

Discovering the bigger picture in chromosomes

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By mapping various genomes onto an X-Y axis, a team comprised mostly of Kansas State University researchers has found that Charles Darwin and a fruit fly -- among other organisms -- have a lot in common genetically.

Their discovery, "Chromosome Size in Diploid Eukaryotic Species Centers on the Average Length with a Conserved Boundary," was recently published in the journal [Molecular Biology and Evolution](#). It details a project that compared 886 chromosomes in 68 random species of eukaryotes -- organisms whose cells contain a nucleus and are enclosed by [cellular membranes](#). The researchers found that the chromosome sizes within each eukaryotic species are actually similar rather than drastically different as previously believed. They also found that the chromosomes of these different organisms share a similar distribution pattern.

Because chromosomes are the genetic building blocks for an organism and its traits, the information will be beneficial to understanding the core components of biological evolution -- especially in genetics and genome evolution, said Jianming Yu, associate professor of agronomy at Kansas State University. With this data, scientists can now better predict the evolutionary adaptations of an organism.

"Basically what this all means is that if the chromosome number of a species can be given, the relative sizes of all the chromosomes can instantly be known," Yu said. "Also, if you tell me the genome size in the

chromosome base pair, I can tell you the base pair length of each chromosome."

According to Yu, the most surprising finding is the extremely consistent distribution pattern of the chromosomes, a result from comparing the full sets of chromosomes -- called genomes -- of the 68 random eukaryotes. The team found that nearly every genome perfectly formed an S-curve of ascending chromosomal lengths when placed on a standardized X-Y axis. That meant the genome from a species of rice expressed the same pattern as the genome from a species of maize, sorghum, fruit fly, dog, chimpanzee, etc.

In order to reach these findings, though, the team started by comparing various genomes of species from multiple organisms, looking for similarities. The genomes selected were from eukaryotes; prokaryotes -- organisms like bacteria that contain no cell nucleus; vertebrates -- organisms with a spine; invertebrates -- organisms without a spine, such as insects; vascular plants -- plants that can transport food and material throughout their tissue; and unicellular organisms.

From there the team looked specifically at the chromosomes of 68 random eukaryote genomes. This amounted to observing 886 chromosomes, 22 of which were human autosomes -- any chromosome other than a sex chromosome. The sex chromosomes of each species were omitted because of their vastly different evolutionary history from other chromosomes, Yu said.

The researchers placed each fully sequenced eukaryote genome onto an X-Y axis, hoping to find similarities between the various organisms. To help generalize the vast amount of information, the X-Y axis graph was standardized with each species.

"It eliminated a scale effect and made it possible to compare a species

with several dozen chromosomes to a species with much fewer chromosomes," said Xianran Li, research associate in agronomy.

That's when the team noticed the shockingly consistent distribution pattern.

"We could not believe this the first time the plot was generated," said Chengsong Zhu, research associate in agronomy.

The only genomes that deviated from forming an S-curve were that of the platypus -- an organism that contains characteristics of birds, reptiles, mammals, amphibians and fish -- and those of birds. Birds are unique because in addition to their usual chromosome sequences, they contain one additional set of minichromosome sequences, according to Zhongwei Lin, research associate in agronomy.

By finding normal distribution in nearly all of the genomes they used, geneticists can now say that if a species has a particular number of chromosomes, the [chromosomes](#) have to be distributed in this order because it's dictated by the laws of mitosis, meiosis and cell division, according to Guihua Bai, adjunct professor of [agronomy](#) at Kansas State University and research geneticist of the U.S. Department of Agriculture-Agricultural Research Service.

"The integration of biology and statistics holds enormous promises to gain insights from genomic data and life processes," said Min Zhang, associate professor of statistics from Purdue University and a co-author of the paper.

"We're in the genomic age, where sequencers and computers are constantly running and completing new [genome](#) sequences every day," Yu said. "We're expecting this information can help when it comes to finding similarities in those genomes. This type of broad analysis across

[species](#), taxonomic and disciplinary boundaries is really exciting in terms of discovering fundamental principles out of teeming genomic data."

More information:

mbe.oxfordjournals.org/content/28/6/1901.abstract

Provided by Kansas State University

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