Timeline

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**Digging Data: Artificial selection**

In the evolutionary process of artificial selection, humans (instead of nature) select which organisms get to reproduce, favoring those with traits we desire. Over many generations, this process causes gene versions that encode preferred traits to become more common in the population, and hence, causes evolutionary change in the selected population. Domestic dogs evolved from ancient, now-extinct wolf ancestors tens of thousands of years ago[[1]](#footnote-1) – and then, over the last 200 years, humans applied artificial selection to different subsets of dogs, creating Great Danes, Chihuahuas, and the full gamut of more than 450 breeds.

A picture containing person, outdoor, dog, mammal

Description automatically generatedA dog carrying a bird in its mouth

Description automatically generated

*Chihuahua (left) and Chesapeake Bay Retriever (right). Photos provided by Dayna Dreger.*

During the process of developing different breeds, the focus was on traits. We didn’t know which genes bestowed, for example, swimming skills or rat-catching ability; we just knew that we wanted dogs that were better at pulling fishing nets (leading to Chesapeake Bay Retrievers and Portuguese Water Dogs) and clearing out pests (leading to the Rat Terrier). In recent decades, scientists have been able to track down some of the genes that we unwittingly selected for in different breeds. Elaine Ostrander, a biologist at the National Institutes of Health, is one of these scientists. She studies dogs in order to answer basic questions about genetics that have implications for human health.

A person holding a dog

Description automatically generated with medium confidenceA picture containing person, wall, indoor, posing

Description automatically generatedA person holding a dog

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A person sitting on a couch with a dog

Description automatically generated with medium confidenceA person holding a dog

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*The team of scientists behind the study: Elaine Ostrander, Jaemin Kim, Dayna Dreger (top row), Jocelyn Plassais, Brian Davis, and Heidi Parker (bottom row). Falina Williams, also an author on the study, is not pictured. Photos provided by Ostrander lab.*

In one study, Elaine and a team that included Jaemin Kim, Falina Williams, Dayna Dreger, Jocelyn Plassais, Brian Davis, and Heidi Parker focused on sport hunting dogs, which are an active group of breeds that perform many different jobs. This group includes spaniels, retrievers, and hunting dogs. The team identified 59 genes that seem to have been the targets of recent selection in these dogs.[[2]](#footnote-2) A variant (i.e., an allele) in one of these genes – called *ROBO1* – was common in the most agile breeds. These athletic breeds were unusually likely to have an A base at a location in the gene where other breeds were more likely to have a C base. **The initial data suggested that *ROBO1* was one of the genes that humans unwittingly affected when they artificially selected breeds for different sorts of athletic abilities, but the team wanted more evidence.**

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**Background:** Broadly, agility is the ability to move quickly and easily, but for dogs, it can have a more specific meaning. Agility is a sport in which a person directs a dog to run through a complex obstacle course. For a dog to perform well in agility competitions, it must have both the athletic skills to make it through the course quickly and the mental skills to respond nimbly to commands and assess obstacles.

A dog jumping over a yellow fence

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*Australian Shepherd in an agility competition. Photo by Ron Armstrong from Helena, MT, USA, CC BY 2.0, via Wikimedia Commons.*

*ROBO1* may be related to those mental skills. It is a gene involved with brain development that we know about from studies of humans. Carrying different versions of *ROBO1* affects how the brain works and learns. For example, disruptions of *ROBO1* seem to contribute to dyslexia, a condition where people have trouble reading.

**Hypothesis:** The team had identified the A version of *ROBO1* based on a relatively small sample of breeds. This led to the hypothesis that **the A version of the gene was favored by artificial selection in breeds in which humans desired traits that lead to high agility**.

**Data:** To assess agility, the team used records of which breeds were entered in agility competitions and which breeds actually won agility titles. For each breed, they calculated the number of titles won per dog of that breed entered in competition. They then divided breeds into eight groups according to how likely each breed was to win agility titles:

Chart, scatter chart

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Top performers (like Border Collies and Pumis, both herding dogs) were in the red group, and breeds that never or very rarely won competitions (like the Greyhound and Anatolian Shepherd) were in the blue group.

A dog running on grass

Description automatically generated with medium confidence

*Greyhound. Photo provided by Dayna Dreger.*

To figure out how common the A gene version of *ROBO1* was in these different groups of dogs, the team turned to a database of dog DNA sequences. They found *ROBO1* data for 1243 dogs of breeds in one of the eight groups. These were not dogs that had necessarily competed in agility trials themselves; they were just dogs that were members of the same breeds as competitors. For each of the eight groups, the team calculated how common the A gene version of *ROBO1* was compared to other gene versions. Here is what they found:

Chart, scatter chart

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*Graph 1*

On this graph, the x-axis orders the eight breed groups from least likely to win agility titles to most likely. The y-axis shows how common the A gene version is in that group – so, for example, a frequency of 0.4 means that the A gene version was found in 40% of the sequences from dogs of that group. R2 indicates how well the frequency of different gene versions is explained by the breed group. R2 of 0 would indicate that breed group cannot predict the frequency of the A gene version at all. R2 of 1 would indicate that one can precisely predict the frequency of the A gene version based on breed group. In this case, 77% of the variation in the frequency of the A gene version is explained by breed group.

**Stepping into science**: When Elaine Ostrander learned about genetics as a sophomore in high school, she knew she’d found her calling. She wanted to be a scientist. But she didn’t have any role models around her: no parent or friends were scientists. So Elaine forged her own path. Throughout high school and college, she worked all sorts of jobs – tutor, waitress, janitor, dishwasher – so she could get the training she needed for her dream career. And she made it. Elaine now leads her own lab, where she helps train the next generation of scientists and builds new knowledge about genetics.

**Reference**: Kim, J., Williams, F. J., Dreger, D. L., Plassais, J., Davis, B. W., Parker, H. G., and Ostrander, E. A. (2018). Genetic selection of athletic success in sport-hunting dogs.  *Proceedings of the National Academy of Sciences.* 115: E7212-E7221.

**Comprehension questions:**

1. In your own words, explain what artificial selection is.
2. What is the key difference between natural and artificial selection?
3. Do some research about a dog breed not mentioned in this article. Briefly describe the breed and what traits humans selected for as this breed evolved.

**Data interpretation questions:**

1. The scientists found 59 genes in domestic dogs that seemed to be the target of recent selection. They thought that the gene *ROBO1* might be related to agility.
   1. As a first step, the scientists compared more agile breeds to less agile breeds. When they did this, what difference did they notice relating to the gene *ROBO1*?
   2. What hypothesis did the observation above lead the team to explore?
   3. In general terms, how did the team decide to test their hypothesis?
   4. How did the team assess the agility of a breed?
   5. If the hypothesis outlined above were true, what would you expect to observe with respect to *ROBO1* when comparing this gene across many breeds?
2. Examine Graph 1. Describe the overall pattern that it shows.
3. Does this finding support the hypothesis, contradict the hypothesis, or do neither? Explain your answer.
4. List one question relating to dog evolution and *ROBO1* that you are still curious about.

1. Scientists are still working on untangling exactly how many wolf populations were involved in this process and where and when it occurred. [↑](#footnote-ref-1)
2. Identifying these genes was a big part of the study, though not the focus of this Digging Data article. The process involved comparing the genomes of many sport-hunting dogs to the genomes of terriers (breeds selected to hunt vermin). The team looked for areas in the genome where 1) sport-hunting dogs tended to have one sequence and terriers tended to have a different sequence (suggesting that the two groups have evolved genetic differences from one another) and 2) the stretch of DNA sequence common in one of the groups of dogs was unusually long – that is, many dogs in one of the two groups (but not the other) had chromosomes with the exact same long genetic sequence at a particular location. This suggests that somewhere in that sequence is a genetic variant (allele) that was so advantageous that it became common quickly – so quickly that recombination didn’t have time to mix up the sequence near the useful variant. This process is known as a selective sweep. So, in short, the team looked for parts of the dog genome where there was evidence of genetic differences between sport-hunting dogs and terriers and evidence that a selective sweep caused those differences to evolve. [↑](#footnote-ref-2)