

How did you decide on your current research topics? When I moved to Tohoku University in 2015, I decided to take on a new challenge: exploring the evolution of hormone function, using strigolactone as a model. I expanded my research beyond angiosperms to include algae, bryophytes, ferns, and gymnosperms.

One of the greatest hurdles for early plants colonizing land was nutrient-poor soil. A key innovation was symbiosis with mycorrhizal fungi — a strategy now used by roughly 80% of land plants. Strigolactones were known to induce this symbiosis. Their identification as a class of plant hormones revealed them to be unique dual-function molecules: they act as interspecies signals that promote symbiosis in the soil, while also regulating shoot branching within the plant. We showed that this interspecies signaling role represents the ancestral function of strigolactones. We are now investigating how strigolactone signaling evolved from more ancient pathways to acquire its role in regulating plant architecture as a plant hormone.

Who was a key early influence on you? My late mentor, Ko Shimamoto, had a contrarian spirit — he deliberately avoided doing what everyone else was doing. At the time, I sometimes found this challenging. Yet his attitude profoundly shaped me. I did not follow the mainstream path of working on *Arabidopsis*, nor did I focus on auxin, the 'king' of plant hormones. In retrospect, that independence suited my personality. If I take on a problem, I want to pursue it thoroughly and see it through to the end. That determination is something I inherited from him.

What is the most useful advice you have come across? When I was young, I loved reading Kurt Vonnegut. I was drawn to his slightly ironic tone. In his novels, the phrase "So it goes" appears again and again. Research does not always proceed as we hope — sometimes it moves forward, and sometimes it does not. That simple phrase has helped me accept setbacks without frustration or haste. It reminds me to keep going steadily, without losing perspective.

At the same time, I have often returned to Dobzhansky's famous statement: "Nothing in biology makes sense except in the light of evolution." When observing the remarkable diversity of living organisms, I have repeatedly felt the depth of this insight. In fact, it was one of the motivations that led me to pursue evolutionary research.

What are the next challenges in plant developmental biology? We have made significant progress in understanding how plants grow in response to specific environmental cues. Yet much of this knowledge comes from controlled laboratory conditions — effectively snapshots of a far more dynamic reality. A major challenge is to understand plant growth as an integrated, multidimensional response to continuously fluctuating environments. Capturing that complexity will require new conceptual and experimental frameworks.

What advice would you offer young scientists? For many years, research in both animal and plant biology has focused on a small number of model organisms. Yet life on Earth is extraordinarily diverse. Each species has evolved unique survival strategies, while sharing deep common principles. There remain countless original questions waiting to be explored. I encourage young scientists to look beyond established systems and pursue questions that illuminate both the uniqueness and the universality of living organisms.

DECLARATION OF INTERESTS

The author declares no competing interests.

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Quick guide

Gene tree discordance

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What is gene tree discordance? Gene tree discordance occurs when the tree describing relationships among species differs from locus to locus, or between the species tree and the tree when only a specific gene is considered. Researchers usually do think there's a species tree that reflects the history of splitting among lineages, but not all genes have to have this same tree topology. As a result, this pattern is also called 'gene tree–species tree discordance' (though exactly how to hyphenate the phrase is debated).

What's a good example? Consider the relationships between humans, chimpanzees, and gorillas. The generally accepted species relationships put human and chimp together as the most closely related pair, with each equally distantly related to gorilla (Figure 1). This is almost certainly true. However, about 30% of the genome doesn't show this relationship, but rather one of the other two possible trees: either human+gorilla together (~15%) or chimp+gorilla together (~15%) (Figure 1).

Does this only happen in genes? No, the name 'gene tree discordance' simply dates back to a time when researchers couldn't imagine getting DNA sequences outside of genes for phylogenetic analysis. Now, we use it to refer to the tree describing relationships for any piece of DNA. In fact, every single base in the genome has a gene tree — this is its genealogical history. Recombination events allow the tree to possibly change between neighboring bases.

Is it all down to error? No, there really are different tree topologies in different parts of a genome. We know this both because of well-accepted theoretical models and because of careful empirical work. However, inferring gene trees from DNA sequences is still a messy business, so error definitely plays a role. In general, we can much more accurately estimate gene trees (and therefore gene tree discordance) among more closely related

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species. The deeper the splits among species, the harder it gets.

What are the biological causes of discordance? There are multiple biological reasons that gene trees can differ, the main three of which are introgression (i.e. hybridization and backcrossing), horizontal gene transfer (HGT), and incomplete lineage sorting (ILS). If we're considering changes in the number of gene copies among gene trees, then duplication and loss also play a role in generating discordance.

How does it come about? The ways that introgression and horizontal gene transfer cause discordance are probably immediately obvious. Genetic material found in one organism traces its ancestry back through another organism — the donor of the foreign genetic material. While introgression usually happens through sexual reproduction and horizontal gene transfer via conjugation or other non-sexual mechanisms, the result of both is often a discordant gene tree. It should be mentioned that sequence convergence is not a biological cause of discordance. While convergent DNA changes might lead you to infer the wrong tree, the underlying relationships among sequences have not changed.

What about incomplete lineage sorting? Incomplete lineage sorting is definitely the most common, and probably the most confusing, cause of gene tree discordance. The name doesn't help, as it does not seem to evoke a clear picture for most people (it is also referred to as 'deep coalescence' or 'shared ancestral polymorphism', if either of those help).

So what is incomplete lineage sorting? The best way to explain it is to think about the relationships between two sequences (in this case let's take one sample each from human and chimp) looking backwards in time. If we trace the history of these lineages, they are obviously separate when they're in the tip branches of the tree, but at some point they both enter the population representing the shared human/chimp ancestor (colored blue in Figure 1). At this point these lineages represent two random individuals that existed in this ancestral population, individuals who shared a common ancestor hundreds of thousands to millions of years earlier. Importantly, because of recombination, the time to the common ancestor differs among loci (this is also true of any two individuals sequenced today). When two lineages find a common ancestor we say that they have 'coalesced', and in fact the coalescent model describes the distribution of waiting times to a common ancestor among loci. As another way to think about it, just because humans and chimps split six million years ago doesn't mean that any particular sequence in these two species also split six million years ago — it still has to wait a long time to coalesce in the ancestral population (hence 'deep coalescence').

But we still haven't gotten to incomplete lineage sorting. As soon as those two lineages enter the human-chimp ancestral population (still looking backwards in time), a clock starts ticking because the split from gorilla was only ~10 million years ago. If the 'human' and 'chimp' lineages in this ancestral population coalesce quickly, great — the gene tree will definitely match the species tree. We say that these lineages have 'sorted'. But if they don't coalesce before reaching the ancestral population they share with gorilla (colored yellow-orange in Figure 1), then either of them can coalesce with a lineage ancestral to current-day gorilla samples, which would lead to a discordant gene tree. This lack of coalescence in the human-chimp ancestral population is called 'incomplete lineage sorting'.

All of this means that the probability of incomplete lineage sorting is determined by the time between speciation events: the shorter the time, the more opportunity for incomplete lineage sorting and discordance. It's also important to note that this genealogical pattern doesn't go away: no matter how long the tip branches are, the discordance is still there because the internal branch of the tree was short. So incomplete lineage sorting can occur at any time in the past.

How much discordance is there? A lot. Most genome-scale datasets find at least some discordance due to incomplete lineage sorting, and in several studies of species radiations (where the time between multiple speciation events is very short) no single gene tree matches the species tree. And this is not an error — it's expected under incomplete lineage sorting alone!

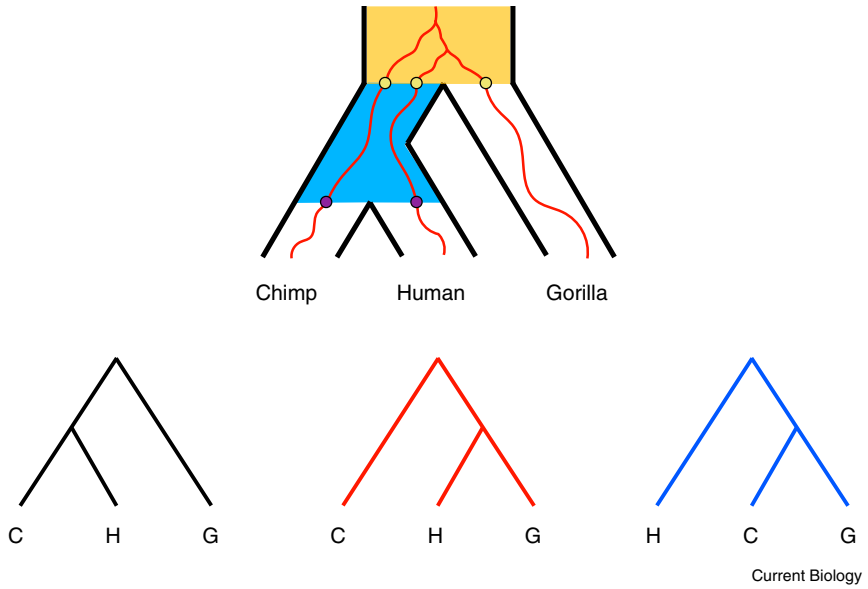


Figure 1. Gene tree discordance and incomplete lineage sorting (ILS) in the great apes. (Top) Accepted species relationships and an example gene tree (red lines). When the chimp and human lineages of the gene tree reach their shared ancestral population (blue) but do not coalesce, there is ILS. When the chimp, human and gorilla gene tree lineages reach their shared ancestral population (yellow), all three must coalesce. (Bottom) Only the left-most gene tree is concordant with the species tree and is the only topology generated without ILS. The others are discordant and are generated with equal frequency under ILS.

So what's the big problem? For a long time, researchers thought that genomic data would provide unambiguous answers about the Tree of Life. To a certain degree this has come true — most contentious sets of relationships have been resolved into a well-supported species tree. But knowing the species tree does not mean you know the history of genes and traits, and so now there is a major effort to understand what we might call the 'Gene Trees of Life'.

Beyond the need to simply describe discordance, it turns out that ignoring it can have dire consequences for many types of analyses. For instance, ignoring gene tree discordance can lead to the wrong answer when inferring species trees, positive selection, the occurrence of convergent evolution, rates of evolution for both DNA sequences and quantitative traits, as well as the number of gene duplications and losses that have occurred. Discordance is here to stay, so we have to find a way to understand and deal with it.

Where can I find out more?

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DECLARATION OF INTERESTS

The author declares no competing interests.

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Essay

Storms, budworms and vagrant birds in a changing world

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The seasonal migration of billions of birds is one of the most spectacular events in the natural world's annual cycle. Migration lets birds exploit spatiotemporally dynamic resources and involves complex trade-offs for survivorship. The migratory movements of individual birds are routinely influenced by atmospheric and ecological connections across long distances. Suboptimal conditions during active migration often lead to bird displacement, sometimes *en masse*. Birds that are displaced outside of their regular geographic ranges are known as vagrants, arguably the most spectacular instances of which involve transoceanic and transhemispheric movements of small songbirds. Vagrants have been catalogued by amateur ornithologists for decades, but there is now a renewed scientific interest in the causes and consequences of vagrancy — in particular as a prelude to range shifts that are prone to become more likely under global change. Against the backdrop of an unprecedented arrival of vagrant North American songbirds in Western Europe in September 2023, we discuss the environmental drivers that influenced this transoceanic movement and the latest scientific literature exploring the phenomenon.

Bird migration has captivated the human imagination for millennia and commanded scientific interest for centuries. The scale of these movements remains vast, despite widespread population declines in many migratory species[1]. For example, almost half of all Nearctic species migrate to the Neotropics annually[2], and over two billion individual landbirds cross the Sahara each autumn *en route* from the Palearctic to the Afrotropics[3]. Seasonal migration offers opportunities to exploit seasonally available resources, such as emerging insects or ripening fruits, but it also exposes individual birds to risks during periods of movement, including displacement by inclement or extreme weather[4]. This risk applies especially to terrestrial birds that travel along coasts or cross oceans and thus are vulnerable to displacement by storm systems over water where, unlike seabirds, they cannot land. For example, several hundred million birds migrate annually in autumn over the western North Atlantic[5]; some species, notably Blackpoll Warblers (*Setophaga striata*), may undertake southbound migration in a single, uninterrupted flight of up to 2500 km over the Atlantic Ocean[6]. These migrants' transoceanic routes likely evolved as an accident of geography — an overwater movement takes many species directly on a great circle route to wintering grounds in the Caribbean or South America. Migration flows across eastern North America may exceed one billion birds in a single night[7] and even species that do not habitually move along coastlines or offshore may be vulnerable to wind drift associated with storm events and strong pre- or post-frontal winds[8].

Every autumn, small numbers of vagrant Nearctic-Neotropical landbirds arrive on the western European seaboard (often on headlands and coastal islands) after completing a flight across the North Atlantic, with more arriving on the mid-oceanic archipelago of the Azores[9]. The ultimate mechanism underlying these movements is the passage of strong storm systems moving from North America to Europe that carry birds across the Atlantic[10], but misorientation may be a complementary mechanism. This mechanism led to an exceptional arrival of vagrant Nearctic passerines in Britain and Ireland in autumn 2023, with a total of ~99 individuals of 27 species (Figures 1 and 2), the highest ever autumn total; this season also saw record numbers and diversity for the Azores, which hosted 181 individuals of 36 species[11],

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