Rapid genetic change in the passerine germline restricted chromosome

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The passerine germline-restricted chromosome (GRC) represents a taxonomically widespread example of programmed DNA elimination. This chromosome’s apparent ubiquity in the order suggests that it is indispensable, but we know little about the GRC’s genetic composition, function, and evolutionary significance. We sequenced the testis (with the GRC) and kidney (without the GRC) of the closely related common and thrush nightingale and compared the sequencing libraries to identify GRC derived reads and assemble the two GRC. In total we identify 192 different genes across the two GRC, with many of them present in multiple copies and often appearing as pseudogenized fragments. Interestingly, the genetic content of the GRC differs dramatically between the two species, despite only 1.8 million years of species divergence. Only one gene, cpeb1, has a complete coding region in all examined individuals of the two species and shows no copy number variation. The acquisition of this gene by the GRC corresponds with the earliest estimates of the GRC origin. Altogether, this suggests that the GRC is under little selective pressure, with rapid changes in genetic content observed and many genes potentially being non-functional pseudogene fragments. The standout nature of cpeb1, a gene known to play a function during oocyte maturation and early embryonic development, makes it a good candidate for the functional indispensability of the passerine GRC.