

Contemporary loss of migration in monarch butterflies

Ayşe Tenger-Trolander^{a,1}, Wei Lu^a, Michelle Noyes^a, and Marcus R. Kronforst^{a,1}

^aDepartment of Ecology & Evolution, The University of Chicago, Chicago, IL 60637

Edited by Nancy A. Moran, University of Texas at Austin, Austin, TX, and approved April 17, 2019 (received for review March 21, 2019)

The annual migration of the monarch butterfly *Danaus plexippus* is in peril. In an effort to aid population recovery, monarch enthusiasts across North America participate in a variety of conservation efforts, including captive rearing and release of monarch butterflies throughout the summer and autumn. However, the impact of captive breeding on monarchs remains an open question. Here, we show that captive breeding, both commercially and by summer-time hobbyists, causes migratory behavior to be lost. Monarchs acquired commercially failed to orient south when reared outdoors in the autumn, unlike wild-caught North American monarchs, yet they did enter reproductive diapause. The commercial population was genetically highly divergent from wild-caught North American monarchs and had rounder forewings, similar to monarchs from nonmigratory populations. Furthermore, rearing wild-caught monarchs in an indoor environment mimicking natural migration-inducing conditions failed to elicit southward flight orientation. In fact, merely enclosing indoors after an otherwise complete lifecycle outdoors was enough to disrupt southern orientation. Our results provide a window into the complexity—and remarkable fragility—of migration.

Danaus plexippus | captive breeding | behavior | migration | population genetics

The monarch butterfly *Danaus plexippus* is famous for its annual mass migration across North America (1, 2). Unfortunately, the number of overwintering monarchs in Mexico has declined drastically over the past 25 y (3, 4). Out of concern that the monarch migration may go extinct in the foreseeable future (5), the US Fish and Wildlife Service is currently considering whether to list the monarch butterfly as a threatened species under the US Endangered Species Act (6). While there is some disagreement about primary drivers of monarch population decline (7–16), the public maintains a keen interest in monarch conservation and undertakes a variety of activities every year to aid them, including reporting sightings online, planting milkweed, creating migratory waystations, and even raising monarchs for release.

However, captive rearing of monarchs is a contentious practice. Summertime hobbyists raise monarchs in their homes throughout the summer and autumn and then release them, hoping that they or their offspring will fly south to Mexico and ultimately contribute to population recovery. Conservation groups and scientists have expressed concern that captive rearing may result in higher parasite loads and even adaptation to captive conditions (17–21). Formal captive breeding programs, which are sometimes implemented to aid recovery of threatened or endangered species, do not exist for the monarch butterfly, but there are multiple commercial companies that breed monarchs year-round and sell them for release. These commercial monarchs are raised and released by school children across the United States, again with the belief that they will fly to the overwintering ground. These monarchs are also released at special events like weddings and monarch-themed fall festivals. However, the impact of captive breeding on monarch migration biology has not been investigated. In this study, we explored whether monarch breeding by commercial facilities and hobbyists affects migration phenotypes and genetics of captive-reared monarchs.

Results and Discussion

To investigate the migratory status of commercially bred monarchs, we reared both commercially sourced and wild-caught North American (NA) monarchs in a common garden experiment. We ordered adult monarchs from a commercial breeder and caught adult wild NA monarchs in July 2016. We raised the offspring of both groups over two successive generations, summer and autumn, in outdoor insectaries in Chicago, IL. Our experiment focused on comparing the descendants of commercial and wild-caught NA monarchs and of crosses between the two groups, raised at the same time in the same outdoor conditions. The monarch migratory syndrome is a multifaceted phenotype, encompassing behavioral, physiological, and anatomical traits. We assessed all three of these components by measuring flight orientation, reproductive status, and wing shape.

To measure orientation behavior, we tested monarchs in a monarch flight simulator (Fig. 1A) (22). Previous work using the simulator has shown that summer-generation monarchs do not have a group direction, whereas autumn-generation monarchs fly south (22–26). We calculated the group mean vector (0° to 359°), weighted by the strength of each individual's vector (0 to 1), as well as the group vector strength. We then used the Rayleigh test to determine whether each group was directional. NA monarchs behaved as expected. NA monarchs that emerged in October flew directionally south (Fig. 1B; $\sigma = 181^\circ$, $n = 25$, $r = 0.65$, Rayleigh test, z score = 10.65, $P < 0.001$), and those that emerged in August flew weakly south (Fig. 1B; $\sigma = 161^\circ$, $n = 19$, $r = 0.37$, Rayleigh test, z score = 2.6, $0.05 < P < 0.1$). Surprisingly, commercial monarchs that were raised side-by-side with

Significance

Captive rearing and release of monarch butterflies is a cultural phenomenon in the United States, where commercial breeders sell monarchs for release by school children and hobbyists raise wild monarchs in an effort to boost dwindling numbers. Our research shows that the captive breeding of monarchs disrupts critical aspects of their migratory behavior. The results are important because they reveal that different components of the migratory syndrome are easily decoupled and that migratory behavior is remarkably sensitive to genetic and environmental change. These results are relevant to conservation efforts, especially as the US Fish and Wildlife Service considers whether to list the North American monarch as a threatened species under the US Endangered Species Act.

Author contributions: A.T.-T. and M.R.K. designed research; A.T.-T., W.L., and M.N. performed research; A.T.-T., W.L., and M.N. analyzed data; and A.T.-T. and M.R.K. wrote the paper.

The authors declare no conflict of interest.

This article is a PNAS Direct Submission.

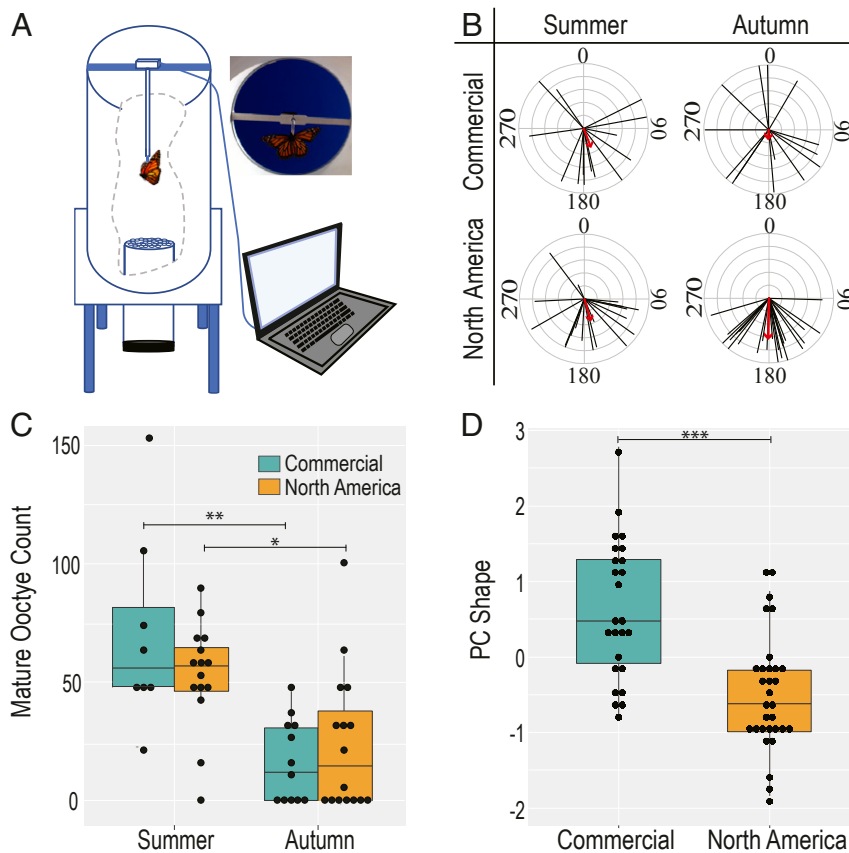
Published under the PNAS license.

Data deposition: The whole-genome sequences reported in this paper have been deposited in the National Center for Biotechnology Information, <https://www.ncbi.nlm.nih.gov/bioproject> (BioProject accession no. PRJNA509269).

¹To whom correspondence may be addressed. Email: atenger@uchicago.edu or mkrnforst@uchicago.edu.

This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1904690116/-DCSupplemental.

Published online June 24, 2019.



Our results indicate that either (i) long-term captive breeding of this commercial monarch population resulted in the loss of migratory behavior and a change in wing morphology, or (ii) the commercial population in our study was originally founded by or supplemented with monarchs from a nonmigratory population. Over the past hundreds or thousands of years, NA monarchs dispersed out of North America at least three times, once south into Central and South America and the Caribbean, once west across the Pacific Islands and into Australia, and once east into southern Europe and North Africa (29). Each of these dispersal events produced populations that reproduce year-round and do not migrate. It remains unknown whether these populations do not migrate because they have lost the ability or because they do not experience the relevant environmental cues. To determine the ancestry of the commercial population, we generated whole-genome sequencing (WGS) data from 15 commercial specimens, 14 of which successfully completed an autumn flight test, and compared them to a worldwide sample of monarch genomes (29). After filtering, our analysis was based on 4,593,379 single-nucleotide polymorphisms (SNPs) with an overall genotyping rate of 0.995. Principal component analysis (PCA) showed that the commercial lineage did not cluster with any other known monarch population, including North America (29) (Fig. 2A). Using a pruned dataset of 1 million variants, we inferred population subdivision and admixture using Frappe, version 1.1 (30).

Consistent with previous work, we found that samples collected from around the world represent at least four distinct populations: North America, Central/South America, Pacific, and Atlantic (29). The commercial individuals represent a distinct and previously unknown population of monarchs (Fig. 2B). We also found evidence that the commercial breeder does introduce NA genetic variation into their captive population, as two of the 15 commercial samples shared ancestry with NA monarchs (Fig. 2B). However, this supplementing of genetic variation does not appear to have a lasting impact on the commercial population.

Subsequent phylogenetic analyses indicate that the commercial monarch population was originally derived from North America and there has been no appreciable gene flow into the commercial population from nonmigratory populations. For instance, our phylogenetic analysis recovered the signatures of independent dispersal events out of North America in the founding of worldwide monarch populations, with the addition of a fourth independent event leading to the origin of the commercial population (Fig. 2C). Furthermore, analysis with TreeMix (31) found no evidence of gene flow between the commercial population and any nonmigratory population (*SI Appendix, Fig. S5*). Consistent with the inferred NA ancestry of the commercial population, we found that the commercial samples that we sequenced were fixed for the NA haplotype at a migration-associated collagen gene, suggesting there is more than one way to become nonmigratory

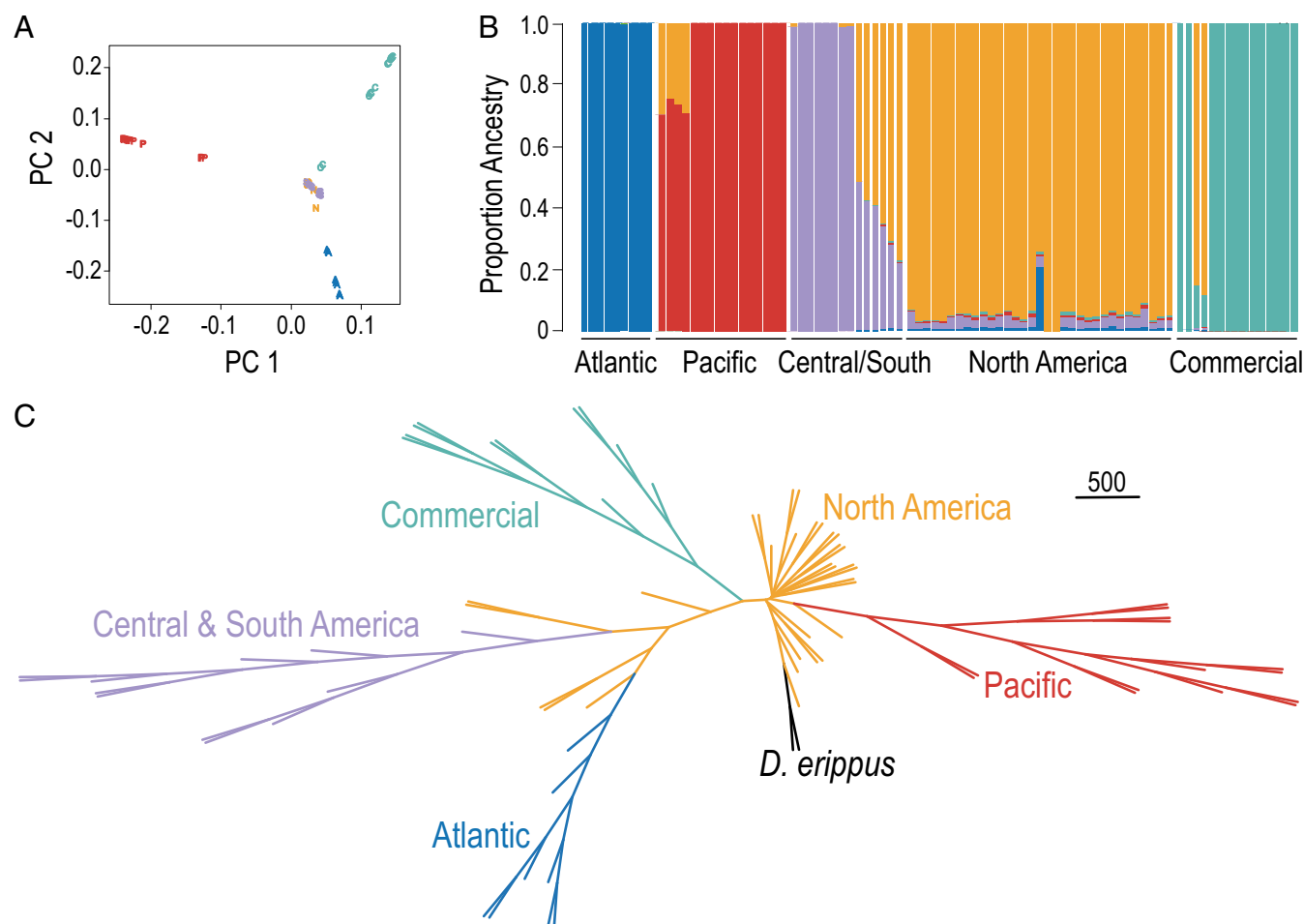


Fig. 2. Commercial monarchs represent a distinct population of monarch butterflies derived from NA monarchs. (A) PCA of SNPs. Principle component 1 (PC1) accounts for 12.3% of the variation in the data, and PC2 accounts for 10.7%. (B) Analysis of SNP structure using Frappe. Each bar represents a single individual, and the colors represent the proportion of ancestry for five populations. (C) Neighbor-joining consensus tree based on SNP data. (Scale bar is equivalent to 500 bootstraps.)

(29). The population genetic consequences of commercial rearing appear to mirror natural dispersal; the commercial lineage, similar to the Atlantic and Pacific populations, was genetically differentiated from NA monarchs and had reduced nucleotide diversity (π) (*SI Appendix, Table S1*).

We do not know what effect the introduction of nonorienting monarchs might have on the wild NA population or whether these results apply more generally to commercial monarch breeding. However, our results indicate that at least one group of commercially bred monarchs are much less likely to migrate than wild NA monarchs. Nonorienting monarchs released in the autumn are unlikely to migrate successfully and will not contribute to monarch population recovery or to the gene pool. However, nonorienting monarchs released in the summer could mate with wild NA individuals, leading to the introduction of nonmigratory variation that may not be purged. We suspect that without the strong annual selective pressure of migration, migration-associated traits can be lost in captivity.

Unlike commercial breeders, hobbyist breeders tend to collect wild eggs throughout the spring and summer and rear them for immediate release or for a few generations during the summer and autumn. When released, autumn-generation butterflies are expected to fly south and experience the same selection pressures as wild individuals. However, we do not know whether rearing a monarch butterfly indoors, where natural environmental cues (temperature, light, etc.) may be absent, affects the induction of migratory behavior. To determine whether indoor captive rearing affects migration, we reared NA monarchs indoors in both an autumnlike (18 °C with a 14-h day) and a summerlike (25 °C with a 16-h day) environmental chamber in 2018. We also reared a summer and an autumn generation outdoors and caught wild autumn-generation monarchs as they migrated south through Chicago in mid-September to act as controls. As expected, outdoor-summer and chamber-summer groups did not orient in a specific direction (Fig. 3A; outdoor $\sigma = 348^\circ$, $r = 0.12$, $n = 16$, Rayleigh test, z score = 0.23, $P > 0.5$; chamber $\sigma = 124^\circ$, $r = 0.295$, $n = 19$, Rayleigh test, z score = 1.65, $P > 0.1$). In contrast,

outdoor-reared autumn-generation and wild-caught autumn-generation monarchs showed southern group orientation (Fig. 3A, outdoor $\sigma = 185^\circ$, $r = 0.4$, $n = 9$, Rayleigh test, z score = 1.44, $P > 0.2$; Fig. 3B, wild $\sigma = 164^\circ$, $r = 0.39$, $n = 14$, Rayleigh test, z score = 2.13, $P > 0.1$). Our sample sizes for these groups were limited but they did have a significant southward direction when combined (autumn positive controls: $\sigma = 172^\circ$, $n = 23$, $r = 0.39$, Rayleigh test, z score = 3.50, $P < 0.05$). Unexpectedly, monarchs reared in the autumnlike chamber did not orient south (Fig. 3A; $\sigma = 295^\circ$, $r = 0.21$, $n = 17$, Rayleigh test, z score = 0.75, $P > 0.2$). The distributions of individual directions and group vector strengths differed between autumn chamber monarchs and autumn positive controls (Wallraff test, Kruskal–Wallis $\chi^2 = 5.970$, $P = 0.015$; *SI Appendix, Fig. S1B*).

Because reproductive diapause is also an important component of the migratory syndrome, we counted mature oocytes in our chamber- and outdoor-reared monarchs. As expected, the autumn females reared outdoors averaged 35.6 ± 11.7 (SE) mature oocytes ($n = 7$), a marked decrease from those reared in the summer, which averaged 77.2 ± 7 (SE) ($n = 9$) (*SI Appendix, Fig. S6*). Unlike the outdoor-reared group, the autumnlike chamber females did not have lower egg counts compared with the summerlike chamber females, averaging 60.4 ± 16.5 (SE) ($n = 8$) oocytes and 69.9 ± 10.8 (SE) ($n = 13$), respectively (*SI Appendix, Fig. S6*). Although some autumn chamber-reared individuals entered diapause, the cool temperature and early-autumn day-length conditions were not sufficient to induce diapause in the entire group, suggesting a missing environmental cue.

We do not know what specifically about the indoor environment prevents the development of migration behavior. Perhaps there are critical developmental periods or environmental conditions that prime monarchs to develop as migratory individuals. We do, however, have one additional observation that illustrates the fragility of migratory orientation behavior. On October 24, 2016, we moved a number of outdoor-reared NA pupae indoors to an autumnlike chamber kept at 21 °C and with an 11-h day (0700 to 1800 hours) to mimic the outdoor environment. The

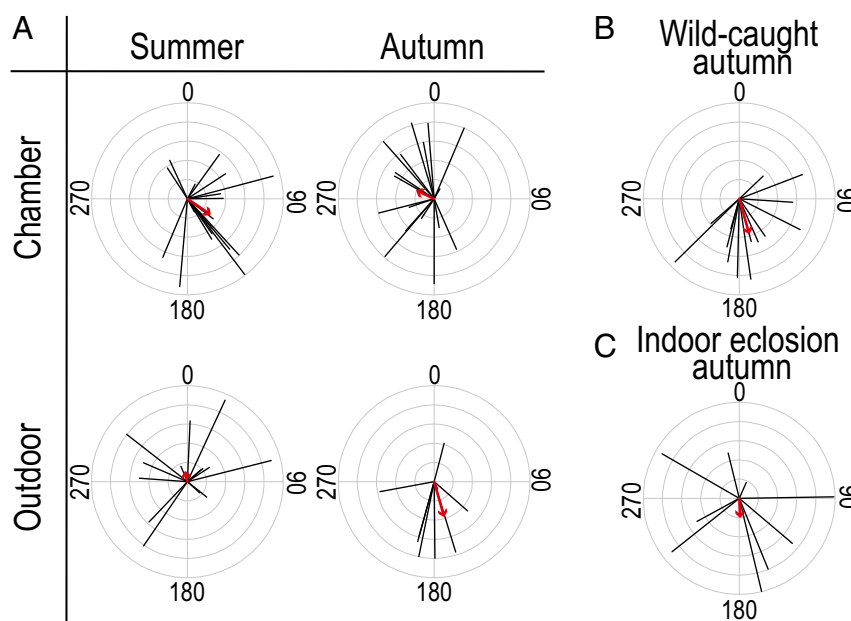


Fig. 3. NA monarchs reared in environmental chambers do not orient south. (A) Orientation plots of NA monarchs raised in a summerlike and an autumnlike chamber and NA monarchs raised outdoors in both a summer and an autumn generation. Each black line indicates the mean direction (0° to 359°) of an individual butterfly, and the length of the line represents the strength of that direction (0 to 1). The red arrow indicates the mean direction of the group, and the length of the arrow indicates the strength of the group direction. 0° is north. (B) Orientation plot of wild NA monarchs caught along their migration route through Chicago, IL. (C) Orientation plot of NA monarchs raised outdoors but brought indoors for eclosion.

1. Reppert SM, Gegeer RJ, Merlin C (2010) Navigational mechanisms of migrating monarch butterflies. *Trends Neurosci* 33:399–406.
2. Reppert SM, de Roode JC (2018) Demystifying monarch butterfly migration. *Curr Biol* 28:R1009–R1022.
3. Brower LP, et al. (2012) Decline of monarch butterflies overwintering in Mexico: Is the migratory phenomenon at risk? *Insect Conserv Diversity* 5:95–100.
4. Vidal O, Rendón-Salinas E (2014) Dynamics and trends of overwintering colonies of the monarch butterfly in Mexico. *Biol Conserv* 180:165–175.
5. Semmens BX, et al. (2016) Quasi-extinction risk and population targets for the Eastern, migratory population of monarch butterflies (*Danaus plexippus*). *Sci Rep* 6:23265.
6. The Center for Biological Diversity (2014) Petition to protect the monarch butterfly (*Danaus plexippus plexippus*) under the Endangered Species Act. Available at https://www.biologicaldiversity.org/species/invertebrates/pdfs/Monarch_ESA_Petition.pdf. Accessed December 6, 2018.
7. Agrawal AA, Inamine H (2018) Mechanisms behind the monarch's decline. *Science* 360:1294–1296.
8. Badgett G, Davis AK (2015) Population trends of monarchs at a northern monitoring site: Analyses of 19 years of fall migration counts at Peninsula Point, MI. *Ann Entomol Soc Am* 108:700–706.
9. Boyle JH, Dalglish HJ, Puzey JR (2019) Monarch butterfly and milkweed declines substantially predate the use of genetically modified crops. *Proc Natl Acad Sci USA* 116:3006–3011.
10. Davis AK (2012) Are migratory monarchs really declining in eastern North America? Examining evidence from two fall census programs. *Insect Conserv Diversity* 5:101–105.
11. Inamine H, Ellner SP, Springer JP, Agrawal AA (2016) Linking the continental migratory cycle of the monarch butterfly to understand its population decline. *Oikos* 125:1081–1091.
12. Pleasants JM, Williams EH, Brower LP, Oberhauser KS, Taylor OR (2016) Conclusion of no decline in summer monarch population not supported. *Ann Entomol Soc Am* 109:169–171.
13. Ries L, Taron DJ, Rendón-Salinas E (2015) The disconnect between summer and winter monarch trends for the eastern migratory population: Possible links to differing drivers. *Ann Entomol Soc Am* 108:691–699.
14. Saunders SP, Ries L, Oberhauser KS, Thogmartin WE, Zipkin EF (2018) Local and cross-seasonal associations of climate and land use with abundance of monarch butterflies *Danaus plexippus*. *Ecography* 41:278–290.
15. Stenoien C, Nail KR, Oberhauser KS (2015) Habitat Productivity and temporal patterns of monarch butterfly egg densities in the eastern United States. *Ann Entomol Soc Am* 108:670–679.
16. Thogmartin WE, et al. (2017) Monarch butterfly population decline in North America: Identifying the threatening processes. *R Soc Open Sci* 4:170760.
17. Davis A (2018) New statement from monarch conservation groups says—For the love of God, stop mass-rearing monarchs in your kitchens! *The Science of Monarch Butterflies: A blog about monarchs, written by a monarch scientist for people who love monarchs*. Available at <http://akdavis6.wixsite.com/monarchscience/single-post/2018/09/11/New-statement-from-monarch-conservation-groups-says—For-the-love-of-God-stop-mass-rearing-monarchs-in-your-kitchens>. Accessed December 6, 2018.
18. Malcolm SB (2018) Anthropogenic impacts on mortality and population viability of the monarch butterfly. *Annu Rev Entomol* 63:277–302.
19. Pelton E (2018) Keep monarchs wild! Why captive rearing isn't the way to help monarchs. *Xerxes Society for Invertebrate Conservation*. Available at <https://xerxes.org/2018/09/11/keep-monarchs-wild/>. Accessed December 6, 2018.
20. Journey North (2015) Captive breeding and releasing monarchs. Available at https://journeynorth.org/tm/monarch/conservation_action_release.pdf. Accessed January 3, 2019.
21. Monarch Joint Venture (2018) Revised handout. Raising monarchs: Why or why not? Available at <https://monarchjointventure.org/news-events/news/revised-handout-raising-monarchs-why-or-why-not>. Accessed January 3, 2019.
22. Mouritsen H, Frost BJ (2002) Virtual migration in tethered flying monarch butterflies reveals their orientation mechanisms. *Proc Natl Acad Sci USA* 99:10162–10166.
23. Froy O, Gotter AL, Casselman AL, Reppert SM (2003) Illuminating the circadian clock in monarch butterfly migration. *Science* 300:1303–1305.
24. Guerra PA, Reppert SM (2013) Coldness triggers northward flight in remigrant monarch butterflies. *Curr Biol* 23:419–423.
25. Merlin C, Gegeer RJ, Reppert SM (2009) Antennal circadian clocks coordinate sun compass orientation in migratory monarch butterflies. *Science* 325:1700–1704.
26. Zhu H, Gegeer RJ, Casselman A, Kanginakudru S, Reppert SM (2009) Defining behavioral and molecular differences between summer and migratory monarch butterflies. *BMC Biol* 7:14.
27. Goehring L, Oberhauser KS (2002) Effects of photoperiod, temperature, and host plant age on induction of reproductive diapause and development time in *Danaus plexippus*. *Ecol Entomol* 27:674–685.
28. Altizer S, Davis AK (2010) Populations of Monarch butterflies with different migratory behaviors show divergence in wing morphology. *Evolution* 64:1018–1028.
29. Zhan S, et al. (2014) The genetics of monarch butterfly migration and warning coloration. *Nature* 514:317–321.
30. Tang H, Peng J, Wang P, Risch NJ (2005) Estimation of individual admixture: Analytical and study design considerations. *Genet Epidemiol* 28:289–301.
31. Pickrell JK, Pritchard JK (2012) Inference of population splits and mixtures from genome-wide allele frequency data. *PLoS Genet* 8:e1002967.
32. Maeckle M (2018) Five monarch butterflies tagged and released at San Antonio Festival made it to Mexico. Texas Butterfly Ranch. Available at <https://texasbutterflyranch.com/2018/04/25/five-monarch-butterflies-tagged-and-released-at-san-antonio-festival-made-it-to-mexico/>. Accessed December 6, 2018.
33. Freedman MG, et al. (2018) Non-migratory monarch butterflies, *Danaus plexippus* (L.), retain developmental plasticity and a navigational mechanism associated with migration. *Biol J Linn Soc Lond* 123:265–278.
34. Zhan S, Merlin C, Boore JL, Reppert SM (2011). The monarch butterfly genome yields insights into long-distance migration. *Cell* 147:1171–1185.
35. McKenna A, et al. (2010) The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data. *Genome Res* 20:1297–1303.
36. Lefort V, Desper R, Gascuel O (2015) FastME 2.0: A comprehensive, accurate, and fast distance-based phylogeny inference program. *Mol Biol Evol* 32:2798–2800.