# Oliver Allison Ryder III (1946? ) [1]

By:  Love, Karen Bailey, Renee

Oliver Allison Ryder studied chromosomal evolution [2] and endangered species in efforts for wildlife conservation and preservation at the San Diego Zoo in San Diego, California. Throughout his career, Ryder studied breeding patterns of endangered species. He collected and preserved cells, tissues, and DNA from endangered and extinct species to store in the San Diego Frozen Zoo, a center for genetic research and development in San Diego, California. Ryder and his team also sequenced vertebrate genomes under the Genome 10k initiative, a collaborative international program aiming to analyze the complete genomes of over ten thousand species of vertebrate. Ryder?s research has helped preserve species, restore diminished populations of wildlife, and protect biodiversity.

On 27 December 1946, Ryder was born to Elizabeth R. Semans Paine and Oliver A. Ryder Paine. From 1964 to 1968, Ryder attended the University of California in Riverside, California, where he earned a Bachelor of Science degree in biology with high honors. Upon completing his undergraduate degree, Ryder began pursuing a PhD in biology from the University of California in San Diego, California. During that time, Ryder married Cynthia Ryan, with whom he had two children, Kerry and Ryan.

In 1975, Ryder received his PhD in biology from the University of California in San Diego. He completed his degree with financial support from a traineeship in genetics with the Prevention and Public Health Fund, or PPHF, which was established by the Patient Protection and Affordable Care Act. The PPHF allocates educational funding to graduate students in relatively low-volume scientific fields regarding public health services. Ryder?s doctoral research described mechanisms for the replication of DNA within a strain of bacteria called *Escherichia coli* [3] (*E. Coli*). *E. Coli* is the cause of many food-borne illnesses, and researchers study it to understand its cellular mechanisms. By doing that, researchers aim to identify more effective ways of preventing its growth. His dissertation, ?Properties of Membrane-Associated Folded Chromosomes of *E. Coli* Related to Initiation and Termination of DNA Replication,? was published in 1975.

In 1975, after completing his dissertation, Ryder joined the San Diego Zoo as a research fellow. At the San Diego Zoo, Ryder studied the genetic makeup of equines, a broad group of animals encompassing various species of horses, zebras, and donkeys. Ryder focused a large amount of his research specifically on a breed known as Przewalski's horse [4] ( *Equus ferus przewalskii* [5]). In the 1960s Przewalski's horses, which are wild horses native to Mongolia, became extinct in the wild due to poaching, capture, and interbreeding with domesticated horse [4] breeds. Generations of interbreeding between the two horse [4] groups diminished the genetic uniqueness of Przewalski's horse [4], rendering their genetic makeup increasingly similar to that of domesticated horse [4] breeds. Subsequently, a worldwide effort that included the establishment of over seventy captive breeding programs started to reestablish the unique lineage of the Przewalski's horse [4] breed.

During his time at the San Diego Zoo, Ryder made multiple contributions to the Przewalski's horse [4] conservation effort. In the late 1970s, he first examined several genetic features of the Przewalski's horse [4], including cellular protein production, chromosomal composition, and viral activity within cells. Ryder then compared those results against similar information from both domesticated horse [4] breeds and specific breeds of zebras. From that, Ryder concluded that the Mongolian horse [4] shared an ancestor that was more closely related to an ancestor of the wild zebra than any known ancestor of a domesticated horse [4] breed. Soon after, Ryder noted that Przewalski's horses possess sixty-six chromosomes. Przewalski's horses have a fairly high number of chromosomes compared to other equine species, such as the Hartmann's Mountain Zebra (*Equus zebra hartmannae* *[6]*), which contains thirty-two chromosomes. His insight on the genetic and geographic history of the Przewalski's horse [4] breed contributed to optimizing conservation practices of the species.

However, Ryder noted a large problem with captive breeding programs that aimed to conserve species like the Przewalski's horse [4]. Ryder found that it was difficult to achieve genetic diversity within captive breeding programs, as there was a limited availability of mates within those programs. When species have a limited number of mates to choose from, inbreeding results. Inbreeding occurs when two closely related individuals mate and have genetically similar offspring. Any offspring produced through inbreeding is more likely to have negative genetic mutations, such as high susceptibility to disease. To offset the issue of inbreeding in Przewalski's horse [4] herds, Ryder developed a computer program to pair non-related individuals as mates. Ryder also argued for recovering ova, sperm [7], and newly fertilized egg [8] cells from the animals, and for the transfer of that material to zoos for storage. Ryder claimed that maintaining frozen stores of various Przewalski's horse [4] genes [9] would enable researchers to manage future domestic populations more easily, without the restrictions of time or geological locations.

In 1979, Ryder was promoted to a full time research position at the San Diego Zoo. The following year, Ryder and a team of researchers studied a behavior of ribosome evolution [2] that was demonstrated in both humans [10] and apes. A ribosome is a unit found within the cell that creates proteins. Ryder and his team found that genetic changes discovered in human ribosomes were similar to those observed in several species of apes in terms of location and structure. That indicated that there were similarities between human and ape genetic coding regarding ribosomes.

In 1984, continuing on his position at the San Diego Zoo, Ryder began researching the quagga (*Equus quagga quagga* *[11]*). The extinct quagga was a horse [4]-like animal with faint striped markings like those of a zebra. At that time, researchers were uncertain about which species quaggas are related to. After obtaining a piece of muscle from a 140-year-old, salt-preserved quagga skin, Ryder extracted its DNA and cloned it to obtain more DNA to study. Ryder?s analysis of the DNA sample showed that the quagga and zebras are more closely related on the evolutionary tree than quaggas are to domesticated cows. From those experiments, Ryder demonstrated that DNA could be extracted from the remains of extinct species, which researchers could use to hypothesize about evolutionary relationships between other species.

In 1986, Ryder accepted the position of Kleger chair in genetics at the San Diego Zoo Institute for Conservation Research, assuming the role of director of genetics. During this time, Ryder worked with his colleague Kurt Benirschke, a geneticist and pathologist, to bank genetic

material of endangered species in a collection called the Frozen Zoo. The collection is stored at the Beckman Center for Conservation Research in the San Diego Zoo. Established in 1972, the Frozen Zoo keeps deep frozen tissue samples of endangered species as a safeguard against losing the genetic information of those species if they went extinct. As of 2017, the Frozen Zoo houses a large collection of frozen cells from over 10,000 individual vertebrates and over 1,000 species. Cell lines, gametes, and even whole embryos are contained in storage tanks on the premises. Researchers can thaw those gametes and use them for in vitro fertilization [12] or artificial insemination. As the director of genetics, Ryder also became head of the Frozen Zoo program and oversees the collection and storage of DNA samples there.

In 1986, Ryder also published a paper in which he discussed the challenges regarding captive breeding of endangered animals, focusing on the importance of keeping subspecies reproductively pure. Ryder argued that subspecies should not cross-breed with members of other subspecies because it muddles the two distinct DNA lineages. For example, tigers have several subspecies, including the Siberian tiger (*Panthera tigris altaica* *[13]*) and the Bengal tiger (*Panthera tigris tigris* *[14]*). Individuals from one subspecies can breed with individuals of a different subspecies, creating hybrid subspecies, which sometimes results in the loss of genetic traits that are unique to a given subspecies. In his 1986 paper, Ryder detailed the challenges of conserving enough breeding individuals in captivity to keep gene pools from becoming inbred. Ryder discussed the concept of an evolutionarily significant unit, which he described as populations that are genetically distinct from the populations of the same species that can be found nearby. Ryder used the concept of the evolutionarily significant unit to determine how closely subspecies are related. His findings helped determine genetically unique populations from one another in the wild, which improved conservation attempts to bolster breeding wildlife populations in their natural environment.

Although Ryder conducted more research about breeding Przewalski's horse [4] during the late 1980s and early 1990s, Ryder spent most of his time studying the genetics of vertebrates. Ryder researched several different patterns in vertebrate DNA, exploring how DNA is structured and how structural patterns could be useful for profiling the genetics of wild animal populations. In the late 1980s, Ryder used a technique called DNA fingerprinting. DNA fingerprinting was a method of finding specific, repeated sequences of DNA within an animal?s genome [15] that could be analyzed and compared to determine hereditary lines within that population. In 1989, Ryder first successfully used DNA fingerprinting on a population of Galapagos tortoises.

In 1990, Ryder examined the dispersal patterns of telomeric DNA in the non-telomeric regions of chromosomes. Telomeric DNA is DNA that does not actively code for any physical product in the body and is typically found on either end of a chromosome. Telomeric DNA is meant to protect the coding DNA from damage. In 1990 Ryder and his research team found random distributions of telomeric DNA within the central coding portion of a variety of vertebrate species. Ryder and the other researchers speculated the cause of that, but their study yielded no definite conclusions.

Throughout the 1990s, Ryder used mitochondrial DNA, or genetic information stored inside of the mitochondria of a cell, to determine the evolutionary patterns of several species including antlered deer in 1990, orangutans in 1993, and bears in 1994. Mitochondrial DNA is less susceptible to mutations, or naturally occurring changes to the genome [15], than the DNA found in a cell?s nucleus [16]. That means that researchers can use it for more accurate

comparisons between DNA samples over long periods of time. Ryder established several hypotheses tracing the species that he genetically mapped back to potential evolutionary ancestors using mitochondrial DNA. Tracing the evolutionary history of an organism helps researchers establish the genetic similarity between different populations of a species.

In 1991, Ryder collaborated with several researchers to utilize satellite DNA to identify a similar genetic sequence across humans [10] and multiple primate [17] species. Satellite DNA refers to large sections of repetitive, non-coding DNA throughout the genome [15]. Ryder found a DNA sequence with up to 91 percent similarity in the genomes of both chimps and humans [10], but was not that similar in the genomes of gorillas or orangutans. Ryder and his co-authors claimed that the similar sequence they found showed the highest reported degree of similarity between a human and any primate [17] using alphoid subsets, which are a specific type of repetitive satellite DNA.

In 2000, Ryder contributed to multiple publications that argued for the collaborative efforts of DNA banks to store cells, tissues, and genetic information from at risk species, if not all species, to combat loss of biodiversity. He also called for the initiation of a Primate Genome Project, emphasizing the importance of sequencing the hereditary background for what he claimed to be human kind?s closest known genetic relative, the chimpanzee (*Pan troglodytes* *[18]*). According to Ryder, sequencing the chimpanzee genome [15] could provide researchers with insight about human health and diseases.

In 2002, Ryder published a paper ?Cloning advances and challenges for conservation? about cloning [19] technologies for the conservation of endangered species. In 2001, researchers in Cremona, Italy cloned a type of wild sheep [20] called the Mouflon (*Ovis aries* *[21]*). That experiment demonstrated that cloning [19] could be used to preserve genetic variation in rare species, particularly when the captive population is very small. When an individual is cloned, its genetics are kept in the gene pool longer than they would have otherwise been. In the conclusion of his paper, Ryder called for cell banking in zoological institutions and for more research to be conducted on cloning [19] technologies.

Throughout the 2000s, Ryder continued researching the genetics of various animal species, including gorillas, chimps, Mongolian sheep [20], and Przewalski's horse [4]. In 2009, he contributed to the collaborative proposal of the Genome 10k project in the article ?Genome 10K: A Proposal to Obtain Whole-Genome Sequence for 10,000 Vertebrate Species.? Established later that year, the Genome 10k Project is a collaboration run by international scientists. The project aims to fully sequence the genomes of 10,000 vertebrate species by 2019. Samples of vertebrate species are selected from stored collections of frozen genetic material in various bioresource banks of the involved scientists. The Genome 10k project is also part of the larger-scale Vertebrate Genome Project. The Vertebrate Genome Project aims to sequence the complete genome [15] of at least one organism from each of the 66,000 known species of vertebrates in the world. Ryder and his lab have actively contributed to both programs, including the submission of one of the first complete elephant genomes.

Beginning in 2004, Ryder started sequencing entire genomes of the vertebrates he studied. He analyzed and compared those sequences, revealing evolutionary trends and patterns that may have previously gone unnoticed. That new practice was referred to as genomics. In 2012, Ryder used comparative genomics and analysis to study genetic diversity and evolutionary history among populations of orangutans. In 2013 and 2014, he did the same for gorillas, equines, and modern birds [22]. Ryder?s compilations of comparative genomics and

evolutionary trends determine genetic diversity among the populations that he studied, which improves conservation efforts to preserve biodiversity among wildlife.

Ryder served as the executive vice president from 2004 to 2011 of the American Genetic Association headquartered in Newport, Oregon. He also received awards such as Fellow of the American Association for the Advancement of Science [23], the Duale Ullrey Award from the American Association of Zoo Veterinarians, the National Research Service Award, and the Bank of America-Giannini Foundation Medical Research Fellowship.

As of 2017, Ryder studies endangered populations both in captivity and in the field through the San Diego Zoo Institute for Conservation Research. His collections are stored in the Frozen Zoo, located within the San Diego Zoo Institute for Conservation Research.

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## Subject

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