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Tracking the genes underlying seasonal migration

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The problem: Millions of songbirds migrate between tropical and temperate regions each year. Their capacity to undertake these journeys is innate but we know little about the underlying genes. This knowledge gap derives from our inability to track songbirds over the entire year and amplify genome-wide markers in non-model organisms.

Our solution: Motus is an automated radio telemetry system consisting of >800 radio towers (Fig. 1a) located primarily in eastern North America (Fig. 1b). We extended the network west, establishing 16 radio towers across a hybrid zone between Swainson's thrushes that use different migratory routes (Fig. 1c).

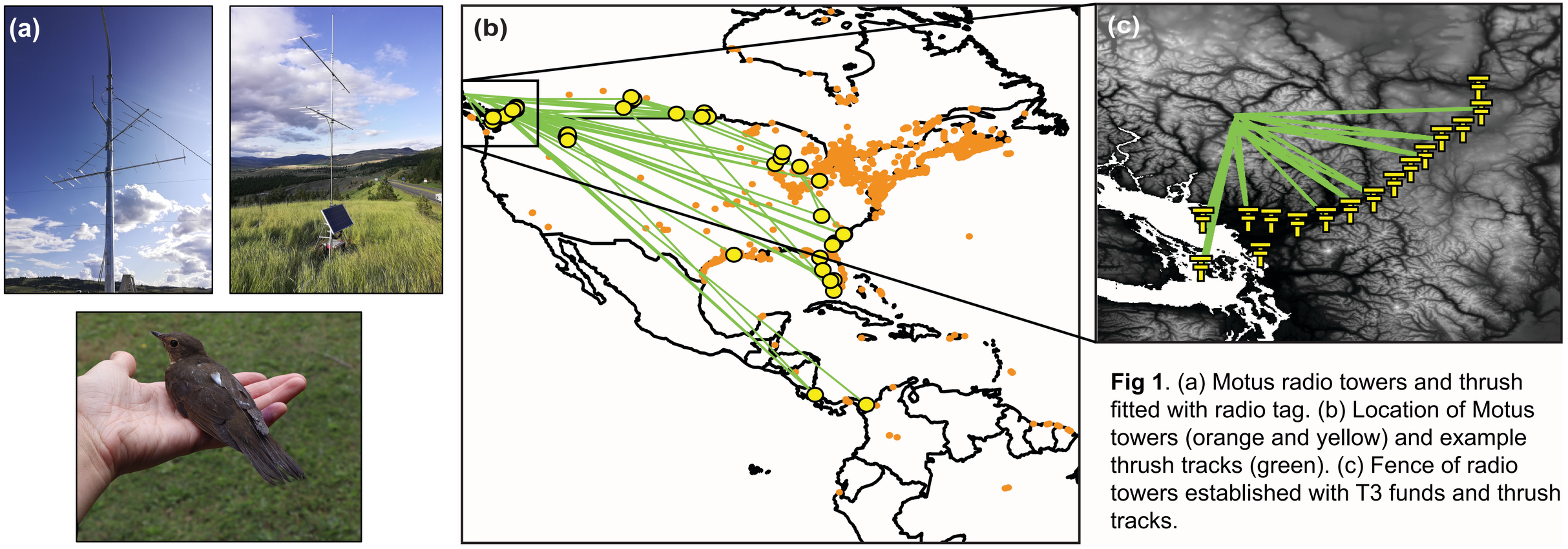

Fig 1. (a) Motus radio towers and thrush fitted with radio tag. (b) Location of Motus towers (orange and yellow) and example thrush tracks (green). (c) Fence of radio towers established with T3 funds and thrush tracks.

Results: We released 240 hybrids thrushes north of the fence; these birds exhibited considerable variation in their migratory routes (Fig. 1bc), spanning the full spectrum of possibilities in pure populations.

Next steps: This kind of phenotypic variation is ideal for admixture mapping. We will harness this variation for admixture mapping, genotyping birds using whole genome resequencing data and an in house bioinformatic pipeline to identify genes underlying migratory timing and orientation.

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