be redrawn would be a map of a dead country.

Last, the map is an argument about what the country is for. We have kept the nourishment note quiet through this whole book, as we keep it quiet through the whole library, and we will keep it quiet now — one sentence, no claim, and then silence. We grow these organisms to carry the most flavor they honestly can and, by the same pathways and the same care, the most nourishment they honestly can, because to us those have never been two projects; and the atlas is, under its coordinates, a record of that single intention mapped across forty-two living things. You do not have to read it that way. The coordinates are true regardless. But a map tells you, if you look, what its makers were looking *for* — and we were looking for a way to grow food that is as good for the body as it is loud on the tongue, and to be able to prove both.

These are computational designs; Scoville Splice's cultivars and constructs have not been experimentally validated in a laboratory. Every coordinate in this atlas is a prediction, a design, an address in flavor-space we are working toward — and the whole value of the Index is that those addresses are precise enough to be returnable, revisable, and honest about what they are.

A word, finally, about the *we* that has narrated this whole volume, because an honest atlas names its surveyors. The computing that found every edit in this book — the language-model scores, the flux models, the folded structures — was one pair of hands at a keyboard. But a survey is more than its instruments, and the work and the table this atlas came from belong to a family: the ones who grew the plants, cooked the results, argued the voice, and asked, one evening, the question that a company then spent years answering. We write as *we* because it is true. The map is a family's map. It always was.

Here is how to read the whole thing, in the end: not front to back, though you can, but the way anyone reads an atlas — by opening it to the place you need, trusting that the scale is honest, and finding your way from there to somewhere you have never been. The territories are surveyed. The meridians are ruled. The capital is built and the frontier is charted. The map is as complete as a map of a living, growing country can ever be, which is to say: complete enough to travel by, and unfinished on purpose at the edge, where the next volume is already being walked into existence. Welcome to the atlas. It is yours now. Go somewhere.