Birds of a Feather: Pigeon Head Crest Findings Extend to Domesticated Doves

Evolutionary biologist Michael Shapiro and his team made international headlines in 2013 when they found that a prominent change in pigeon plumage, head crests, could be traced to a mutation in a single gene.

Now, in the new advanced online edition of *Molecular Biology and Evolution* (Vickrey et al. 2015), the research team has found an almost exact repeat in the evolutionary playbook. A mutation in the same gene, *EphB2*, has led to a similar result in domesticated ringneck doves. The mutation causes the feathers on the back of the head and neck to grow up toward the head in a striking look.

Domesticated rock pigeons have more than 300 varieties that have been bred and chosen for their prized looks and vibrant feather colors. The head-crested birds had one version of the gene, a single mutation that made an aberrant protein (Arg758Cys) responsible for the feather difference between them and uncrested birds.

The researchers performed DNA analyses from 50 crested and 75 uncrested ringneck doves and found a different mutation in the same gene, which led to a single Gly636Arg amino acid substitution. In both cases, a single DNA base change hinders normal protein function by changing an amino acid at a crucial spot, causing the feather to swoop up toward the head rather than tuck neatly down.

“Crested birds from both species have mutations in the same gene, and even in the same functional part of the gene,” said Shapiro. “This suggests that only a limited number of genes—perhaps only genes in the EphB2 pathway—can cause crest formation without causing other problems that affect survival of the embryo or adult. Studying other species will help us understand if this same genetic mechanism is used repeatedly throughout crested bird species, or if it’s a mechanism that’s limited to the pigeon and dove family.”

Given that the ringneck dove is a domesticated species that last shared a common ancestor with the rock pigeon 23–35 Ma, the study shows that the same gene can be implicated as a prime driver of feather variation in completely different species, separated over a great evolutionary distance.

“We know that many genes are involved in feather development, so it’s rather remarkable that the same gene appears to control the same trait in two distantly related species,” said Shapiro.

Next, armed with new DNA banks of bird species, Shapiro’s team will examine how far and wide this unique evolutionary twist may be found among other bird species and wild populations.

Reference

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Melon Genome Study Reveals Recent Impacts of Breeding

An important and delicious crop—melons—has recently revealed their genetic secrets.

The first comprehensive genome analyses of seven melon varieties were completed by a research team led by Josep Casacuberta, Jordi Garcia-Mas and Sebastian Ramos-Onsins, providing breeders new knowledge important for understanding crop traits and helping to increase plant quality yields by selective breeding. The findings were published in the advanced online edition of *Molecular Biology and Evolution* (Sanseverino et al. 2015).

The researchers sought to bridge the gap between expanding the genetic knowledge of melons and understanding important traits, such as flavor, size, and water use.

The study is the first comprehensive analysis of genetic diversity in melon, and describes more than 4.3 million single sequence DNA variants (single nucleotide polymorphisms), together with an important number of structural variants including deletions, inversions, duplications, and mobile element movements. The team proved that highly cultivated and bred lines show the least diversity, with wild melons being the most diverse. Similar studies of corn, rice, and soybeans have shown that the most farmed and domesticated varieties show the least genetic variability.

The study also revealed in great detail, the genomic architecture of the melon genome (which the researcher dub “melonomics”—see melonomics.net). Overall, they found
902 genes that may be affected by DNA structural variations, with 53 genes putatively involved in disease resistance (29), cell-wall metabolism (10), aroma volatiles metabolism (9), sugar metabolism (4), and carotenoid biosynthesis (1).

The mobile elements, gene-hopping structures called transposons, have been very active during recent melon evolution, and the study reports on a number of transposon insertions that may be linked to the variability of important agronomic traits, even between two closely related elite lines.

The melon genome as a whole has evolved under negative evolutionary selective pressure, removing deleterious traits over time to improve fitness and adaptation.

“...This study reveals the high plasticity of the melon genome, and paves the way for future analyses to address melon breeding goals, such as increasing the quality of the fruit, or resistance against pests and diseases. On a more general perspective, studies such as this one will be needed to breed new plant varieties allowing to respond to the challenges in agriculture, including a growing human population, land and water scarcity, and the future impact of climate change,” said Casacuberta.

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