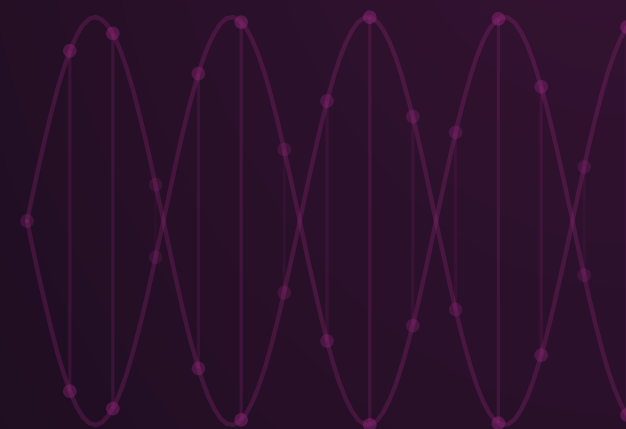


Lesson: the PTC taste test, and why the textbook version is wrong



Biology

Genetics

Statistics

Age 13+

Intermediate

A ready-to-run genetics lesson built on the PTC taste test — free to use in any school, college or university. Forty minutes, one paper strip, and the textbook version of the trait turns out to be wrong in a way that is more interesting than the original.

Free to read, use and adapt. No account, nothing to buy, nothing collected from anyone.

Full lesson, figures and updates: <https://www.mygenelog.com/updates/lesson-the-bitter-paper>

What this is. A ready-to-run genetics lesson, free to use and adapt in any school, college or university. Nothing to buy from us, no account, no data collected from anyone.

- Level: works from about age 13 through first-year undergraduate. The activity is the same at every level; the questions at the end are graded.
- Time: 40–50 minutes. The activity itself takes six.
- You need: commercially prepared PTC or PROP taste-test papers (a science supplier sells them for a few pounds a hundred), and a board to count on.
- It covers: alleles and genotypes, dominance and why it is a simplification, haplotypes, Hardy–Weinberg, expected versus observed, sample size, and how a textbook fact gets revised.

Start here: the accident

In 1931 a chemist called Arthur Fox was working with a powdered compound at a DuPont laboratory. Some of it escaped into the air. A colleague across the room complained about the bitter taste. Fox, who was closer to it, tasted nothing at all.

Most people would have shrugged. Fox went and got more of the compound, and started asking everybody he could find to taste it. Some people recoiled. Others could

not tell it from a blank strip of paper. It ran in families.

That compound was phenylthiocarbamide — PTC — and the argument that started across that laboratory is still going on, ninety-five years later. Your class can join it in the next forty minutes.

A note on the story: this account is repeated in a great many textbooks and we have not been able to check it against the original record. Treat it as the story the field tells about itself, which is a useful thing for students to notice in its own right.

Do this

1. Ask for a prediction first, before anyone tastes anything. "Put your hand up if you think you will taste something." Write the number on the board. You will come back to it, and the gap between what people expect and what happens is half the lesson.
2. Hand out a control strip. Plain paper, no chemical. Everyone touches it to their tongue. Nobody should taste anything. This matters more than it sounds: without it, some students will report a taste from suggestion alone, and you will have taught them the wrong lesson about evidence.
3. Hand out the test strip. Touch to the tongue, no chewing, no swallowing. Follow the supplier's own instructions — they are on the packet, and they are the ones that count.
4. Count three groups, not two: tasted nothing / tasted something faintly / that was horrible. Write all three on the board.
5. Now ask the question that opens the lesson: why are there three groups when the textbook says there are two?

Before you run it. Use commercially prepared test papers from a science supplier and follow their instructions — never make a solution yourself. Check your institution's own policy first. Nobody should be pressed to take part, and a student who would rather not can do the counting, which is the more interesting job anyway.

And this one really matters. Do not record who tasted what against anybody's name, and do not ask students about their families. A taste result is a piece of somebody's genetics. Counting a room is a lesson; a list of names is a record about children that nobody needs and nobody should keep.

What the numbers look like



Most human traits are a single hill — height, blood pressure, almost anything you measure in a class. This one has two, with a valley between them. That shape is the whole reason anybody looked for a gene. Schematic, not measured data.

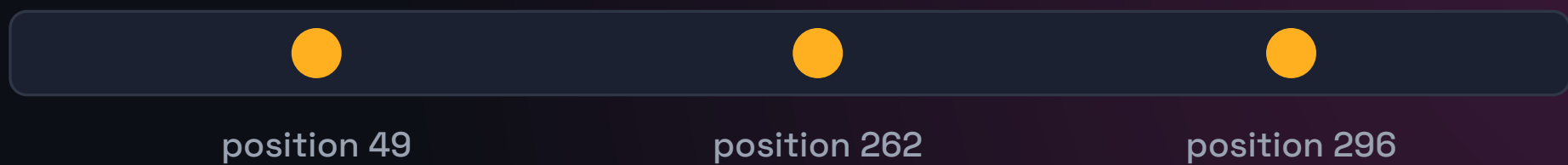
The first thing to notice is the shape. Almost everything you can measure about a class — height, reaction time, how long anyone can hold their breath — makes a single hill: a lot of people in the middle, fewer at each end. This does not. It makes two hills with a valley between them.

That shape is why anyone went looking for a gene. A trait that splits people into two groups is behaving as if something switch-like is behind it, and for seventy years the explanation was the simplest one available: one gene, two alleles, tasting dominant over not tasting.

The part the textbook gets wrong

It is not one gene with two alleles. It is one gene with three variable positions in it, and they are inherited together as a block.

TAS2R38 — one gene, on chromosome 7



PAV Pro · Ala · Val
the receptor works: the paper tastes bitter

AVI Ala · Val · Ile
the receptor barely responds: the paper tastes of paper

Three letters change, in the same gene, and they are inherited as a block. That block is what you actually have two of — one from each parent. Three more combinations exist and are rarer.

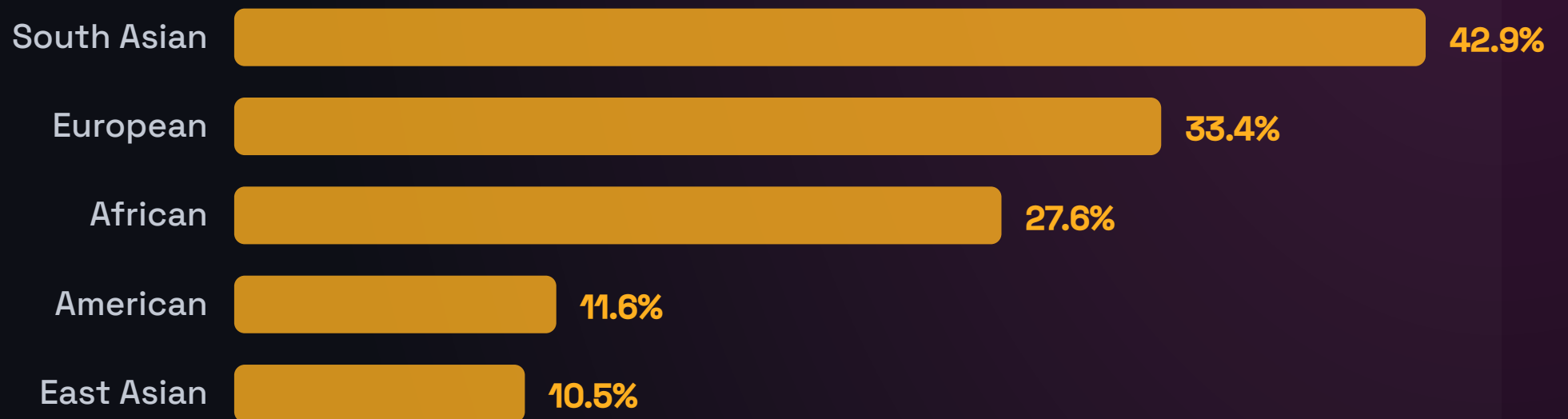
The gene was finally found in 2003. It codes for a bitter taste receptor, and it has three places where the DNA differs between people, each changing one amino acid. Those three positions are close together and travel as a unit — a haplotype — and worldwide there are five of them, of which two are common.

So what a person actually inherits is two haplotypes, one from each parent. Two working copies and the paper is unbearable. Two non-working and it tastes of paper. One of each, and you get the students in the middle — the group the one-gene-two-alleles version has nowhere to put.

The 2003 paper reported that these haplotypes account for between 55% and 85% of the variation in how strongly people taste PTC. That number is worth putting on the board on its own. It is very high for human genetics. It is also not 100%, and the missing part is a real question, not a rounding error.

Compare your class to the world

predicted share who taste nothing



Worked out from real allele frequencies (1000 Genomes, rs713598) using Hardy–Weinberg. It is a prediction from one of the three positions, not a count of anybody’s tongue — which is exactly what makes it useful to compare your class against.

Your class will not match any of those bars, and the reasons why are the best discussion in this lesson.

The bars are a prediction, calculated from allele frequencies using Hardy–Weinberg — and calculated from only one of the three positions, because that is the one with clean public frequency data. The real trait uses all three.

And a class is a small sample. Thirty people is not a population. If your class comes out at 20% when the prediction says 33%, that is roughly what you should expect from thirty coin flips, and demonstrating that to a class that has just produced the number themselves is worth more than any worksheet on sampling error.

The argument that is still open

Here is the question nobody has settled, and it is a good one to end on because the class can argue about it with the same information the researchers have.

Why do non-tasters still exist? Bitterness is a warning system — a lot of plant poisons are bitter. A broken warning system ought to be selected against. And yet every human population that has ever been tested contains people who cannot taste PTC, at substantial frequencies. Something has kept the non-working version around.

The long-standing answer was balancing selection: the non-working version must be good for something, perhaps letting people eat foods that tasters reject, so both versions survive.

Then in 2016 a study of 5,589 people from 105 populations looked for the signature that natural selection leaves in DNA. It found evidence of something ancient — older than modern humans leaving Africa — but nothing since. Its conclusion was that the

modern pattern is explained mostly by where people went and who they had children with, not by selection favouring one version.

That is a genuinely open argument, published in an open-access journal your students can read. Ask them which they find more convincing, and what evidence would settle it. There is no answer at the back of this book.

Questions

To warm up

1. Before anyone tasted anything, how many people predicted they would taste something? How close was the class? Why might people guess wrong about their own tongue?
2. Why did we start with a strip of plain paper? What would have happened without it?
3. Two students disagree about whether they tasted anything. Neither is lying. What does that tell you about measuring a trait?

Core

1. The textbook version says tasting is dominant. Our class had a group in the middle. Does that disprove dominance, or does it mean something more specific? Say exactly what.
2. Three DNA positions sit close together in one gene and are inherited as a block. Why does that make the trait look simpler than it is when you only measure the taste?
3. The haplotypes explain 55–85% of the variation. Give three different things that could account for the rest, and say how you would test one of them.
4. Our class result differs from the predicted bar for our part of the world. Give two reasons that have nothing to do with anybody being unusual.

To stretch

1. Hardy–Weinberg says the share of people with two copies of an allele is its frequency squared. Use the chart to work backwards: what allele frequency gives 33% non-tasters? Now say three assumptions you just made that are not true of any real human population.
2. Design an experiment that would distinguish “natural selection kept the non-working version” from “it is there because of where people migrated”. What would you measure? What result would change your mind?
3. This trait was taught as one gene with two alleles for about seventy years, and that was wrong. It was not a careless mistake — it fitted the evidence available. What does that suggest about the things in your textbook now?

Notes for whoever is teaching — where these questions are going

2. The control strip. Some students report a taste from expectation alone, and the plain strip is what exposes that. If nobody in your class does it, say so — that is also a result.

4. Dominance is not wrong, it is incomplete. Two working copies really do behave differently from one, so the trait is closer to incomplete dominance when you measure intensity rather than yes/no. The "dominant" version survived because early studies recorded a yes or a no, and a faint taste got written down as a yes.
5. Linkage. Because the three positions travel together, they behave like a single unit when you look from the outside, so a trait controlled by three things can look like a trait controlled by one. This is the general idea of a haplotype and it is worth naming.
6. Plenty of good answers: the two rarer haplotypes, differences in how many taste buds people have, age, smoking, whether they had just eaten, measurement error in the reporting itself. The testable ones are the good ones.
7. Sample size first — thirty people is a small sample and the swing is large. Then: the bars come from one position out of three; and the population labels in a reference dataset are a rough grouping, not a description of any actual class.
8. $\sqrt{0.334} \approx 0.58$, so a non-taster allele frequency near 58%. Assumptions include random mating, no selection, no migration, no mutation, and an infinite population — none of which is true of anywhere.
10. The honest answer is: some of it is wrong, we do not know which parts, and the way to find out is the method rather than the memorising. Most students have never been told this directly and it tends to land.

Take it further

- One gene, three answers — the same gene turns up in sinus infections and in how well an antibiotic works. Good extension reading.
- rs713598, rs1726866 and rs10246939 — the three positions, one page each, with the sources.
- What is a SNP — if the class needs the vocabulary first.
- Smell and taste — the rest of the sensory genetics on this site.

Use this freely. Print it, copy it, cut it up, put it on your own worksheet, translate it, change the questions. No permission needed and nothing to pay. If you credit it, mygenelog.com is enough.

If you teach with it and something in it does not work, tell us — that is worth more to us than a thank-you.