# Crazy avian genome, stuttering genes, and why we love nanopore

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Avian genomics is full of mysteries. One of them concerns the apparent absence of many well-known vertebrate genes. This year marks a decade since we first reported that most of these avian “missing” genes do, in fact, exist, yet their sequences are so unusually problematic that they elude detection by standard sequencing technologies. The issue lies in their extreme sequence composition, characterized by a massive accumulation of short repeats and strongly biased nucleotide content. Intriguingly, these genes are found almost exclusively on the so-called avian dot chromosomes,yet another of birds' genomic curiosities.

Subsequent research has revealed that some genes — otherwise conserved across vertebrates — have indeed been lost during avian evolution. And once again, the trail leads back to the avian dot chromosomes, where these genes were originally located.

Apparently, avian dot chromosomes undergo a form of dynamic genetic instability that has not yet been characterized, and whose underlying mechanism remains unknown. So far the only viable approach to studying this phenomenon appears to be nanopore sequencing, which offers at least partial resistance to the extreme sequence bias present in these regions.