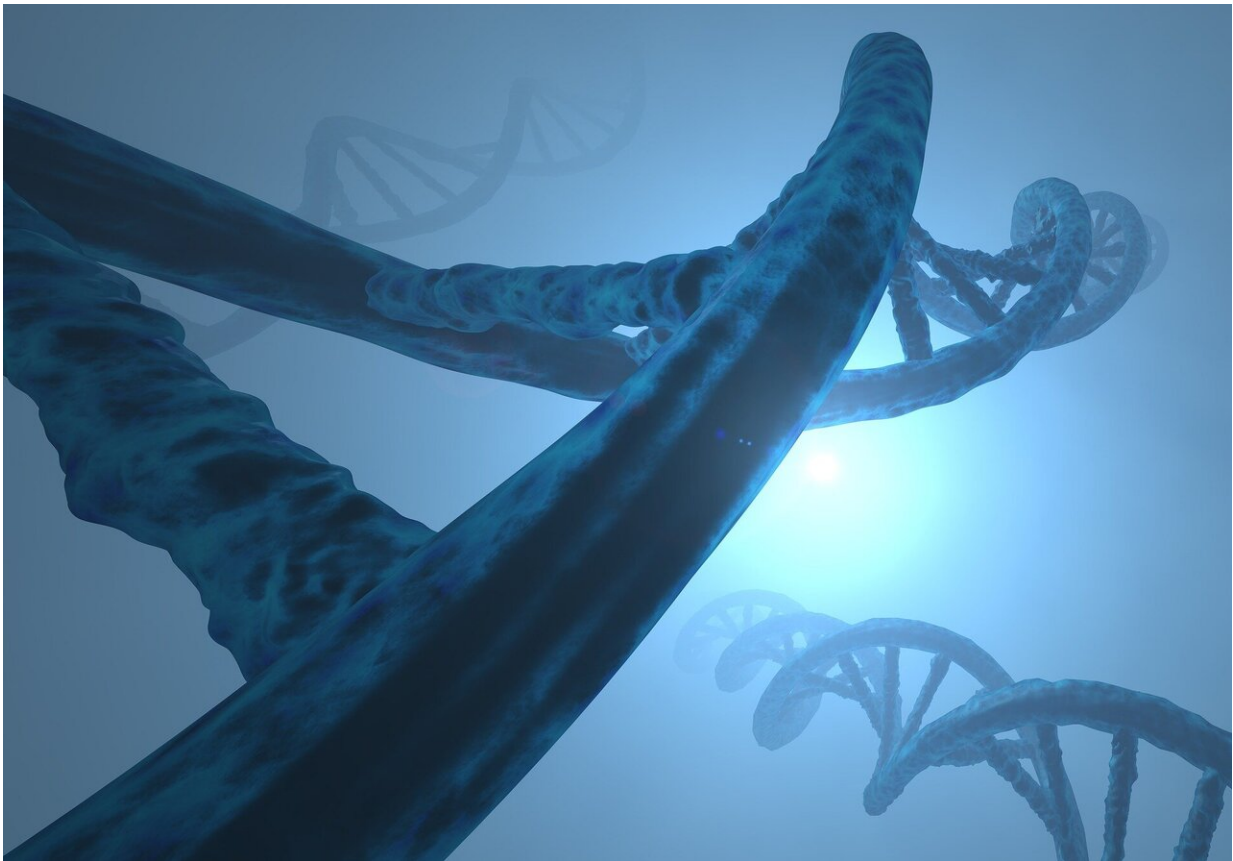


# How chromosomes evolve to create new forms of life

January 27 2021, by John Hewitt

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Credit: Pixabay/CC0 Public Domain

3-D printing is a universal process in the sense that pretty much any part that can be drawn up in a CAD program can be printed, at least within a certain resolution. Machining a part on a mill or lathe, while having the

advantage of greater accuracy and material options, is a slightly less universal process in that many possible designs that exist in theory could never be machined. A hollow sphere can easily be printed, but a ball could never be milled as a single part into a hollow sphere—unless you happen to have a milling machine tiny enough to fit inside the ball. But what about biological parts, and whole animals? How universal, from a design perspective, is growth?

What we are really asking here is: How universal is the [genetic code](#) in its ability to specify viable, and fertile, body plans? Yesterday, we discussed a new project called '[genome](#) in a box' that seeks to create [artificial chromosomes](#) from the ground up, starting with the raw genetic sequence and then adding in appropriate organizing proteins to create a reasonable facsimile of an intact chromosome. One of the main challenges in this endeavor was seen as getting the larger-scale structures, the so-called topologically associating domains (TADs) in the right spots. The question was posed as to whether or not any arbitrary creature like, for example, a dragon, could be fully coded in DNA. If it can, then what might the chromosomes look like, and furthermore, could there be different ways to code for the same organism?

Unfortunately, the closest approximations we have in the fossil record to a dragon (probably an extinct Pterosaur or Brontornis 'terror bird'), don't come with readily sequenceable genomes. However, we do have ample sequence data for what might be the next best thing—namely, their feathered avian descendants. Beyond the raw sequence, what we really want to know, as far as how genomes proscribe real animals, is how genomes change to evolve new forms. It is by now well appreciated that simple base-pair mutations or epigenetic modifications can fine tune minor species incidentals like coloration, parasite resistance and environmental adaptation to temperature or altitude.

However, the real speciation events, those gross affronts that free up the

code to depart radically from a traditional body plan, usually require more drastic adjustments to the karyotype. In other words, any currently stable chromosome table must be sufficiently perturbed through major breakages, fusions, inversions or duplications in order for a species to fork. If significant enough, these processes can cause a loss of universal mating compatibility wherein all newly generated offspring cannot necessarily mate successfully with all the other new offspring. In this case, local backcrossing events with the parental genomes could generate a minimal pool of viable offspring with a new species identity.

For studying the evolution of avian genomes, the chicken has proven to be invaluable. Because of their large and readily obtained eggs, chicks also make a great model for developmental studies. One eminently practical application of chicken genome knowledge has the industrial creation of chicks that can be readily sexed by the color of their plumage. Not to be outdone, students of the avian genome in China have decided to delve deeper into the duck genome, because in their own words, Peking duck makes an amazing dish. In their recent paper in the journal *Gigascience*, researchers from Zhejiang University in Hangzhou report a new mapping of the entire duck genome and all its associated TAD regions.

As far as birds go, the duck genome is intermediate between the chick genome on the one hand, and emu genomes on the other. What really matters, as far as how karyotypes evolve, is sex. In other words, the nitty gritty details lurking behind the origins of large speciation events tend to revolve around the particulars of the sex chromosomes. These details include which autosome fragments fuse in the founding of new sex chromosomes, their relative sizes compared to their complement, their number, pseudogene content, repeat regions and degree of recombination. In the case of the duck, the sex chromosomes are not as highly heteromorphic as those of the chicken, nor quite as homomorphic as those of the emu.

The haploid genome of the Pekin duck is about 1.4 Gb with a karyotype of nine pairs of macrochromosomes (chr1–chr8, chrZ/chrW) and 31 pairs of microchromosomes (chr9–chr39). These specs are very different from those of most mammals, but fairly typical of birds. The small total genome size, the Z/W sex determination system and large number of minichromosomes are also features sometimes found in other species like reptiles and perhaps some dinosaurs. It should be noted that the bird and snake Z/W are unrelated, having evolved from different autosomes. The Z/W system is different from X/Y and X0 systems in which the sperm has the power of sex determination. The ovum controls the sex in the Z/W system, where males are the homogametic sex (Z/Z) and females are the heterogametic sex (Z/W). The Z chromosome is larger and has more genes than the W, much like the X chromosome in the XY system. Curiously, it is the male birds that are the colorful, displaying type, while the female birds are often duller and larger.

As there are no genes shared between avian Z/W and mammalian X/Y chromosomes, both systems likely share a common ancestor from which they independently evolved. The Z chromosome has features more representative of human chromosome 9 rather than X or Y. Gaining more insight into how chromosomes evolve could entail a closer look at some of the more extreme points of the system, like the duck-billed platypus. This monotreme beaver-bird mammal has five separate pairs of XY chromosomes, and is not directly related to beavers or ducks. In male germ cell meiosis, the the platypus sex chromosomes form a chain linked together by homologous regions, which ultimately segregates into XXXXX-sperm and YYYYY-sperm.

The most bird-like pair in the lot, which has some Z chromosome character, shows up on opposite ends of the chain. Additional segments with lesser Z homology are scattered throughout the X3 and X5 chromosomes. From a recent study of the [platypus and echidna](#) genomes, researchers were able to deduce that our own X chromosome

derives from a fusion of the original therian X chromosome with an autosomal region after the divergence from marsupials. As in birds, our sex chromosomes were similarly formed through stepwise suppression of recombination in autosomes. This process resulted in patterns of pairwise sequence divergence between sex determination regions, which are termed "evolutionary strata."

Another useful critical point on the genome landscape is that of the Australian lungfish. [Recent research](#) indicates that its genome is over 43 billion bps long (14 times bigger than humans), making it the largest known genome. Many lungfish chromosomes are each individually larger than our own entire genomes. There are large intergenic regions and introns with high LINE element repeat content ( $\approx 90\%$ ) that bear more resemblance to those of tetrapods than to ray-finned fish. It appears that the lungfish genome is still growing, with continued expansion at its active transposable element sites.

As the lungfish body plan represents a major transition for vertebrate evolution, it is perhaps not surprising that their [chromosomes](#) lug around a lot of extra raw material despite the huge overhead in cell cycle time and exorbitant nucleotide demand. Lungfish terrestrialization involved the new expression of limb-like patterns of genes such as *hoxc133* and *sall1* in preadapted lobed fins. Duplication of gene regions coding for surfactants enabled obligate air breathing, while proliferation of olfactory receptor genes permitted detection of odorants.

To return to the original question of how universal the process of growth, and therefore genetic codes, might be for building animals, one useful conception is that of reversibility. While any 3-D drawn object can be printed, the particular G-code used to print that object can not be readily predicted (G-code is the metonymically established name for the series of "Go" codes to move the tool). The reason is that many possible codes, or toolpaths, could be used to make the same object. It is

therefore not one-to-one, and in that sense, not reversible. It is reversible, however, in the sense that every object does have at least *one* G-code associated with it. But not every possible G-code has a real object associated with it. For example, one can't lay down plastic twice in the same spot, or print in thin air on Earth.

One might suggest that almost all theoretical organisms or body plans that could be drawn on a computer could never actually be coded in DNA and grown. Surely, some animals that have never appeared in the fossil record could evolve in the future given time and resources, but how different can they actually become before the system grinds to a halt? At the upper size limit, things get pretty dull—either giant cetacean cylinders in the sea, or lumbering and surprisingly symmetrical tetrapod giants. Although time and resources are real constraints, the biggest constraint is probably the code itself.

**More information:** Jing Li et al. A new duck genome reveals conserved and convergently evolved chromosome architectures of birds and mammals, *GigaScience* (2021). [DOI: 10.1093/gigascience/giaa142](https://doi.org/10.1093/gigascience/giaa142)

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