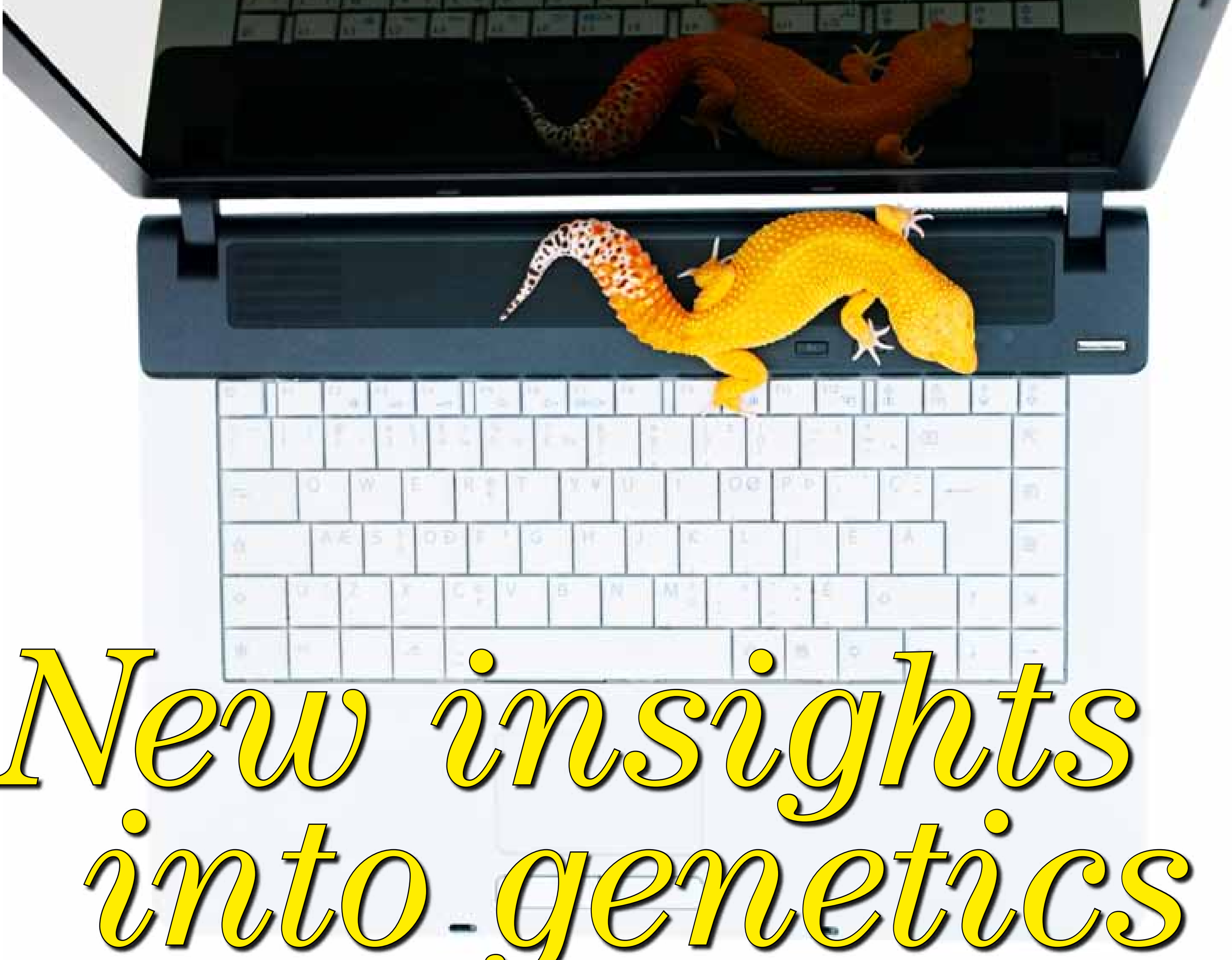


New insights into genetics

As interest in new, more desirable mutations grows, and their availability increases, so it is essential to build a better understanding of the genetics involved and an improved way of being able to describe the genes themselves, argues Andy Tedder.

Incomplete dominant

OK, this is a special type of dominance in which the allele in question creates different phenotypes when present with either a dominant or a recessive allele. It can be represented as an intermediate state. In a number of cases, an incomplete dominant trait may not express itself visually when paired with a dominant allele. This is believed to be the case with the snow mutation which is now well-known in the leopard gecko (*Eublepharis macularius*). The important thing to remember is that in cases of incomplete dominance, the individual's phenotype – appearance – is therefore dependent on the interaction with the other allele.

This can be a difficult concept to understand, but it is believed to be an inbreeding avoidance mechanism, where novel genotypes and phenotypes can arise from closely-related individuals. This becomes particularly important when considering traits such as colouration, in terms of camouflage, or even characteristics such as head size, which impact on the type of prey which is taken.

In the Punnett Square system, incomplete dominant traits are recorded using the same letter as the "normal"

A T-positive form of the Colombian boa constrictor.

> *"A well-known example of co-dominance is the trait of hypomelanism in the Colombian boa constrictor (***Boa constrictor imperator***)."*

dominant trait, but with the addition of an apostrophe. This is known as a "prime". In our examples here, an incomplete dominant form of hypomelanism is notated as H', pronounced "H prime".

		Male	
		H'	H
Female	H	H'H	HH
	H	H'H	HH

A well-known example of co-dominance is the trait of hypomelanism in the Colombian boa constrictor (*Boa constrictor imperator*). In the Punnett Square above, we cross a male "hypo" morph to a normal female.

Statistically, this cross will produce 50 per cent hypomelanistic specimens. As always, each of the resulting offspring received one allele from each parent. Thus half are heterozygous for hypomelanism (hypomelanistic, H'H), and half of the offspring are normal (HH).

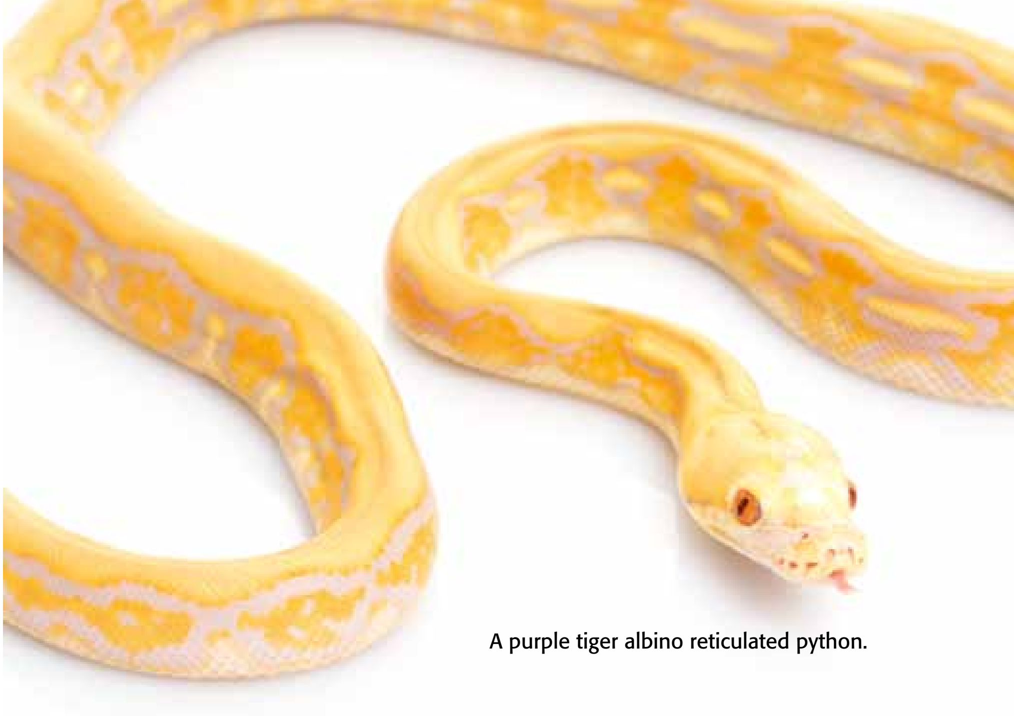
When two hypomelanistic specimens are bred together, the results below are the same genetically as any other pairing of two heterozygous specimens.

- 25% are HH (completely normal)
- 50% are H'H (heterozygous for hypomelanism)
- 25% are H'H' (homozygous for hypomelanism)

		Male	
		H'	H
Female	H'	H'H'	H'H
	H	H'H	HH

Remember that the appearance of these animals will be quite different, as the incomplete dominant trait expresses itself visually even in the heterozygous state. The normal (HH) animals will appear completely normal, while the heterozygous specimens (H'H) will appear hypomelanistic. In the case of the Colombian boa constrictor, homozygous for hypomelanism animals (H'H') will exhibit a much greater influence on appearance and are trade-named "super-hypo".

Another classic example is the "tiger" and "super-tiger" morphs of reticulated python (*Python reticulatus*) developed by Al & Cindy Baldogo. When the original tiger retic was bred to a normal snake, half the offspring were tigers! Knowing full-well that the odds of the normal snake being heterozygous for "tiger" were astronomical, the Baldogos believed (correctly) that this trait was a incomplete dominant recessive. This was later proven when two of them were bred together. This breeding yielded yet another surprise when one-fourth of the offspring exhibited a new appearance - that of the "super-tiger". These animals are now known to be homozygous for the "tiger" trait, while tigers are heterozygous for the same trait.



A purple tiger albino reticulated python.

Exploratory pairings required

In other species where co-dominance is recognised, there may be no difference in appearance between heterozygous and homozygous individuals, although much more research is needed in this area. This finding has severe consequences for the breeder, as it is possible that his or her cherished animal may in fact be heterozygous (H'H), rather than homozygous (H'H'). When this is the case, the only way to distinguish the two is through several breedings and tabulating the outcomes. Many of these genotypes have been inadequately explored, and there is still much room for new discoveries.

This is most likely the case with the two related traits in leopard geckos known as hypomelanism and hyperxanthism. Both these traits have been demonstrated by breeding experiments to be incomplete dominant recessive traits when expressed against 'normal' genotypes.

Breeding two hypomelanistic or two hyperxanthic leopard geckos together does not always result in similar offspring. However, the resultant ratios of offspring are fairly consistent with expected results if these traits were incomplete dominant against normal traits. Confusingly though, they also appear to be to incomplete dominant with each other! In other words, all three traits have an equal chance of expressing themselves visually when combined. Additionally, it appears that hypomelanism and hyperxanthism can be expressed visually in the same animal, at the same time, yielding astonishing results. Much more study is again needed on this subject – that is part of the appeal of working with these types of animals.

The normal dominant situation

This is a much more straightforward situation, with a dominant gene altering the appearance of an individual when only one copy of that gene is present. It will equally alter the appearance if two copies are present. There is no "super'" form of appearance. Needless to say, this makes determining whether such a specimen has one copy (a heterozygous individual) or two copies (the homozygous state) a real challenge. Breeding trials to normal specimens are the only way to be certain.

What does all this mean? Simply put, it means that you better know your breeder when buying these animals! Moreover, you better make sure the breeder understands all of this – as many don't, and may misrepresent their stock accordingly.

New thinking

But it is also clear now that a simplified understanding of genetics can lead to serious errors. As our understanding of reptile mutations continues to evolve, we begin to see various outcomes of breeding trials which yield seemingly unexpected results. In reality however, these results are perfectly understandable with an increased knowledge of the complexity of genetics.

Think of it like this: all humans look pretty much alike because each locus stays in order, yet each human has recognizable variations as a result of the different alleles present at each locus. For example, there are several alleles available for the eye colour locus. Thus we have friends with blue eyes, green eyes, brown eyes and so on – but they all have eyes because regardless of changes in the allele, the locus is still there.

If we were to reduce the number of possible alleles at every locus to only one however, then all of us would be identical! This is exactly what happens when a clone is created, because every allele at every locus is identical to the original – not very realistic in practice, but makes for some great sci-fi movies!

How does all this change anything?

Well, let me give an example:-
Recently a number of cornsnake breeders attempted to resolve the confusion over what appeared to be several types of ▶

Hypomelanistic leopard geckos have their spotted patterning restricted to their banded areas.

hypomelanism and a strange looking new albino form derived from one of these hypomelanistic varieties. What was discovered could not be explained by a conventional knowledge of genetics as understood by most reptile breeders.

It seems that one type of hypomelanism (named 'ultra hypo') when bred to another of the same would produce more ultra hypo specimens. No surprise there. The surprise comes in when one of these snakes is bred to an amelanistic (albino) specimen. Conventional wisdom would lead the breeder to expect all of the offspring from this crossing to appear normal, and each to be heterozygous for both ultra hypo and albino.

Instead, all of the babies appeared to be a strange new type of albino, named ultramel. And when an ultramel was bred back to either an albino or or an ultra, half the resulting offspring looked like each parent! Using conventional 'reptile breeder knowledge' of genetics, this should be impossible!

Ok, so clearly something interesting was going on and it seems that the new form of hypomelanism (ultra) shared the same locus as amelanism. They were different alleles residing at the same locus. Thus ultra specimens have two copies of the ultra allele at that locus, while the albino specimens have two copies of the amelanism allele at that same locus. Ultramel specimens have one copy of each type at that same locus.

Many readers would ask: "If these ultramels have only one copy of each trait, they must be heterozygous for these traits, and why don't they appear as wild-type cornsnakes?" The answer is simple: since there is one copy of each allele present at the locus, there can be no copy of the wild-type allele at that locus to control the appearance!

Hypomelanistic corn snake.

A new language

While it's great to have figured this out, it's also forced another problem upon us. Reptile breeders have grown accustomed to using a very simplified method of representing the genes involved in these mutations with a single letter. This system of notation for genes (as used in our example Punnett Squares) does not take into account the concept of different alleles being able to reside at the same loci. It assumes that each loci can have one of two alleles, the normal or wild-type and the mutation involved with that loci. But as we've just seen, more than one type of mutated allele can reside at the same loci.

So a more proper form of notation is being offered to the reptile community. It was initially set out in the 2005 Cornsnake Morph Guide, and is something that has recently been made up. It's the way it SHOULD have been presented to the reptile community from day one. Many mysteries could have been avoided if this system had been in place.

It works like this: large letters represent each loci, with smaller superscripted letters representing the alleles for that loci. Normal or wild-type alleles are represented with a +. An example for an amelanistic specimen would be aaaa, whereas using the previously accepted method of notation, it would simply be aa. A specimen heterozygous for amelanism would therefore be represented as A+aa.

While this may appear only to be twice the letters and nothing more, the real value can be seen when used to describe the various ultra, ultramel, and albinos from the example above. This gives aaaa= albino; auau= ultra; aaau=ultramel. Notice that we can now see that all involve the same loci (a) but the different alleles can now be seen at that loci (a or u). Better still, we can now see the various allele combinations present and easily predict what offspring we will produce from any given pairing! This would be impossible with the older system. ■

**Andy Tedder is an enthusiastic breeder of geckos, and has a particular interest in genetics. You can find his website at www.glasgowgecko.co.uk*