

Advances in genomic and molecular tools have transformed monarch research, enabling detailed investigation of the genetic and regulatory bases of complex traits (Li et al., 2025). High-quality reference genomes, long-read sequencing, and chromosome-scale assemblies now provide near-complete maps of coding and non-coding regions, structural variants, and neo-sex chromosomes (Zhan et al., 2011; Mongue et al., 2017; Zhan et al., 2020). Transcriptomic approaches, including tissue-specific and developmental-stage RNA sequencing, reveal dynamic gene expression patterns underlying migration, diapause, and chemical defense. Functional genomics techniques such as RNA interference, TALENs, and CRISPR/Cas9 genome editing have made it possible to experimentally validate candidate genes and regulatory elements, linking genetic variation to phenotypic outcomes (Markert et al., 2016; Zhang and Reed, 2016). Complementary population genomic analyses, leveraging resequencing, Genome Wide Association Studies (GWAS; Uffelmann et al., 2021), and selection scans, are uncovering polygenic architectures for migratory behavior, adaptation to host-plant chemistry, and responses to parasites. Together, these tools provide a comprehensive framework for connecting genotype to phenotype, enabling integrative studies that span molecular mechanisms, ecological interactions, and conservation applications (Li et al., 2025).

In this review, we synthesize current knowledge of monarch ecology, genetics, and metabolomics (Figure 1) across seven major domains: (1) the development of genomic resources and functional tools, (2) the genetic basis of migration and seasonal behavior, (3) molecular evolution of chemical defense and host-plant specialization, (4) sex-chromosome and structural genome evolution, (5) eco-genomic interactions involving parasites, microbiota, and host plants, (6) population genomic signals that inform conservation, and (7) metabolomic perspectives on host-plant chemistry and monarch sequestration. We also highlight methodological frontiers - from long-read pan-genomics to CRISPR-based functional validation, single-cell genomics, and integrated metabolomics - that are poised to resolve outstanding questions about how the monarch's remarkable life history is encoded in its genome and shaped by ecological interactions. Overall, this review aims not only to synthesize recent advances in monarch genomics and chemical ecology, but also to identify conceptual and methodological gaps that must be addressed to link molecular mechanisms to ecological function and conservation outcomes.

Integrative Overview of Monarch Migration, Genomics, and Chemical Ecology

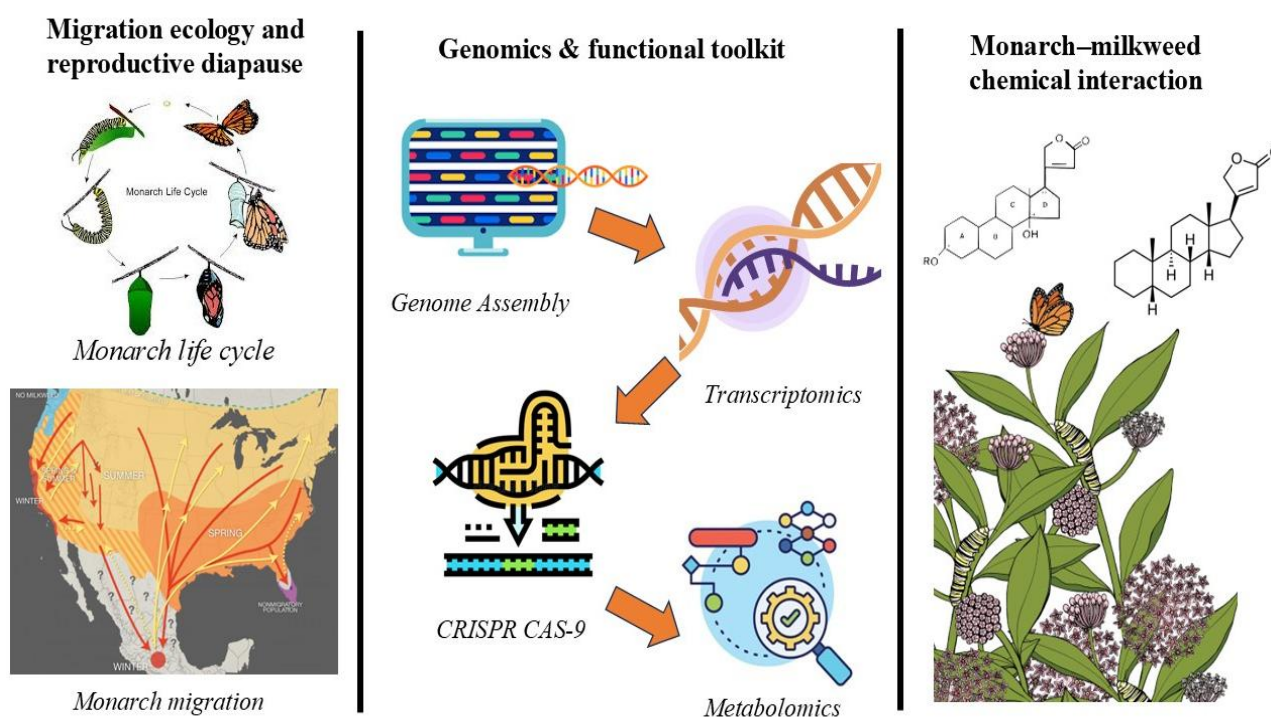


Figure 1 Conceptual model integrating *D. plexippus* migration ecology, genomics, and plant-insect chemical interactions