



Dispersal evolution: behavioural and genetic integration

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Abstract. Dispersal is a complex and evolutionarily important phenotype that integrates behavioural, physiological, genetic, and ecological processes across its three major stages: departure, transfer, and settlement. Rather than representing a random subset of individuals, dispersers frequently differ from residents in personality traits such as boldness, exploration, aggression, risk-taking, and sociability, giving rise to personality-dependent dispersal syndromes. Increasing evidence indicates that dispersal has a substantial genetic component and is generally governed by a polygenic architecture, with candidate genes and molecular pathways associated with circadian regulation, neurobiological function, locomotor performance, and other physiological processes. The expression and evolutionary consequences of dispersal are strongly context-dependent, reflecting interactions between genetic variation, environmental conditions, habitat dynamics, and life-history trade-offs. Dispersal also co-evolves with social behaviour and can generate persistent behavioural and social polymorphisms within populations. At the population level, variation in dispersal directly influences gene flow, kin structure, genetic diversity, inbreeding, population differentiation, colonization, and local adaptation. Anthropogenic habitat modification can further alter dispersal phenotypes and their genetic consequences, demonstrating that changes in landscape dynamics may generate substantial eco-evolutionary effects. Overall, dispersal should be regarded not simply as movement between populations, but as an integrated behavioural and genetic trait whose evolution can reshape both individual fitness and population genetic structure. Understanding these interactions requires approaches that combine behavioural ecology, quantitative genetics, molecular genomics, demography, and environmental context.

Keywords: personality-dependent dispersal, dispersal syndromes, behavioural ecology, genetic architecture, polygenic inheritance, gene flow, population genetic structure, local adaptation, eco-evolutionary dynamics, social behaviour, phenotypic plasticity.

Introduction. Dispersal is a complex, multivariate phenotype whose three stages - departure, transfer, and settlement - are each under selection to reduce movement costs and maximize fitness (Bonte & Doherty, 2016; Saastamoinen et al., 2017). Because dispersal determines gene flow, shapes kin structure, and influences local adaptation, its evolution is tightly linked to personality, social behaviour, and population genetic structure (Mullon et al., 2017; Cayuela et al., 2020; Cayuela et al., 2018; Păpuc, 2023).

Aim and Scope of the Review. The aim of this mini-review is to synthesize current evidence on the behavioural and genetic integration of dispersal and to highlight the mechanisms through which dispersal variation is generated, expressed, and maintained in natural populations. Particular attention is given to the non-random nature of dispersal, emphasizing the associations between dispersal propensity and personality traits such as exploration, boldness, aggression, risk-taking, and sociability. The review

further examines the genetic architecture and molecular mechanisms underlying dispersal, including evidence for polygenic inheritance, candidate genes, gene expression, and physiological pathways involved in dispersal-related phenotypes.

A second objective is to examine how ecological context and life-history constraints influence the expression and fitness consequences of dispersal. The review considers dispersal as a multistage process involving departure, transfer, and settlement, with selection acting at each stage to reduce movement costs and enhance fitness. It also addresses the co-evolution of dispersal with social behaviour and the consequences of dispersal for gene flow, kin structure, genetic diversity, population differentiation, and local adaptation.

Finally, the review aims to emphasize the importance of an integrative eco-evolutionary perspective. By connecting individual behavioural variation with genetic architecture, environmental heterogeneity, demographic processes, and population genetic structure, it seeks to demonstrate that dispersal is a central mechanism linking individual-level behavioural variation to broader evolutionary and population-level outcomes.

Who Disperses: Personality-Dependent Dispersal. Dispersers are not a random subset of the population. Across taxa, dispersal tendency covaries with boldness, aggressiveness, exploration propensity, and sociability, forming what is termed personality-dependent dispersal (Bourne & Sammons, 2008; Cote et al., 2010; Nicolaus et al., 2022; Petrescu-Mag, 2023, 2025abc; Petrescu-Mag et al., 2006). In several species, these behavioural differences appear at the onset of dispersal and persist throughout the life cycle, suggesting that dispersers and residents represent distinct behavioural types rather than transient states (Cote et al., 2010). A cross-species experiment spanning 15 organisms from protists to vertebrates confirmed a general phenotypic dispersal syndrome: dispersers are larger, more active, and possess locomotion-oriented morphology, with the link between dispersal and phenotype strengthening under environmental harshness (Cote et al., 2022).

The specific personality dimension linked to dispersal varies across systems. In great tits (*Parus major*), a strongly positive genetic correlation between local dispersal distance and exploration rate demonstrates genetic coupling of dispersal and exploration, even though the phenotypic correlation is weak and non-significant (Korsten et al., 2013). In western bluebirds (*Sialia mexicana*), male dispersal propensity in expanding populations is genetically correlated with aggression rather than exploration (Korsten et al., 2013). In Alpine swifts (*Apus melba*), a negative phenotypic and genetic correlation exists between natal dispersal propensity and nest-defence behaviour, suggesting that risk-averseness benefits dispersers settling in unfamiliar environments (Bize et al., 2017). In pied flycatchers (*Ficedula hypoleuca*), forced dispersers behaved more aggressively in their first breeding year, but this syndrome was remodelled via adaptive plasticity depending on local breeding experience and year-specific ecological conditions (Nicolaus et al., 2022) (Table 1; Figure 1).

Table 1
Personality traits genetically and phenotypically linked to dispersal across vertebrate species, showing trait specificity and direction of association

Species	Personality trait linked to dispersal	Direction	Evidence type
Great tit (<i>Parus major</i>)	Exploration rate	Positive genetic correlation	Quantitative genetics, pedigree (Korsten et al., 2013)
Western bluebird (<i>Sialia mexicana</i>)	Aggression	Positive genetic correlation	Field study, expanding population (Korsten et al.,

Species	Personality trait linked to dispersal	Direction	Evidence type
			2013)
Alpine swift (<i>Apus melba</i>)	Nest-defence (risk-taking)	Negative genetic correlation	Long-term colonial study (Bize et al., 2017)
Pied flycatcher (<i>Ficedula hypoleuca</i>)	Aggression	Positive, plastic	Forced dispersal experiment (Nicolaus et al., 2022)
Yellow-bellied toad (<i>Bombina variegata</i>)	Boldness, exploration	Positive, transgenerational	Common garden experiment (Cayuela et al., 2020).

Genetic Architecture and Molecular Mechanisms. Dispersal has a detectable genetic basis across organisms from bacteria to plants and animals, with significant genetic variation for dispersal or dispersal-related phenotypes documented in many natural populations (Saastamoinen et al., 2017). The trait is typically polygenic, though genes of moderate to large effect can influence specific aspects of the dispersal process (Saastamoinen et al., 2017). In house sparrows (*Passer domesticus*), a genome-wide association study identified a SNP near genes regulating circadian rhythm, glycogenesis, and exercise performance, but this variant explained only 3.8% of variance, reinforcing the polygenic architecture (Saatoglu et al., 2024). An animal model estimated that additive genetic variation composes 10% of total variation in dispersal probability, with different adaptive potentials across habitat types (Saatoglu et al., 2024).

In common lizards (*Zootoca vivipara*), a multi-omics approach combining quantitative genetics, RAD-seq, and RNA-seq found that natal dispersal is heritable and associated with variation in the carbonic anhydrase gene (CA10) and differential expression of genes involved in central nervous system functioning, including serotonin (SLC6A4) and nitric oxide (NOS1) pathways (San-Jose et al., 2023). Circadian clock genes (CRY2, KCTD21) were also differentially expressed between dispersers and residents, implicating circadian rhythm in dispersal regulation (San-Jose et al., 2023). In silveryeyes (*Zosterops lateralis*), genetic variation at three candidate genes—CLOCK, CREB1, and DRD4—was associated with migratory and dispersal propensity, with CREB1 allele lengths declining over time since colonization, potentially resolving the "paradox of the great speciators" through a rapid genetic reduction in dispersal ability after colonization (Estandía et al., 2023).

Correlations among dispersal traits and between dispersal and other life-history traits are common and may constrain dispersal from evolving to its adaptive optimum (Saastamoinen et al., 2017). The genetic basis of dispersal can be highly environment-dependent, with genetic variation for dispersal plasticity leading to context-dependent expression (Saastamoinen et al., 2017). Theoretical models have historically used simplified single-locus architectures, but recent multi-locus models incorporating dominance and epistasis show that genetic architecture influences evolutionary rates and outcomes, particularly during range shifts (Saastamoinen et al., 2017).

Fitness Consequences and Social Co-Evolution. Natural selection favours the functional integration of dispersal with phenotypic traits that reduce dispersal costs, and the fitness returns of different dispersal strategies are proposed to favour the evolution of animal personalities (Bize et al., 2017). Dispersal is selected as an adaptation to avoid kin competition, reduce inbreeding risk, and spread risk in spatially and temporally varying environments (Bonte & Doherty, 2016). Individuals adjust dispersal decisions according to fitness prospects of a patch, leading to informed, context-dependent dispersal (Cayuela et al., 2020; Unglaub et al., 2021).

DISPERSAL EVOLUTION: BEHAVIOURAL AND GENETIC INTEGRATION

Personality shapes who disperses, genes influence how, and together they structure populations and adaptation

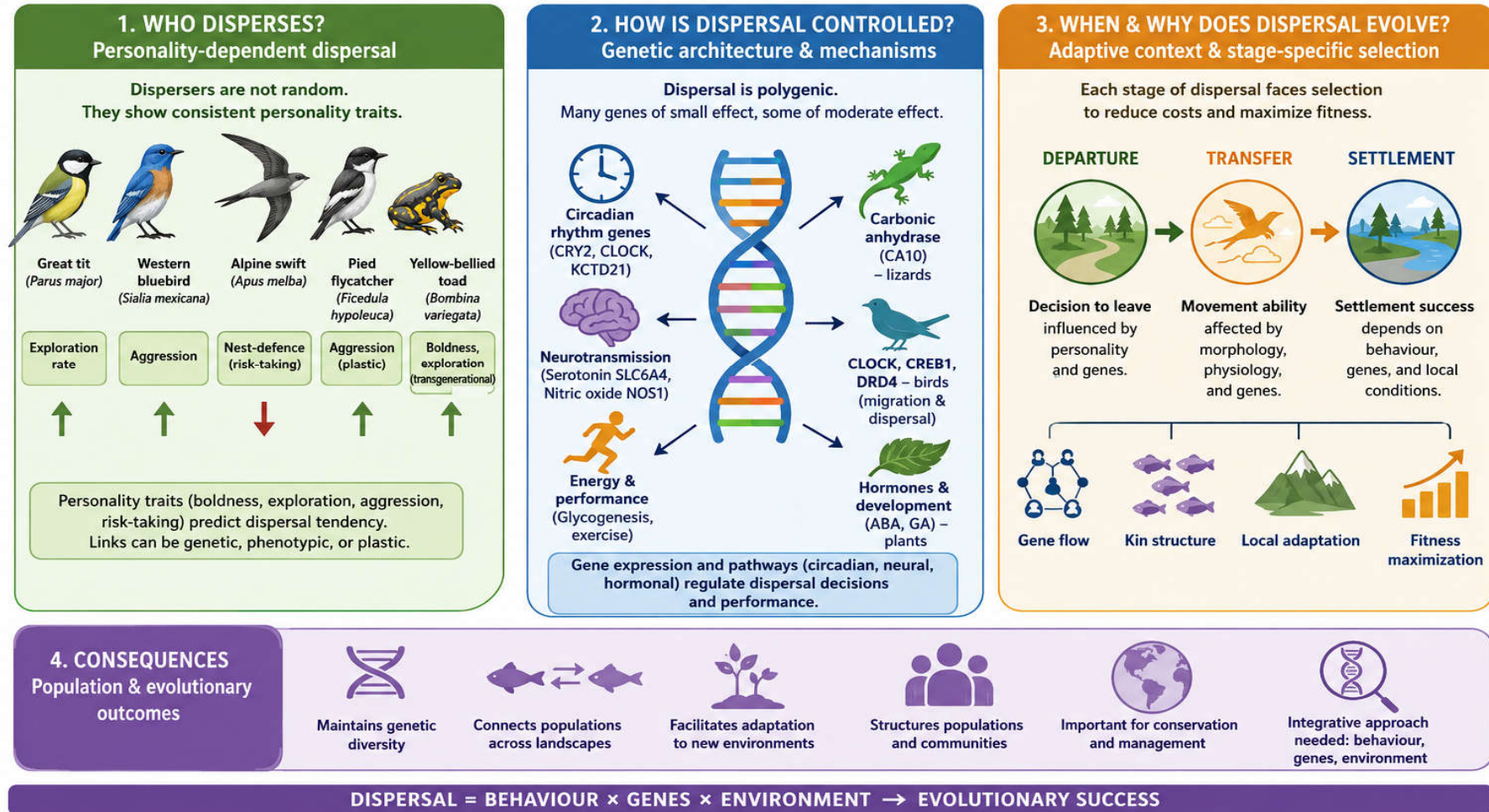


Figure 1. Dispersal evolution: behavioural and genetic integration.

The co-evolution of dispersal and social behaviour can produce stable social polymorphism. Theoretical modelling demonstrates that positive linkage between loci responsible for dispersal and social behaviour leads to two morphs: a sessile, benevolent morph that increases others' reproduction, and a dispersive, self-serving morph that increases its own reproduction (Mullon et al., 2017). This linkage is favoured under a broad spectrum of conditions, predicting that associations between dispersal proclivity and social tendencies should be common in nature (Mullon et al., 2017). Dispersers across a wide range of organisms have indeed been reported to differ in social tendencies from non-dispersers (Mullon et al., 2017).

Dispersal also carries direct fitness costs and trade-offs with other life-history components. Evidence for a consistent, context-independent integration of dispersal into the fast-slow life-history continuum is weak, leading to the proposal that dispersal should be treated as an independent principal axis of life-history variation that is free to evolve separately from other traits (Bonte & Doherty, 2016). Changes in spatial habitat configuration alter movement costs, and adaptations to reduce these costs increase phenotypic divergence among and within populations (Bonte & Doherty, 2016).

Gene Flow and Population Genetic Structure. Dispersal determines the intensity and direction of gene flow, with far-reaching consequences for local genetic diversity and adaptive processes (Cayuela et al., 2020; Saatoglu et al., 2024). Because gene flow shapes kin structure, dispersal is fundamental to the evolution of social behaviours within groups, while dispersal decisions simultaneously depend on kin structure and social interactions (Mullon et al., 2017). The non-random nature of dispersal with respect to genotype means that gene flow can be directional, causing spread rates, colonization success, and population genetic structure to depend strongly on populations' phenotypic composition (Nicolaus et al., 2022).

Anthropogenic landscape modification profoundly alters dispersal evolution and its genetic consequences. In yellow-bellied toads, populations in logging environments with high patch turnover had drastically higher natal and breeding dispersal rates and distances than those in persistent riverine habitats (Cayuela et al., 2020). Common garden experiments revealed transgenerationally transmitted dispersal syndromes, with toadlets from logging populations showing higher boldness and exploration (Cayuela et al., 2020). These logging populations also exhibited higher genetic diversity, larger effective population size, and greater gene flow, with lower intrapatch inbreeding and relatedness (Cayuela et al., 2020). Anthropogenic variation in patch turnover may thus have effects at least as important as landscape fragmentation on dispersal evolution and long-term population viability (Cayuela et al., 2020) (Table 2).

Table 2

Comparative dispersal patterns and genetic consequences across taxa, illustrating how ecological context and life history shape gene flow and population structure

<i>System</i>	<i>Dispersal pattern</i>	<i>Genetic consequence</i>	<i>Key driver</i>
Yellow-bellied toad (logging vs. riverine)	Higher rates and distances in logging habitats	Higher diversity, gene flow, lower inbreeding in logging populations	Patch turnover (Cayuela et al., 2020)
Great crested newt (<i>Triturus cristatus</i>)	High rates, short distances, context-dependent	Weak spatial genetic structure within SSP; strong hierarchical structure regionally	Habitat quality (Unglaub et al., 2021)
Amazonian birds (upland vs. floodplain)	Elevated gene flow in dynamic habitats	Progressively lower genetic structure from upland to	Habitat dynamics (Johnson et al.,

System	Dispersal pattern	Genetic consequence	Key driver
vs. riverine)		riverine	2023)
Anadromous brown trout (<i>Salmo trutta</i>)	55% dispersal, 25% successful straying	Directional gene flow from innermost to outermost fjord populations	Source-sink dynamics (Hawley et al., 2025)
Lake whitefish vs. brook charr	Similar dispersal rates, broader structure in whitefish	Lower effective gene flow in whitefish despite 10× larger N_e	Life history, temperature (Bouchard et al., 2025).

N_e = the “equivalent” number of individuals that effectively contribute to reproduction and, consequently, to the transmission of genetic variation to subsequent generations.

In great crested newts (*Triturus cristatus*), high context-dependent dispersal within a spatially structured population produced weak but significant spatial genetic structure, with individuals preferentially immigrating into high-quality ponds (Unglaub et al., 2021). At the regional level, strong hierarchical genetic structure with very few first-generation migrants suggested independent demographic units, with limited long-distance dispersal capacity increasing genetic structure and demographic isolation in anthropogenic landscapes (Unglaub et al., 2021). In Amazonian birds, species occupying more dynamic habitats—floodplain forest and riverine islands—exhibited progressively lower population genetic structure and elevated gene flow compared to stable upland forest species, suggesting that habitat dynamics drive long-term fluctuations in gene flow (Johnson et al., 2023).

In anadromous brown trout (*Salmo trutta*), a metapopulation of multiple sink populations was primarily supplemented by a single source population, with directional gene flow from innermost to outermost fjord populations and highest rates among neighbouring populations (Hawley et al., 2025). Although most dispersal resulted in unsuccessful spawning, connectivity among demes was significant and likely enhanced metapopulation resilience (Hawley et al., 2025). In a comparison of two subarctic salmonids, lake whitefish and brook charr showed similar dispersal rates and population differentiation, but lake whitefish had effective population sizes approximately ten times larger, meaning that their dispersal resulted in lower effective gene flow despite broader-scale structure and greater long-distance dispersal capacity (Bouchard et al., 2025). Dispersal rates in both species were lower in northern areas, likely due to colder temperatures and shorter growing seasons (Bouchard et al., 2025).

In a continuous great tit population at Wytham Woods, immigrants constituted a substantial portion of the breeding population and were indeed more outbred and less related to neighbours than locally born birds (Estandía et al., 2025). Despite low F_{ST} and no clear genome-wide population structure, immigrants and locals could be distinguished above chance using SNP data, and the population experienced substantial gene flow that maintained high genetic diversity and reduced the possibility of local adaptation at this spatial scale (Estandía et al., 2025). The spatial genetic structure was driven by spatial and temporal clustering of close kin, a pattern continually renewed through high population turnover rather than sustained by a consistent genetic basis (Estandía et al., 2025).

Eco-evolutionary feedbacks further complicate these dynamics. Evolutionary changes in dispersal can alter metapopulation dynamics, population expansion rates, species interactions, and local adaptation, generating feedbacks between ecological and evolutionary processes (Lustenhouwer et al., 2023). Dispersal syndromes—associations between dispersal and suites of morphological, behavioural, and life-history traits—affect ecological processes such as population spread, and evolutionary changes in dispersal may leave a legacy on other demographic parameters (Lustenhouwer et al., 2023).

Experimental evolution approaches, though constrained to small short-lived organisms, can reinforce links between theoretical predictions and empirical observations and advance understanding of dispersal evolution under complex biological scenarios including biotic interactions and dispersal syndromes (Lustenhouer et al., 2023). Integrating demographic and genetic methods provides a unified framework for quantifying both effective and non-effective dispersal and investigating how individual and environmental factors affect each stage of the dispersal process (Cayuela et al., 2018).

Conclusions. Dispersal is best understood as an integrated evolutionary trait rather than as a simple movement behaviour. Its expression reflects the interaction of personality, genetic architecture, physiology, environmental conditions, and life-history trade-offs. Evidence across diverse taxa demonstrates that dispersers are frequently behaviourally differentiated from residents and that traits such as exploration, aggression, boldness, and risk-taking may be genetically correlated with dispersal propensity or expressed through environmentally dependent plasticity.

The genetic basis of dispersal is generally complex and predominantly polygenic, although individual genes and molecular pathways may contribute to particular components of the phenotype. Genetic effects can also be strongly environment-dependent, indicating that dispersal evolution cannot be fully understood independently of ecological context. The integration of behavioural and genetic variation may consequently influence not only an individual's probability of dispersing, but also its movement performance, settlement success, and subsequent fitness.

At the population level, dispersal has profound consequences because it determines the intensity, direction, and spatial distribution of gene flow. Differences in dispersal can alter genetic diversity, relatedness, inbreeding, population differentiation, colonization success, and the potential for local adaptation. Importantly, dispersal is not necessarily equivalent to effective gene flow: movement may occur without successful reproduction, and populations with similar dispersal rates may consequently experience markedly different genetic connectivity.

Environmental change further demonstrates the eco-evolutionary significance of dispersal. Anthropogenic disturbance and habitat dynamics can modify dispersal rates, distances, behavioural syndromes, genetic diversity, effective population size, and gene flow, potentially producing persistent evolutionary differences among populations.

Overall, the available evidence supports a conceptual framework in which dispersal emerges from the interaction of behaviour, genes, and environment and, in turn, feeds back to influence population dynamics and evolution. Future research should therefore integrate behavioural observations, quantitative genetics, genomic and transcriptomic approaches, demographic analyses, and explicit characterization of environmental context. Such integration is essential for understanding how dispersal evolves and how dispersal-mediated processes ultimately shape population persistence, connectivity, adaptation, and evolutionary trajectories.

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References

- Bize, P., Daniel, G., Viblanc, V. A., Martin, J. G. A., & Doligez, B. (2017). Negative phenotypic and genetic correlation between natal dispersal propensity and nest-defence behaviour in a wild bird. *Biology Letters*, 13(7), 20170236. <https://doi.org/10.1098/rsbl.2017.0236>
- Bonte, D., & Dähirel, M. (2016). Dispersal: a central and independent trait in life history. *BioRxiv*, 065151. <https://doi.org/10.1101/065151>
- Bouchard, R., Babin, C., Normandeau, É., Xuereb, A., Boulanger, F., Coxon, A., Diamond, S., Fireman, R., Lameboy, J., Louttit, N., Natawapineskum, G., Okimaw, D., Torio, D., Varty, S., Moore, J.-S., Fraser, D., & Bernatchez, L. (2025). Shared dispersal patterns but contrasting levels of gene flow in two anadromous salmonids along a broad subarctic coastal gradient. *Molecular Ecology*, 34, e17739. <https://doi.org/10.1111/mec.17739>
- Bourne, G. R., & Sammons, A. J. (2008). Boldness, aggression and exploration: evidence for a behavioural syndrome in male pentamorphic livebearing fish, *Poecilia parae*. *Aquaculture, Aquarium, Conservation & Legislation*, 1(1), 39-49.
- Cayuela, H., Besnard, A., Cote, J., Laporte, M., Bonnaire, É., Pichenot, J., Schtickzelle, N., Bellec, A., Joly, P., & Léna, J. (2020). Anthropogenic disturbance drives dispersal syndromes, demography, and gene flow in amphibian populations. *Ecological Monographs*, 90(2), e01406. <https://doi.org/10.1002/ecm.1406>
- Cayuela, H., Rougemont, Q., Prunier, J. G., Moore, J.-S., Clobert, J., Besnard, A., & Bernatchez, L. (2018). Demographic and genetic approaches to study dispersal in wild animal populations: A methodological review. *Molecular Ecology*, 27, 3976-4010. <https://doi.org/10.1111/mec.14848>
- Cote, J., Clobert, J., Brodin, T., Brodin, T., Fogarty, S., & Sih, A. (2010). Personality-dependent dispersal: characterization, ontogeny and consequences for spatially structured populations. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 365, 4065 - 4076. <https://doi.org/10.1098/rstb.2010.0176>
- Cote, J., Dähirel, M., Schtickzelle, N., Altermatt, F., Ansart, A., Blanchet, S., Chaine, A., De Laender, F., De Raedt, J., Haegeman, B., Jacob, S., Kaltz, Laurent, O., Little, E., C., Madec, L., Manzi, F., Masier, S., Pellerin, F., Pennekamp, L., Therry, A., Vong, Winandy, L., Bonte, D., Fronhofer, E. A., & Legrand, D. (2022). Dispersal syndromes in challenging environments: A cross-species experiment. *Ecology Letters*, 25, 2675 - 2687. <https://doi.org/10.1111/ele.14124>
- Estandía, A., Sendell-Price, A. T., Oatley, G., Robertson, F. E., Potvin, D., Massaro, M., Robertson, B., & Clegg, S. M. (2023). Candidate gene polymorphisms are linked to dispersive and migratory behaviour: Searching for a mechanism behind the "paradox of the great speciators". *Journal of Evolutionary Biology*, 36, 1503 - 1516. <https://doi.org/10.1111/jeb.14222>
- Estandía, A., Recalde, N. M., Slate, J., & Sheldon, B. C. (2025). The genetic consequences of dispersal and immigration in a wild great tit population. *Molecular Ecology*, 35(1), e70206. <https://doi.org/10.1111/mec.70206>
- Hawley, K., Thaulow, J., Urke, H. A., Kristensen, T., Barson, N., & Haugen, T. (2025). Dispersal and gene flow among potential spawners: source-sink structure among populations of anadromous brown trout exposed to multifaceted anthropogenic impacts. *Evolutionary Applications*, 18(7), e70130. <https://doi.org/10.1111/eva.70130>
- Johnson, O., Ribas, C., Aleixo, A., Naka, L., Harvey, M. G., & Brumfield, R. T. (2023). Amazonian birds in more dynamic habitats have less population genetic structure and higher gene flow. *Molecular Ecology*, 32, 2186-2205. <https://doi.org/10.1111/mec.16886>

- Korsten, P., Van Overveld, T., Adriaensen, F., & Matthysen, E. (2013). Genetic integration of local dispersal and exploratory behaviour in a wild bird. *Nature Communications*, 4, 2362. <https://doi.org/10.1038/ncomms3362>
- Lustenhouwer, N., Moerman, F., Altermatt, F., Bassar, R., Bocedi, G., Bonte, D., Dey, S., Fronhofer, E. A., Da Rocha, É. G., Giometto, A., Lancaster, L., Prather, R. B., Saastamoinen, M., Travis, J., Urquhart, C., Weiss-Lehman, C. P., Williams, J. L., Börger, L., & Berger, D. (2023). Experimental evolution of dispersal: Unifying theory, experiments and natural systems. *The Journal of Animal Ecology*, 92(6), 1113-1123. <https://doi.org/10.1111/1365-2656.13930>
- Mullon, C., Keller, L., & Lehmann, L. (2017). Social polymorphism is favoured by the co-evolution of dispersal with social behaviour. *Nature Ecology & Evolution*, 2, 132-140. <https://doi.org/10.1038/s41559-017-0397-y>
- Nicolaus, M., Wang, X., Lamers, K. P., Ubels, R., & Both, C. (2022). Unravelling the causes and consequences of dispersal syndromes in a wild passerine. *Proceedings of the Royal Society B*, 289(1974), 20220068. <https://doi.org/10.1098/rspb.2022.0068>
- Păpuc, T. (2023). Shoaling: possible benefits for poeciliids exhibiting social behavior. *Poeciliid Research*, 13(1), 22-24.
- Petrescu-Mag, I. V. (2023). A rival for the guppy in behavioral studies: The pentamorphic fish, *Poecilia parae* Eigenmann, 1894. *Poeciliid Research*, 13(1), 25-31.
- Petrescu-Mag, I. V. (2025a). Aggression, sexual selection, and neuroendocrine regulation in *Betta splendens*: an integrative mini-review. *Studia Universitatis Vasile Goldiș Seria Științele Vieții*, 35(3), 117-120.
- Petrescu-Mag, I. V. (2025b). Behavioral plasticity, honest signaling, and parental investment in *Betta splendens*: an integrative review across environmental and evolutionary contexts. *Studia Universitatis Vasile Goldiș Seria Științele Vieții*, 35(3), 121-130.
- Petrescu-Mag, I. V. (2025c). Sexual selection in animals: pigment-based signaling and eco-evolutionary trade-offs. *Studia Universitatis Vasile Goldiș Arad Seria Științele Vieții*, 35(3), 106-116.
- Petrescu-Mag, I. V., Hărșan, R., & Pojar, T. N. (2026). Animal personality in *Betta splendens*: boldness, aggressiveness, syndromes and domestication. *Aquaculture, Aquarium, Conservation & Legislation*, 19(3), 964-978.
- Saastamoinen, M., Bocedi, G., Cote, J., Legrand, D., Guillaume, F., Wheat, C.W., Fronhofer, E.A., Garcia, C., Henry, R., Husby, A., Baguette, M., Bonte, D., Coulon, A., Kokko, H., Matthysen, E., Niitepõld, K., Nonaka, E., Stevens, V. M., Travis, J. M. J., Donohue, K., Bullock, J. M. and del Mar Delgado, M. (2018). Genetics of dispersal. *Biological Reviews*, 93, 574-599. <https://doi.org/10.1111/brv.12356>
- Saatoglu, D., Lundregan, S. L., Fetterplace, E., Goedert, D., Husby, A., Niskanen, A., Muff, S., & Jensen, H. (2024). The genetic basis of dispersal in a vertebrate metapopulation. *Molecular Ecology*, 33(6), e17295. <https://doi.org/10.1111/mec.17295>
- San-Jose, L. M., Bestion, E., Pellerin, F., Richard, M., Di Gesu, L., Salmona, J., Winandy, L., Legrand, D., Bonneaud, C., Guillaume, O., Calvez, O., Elmer, K., Yurchenko, A., Recknagel, H., Clobert, J., & Cote, J. (2023). Investigating the genetic basis of vertebrate dispersal combining RNA-seq, RAD-seq and quantitative genetics. *Molecular Ecology*, 32, 3060 - 3075. <https://doi.org/10.1111/mec.16916>
- Unglaub, B., Cayuela, H., Schmidt, B. R., Preißler, K., Glos, J., & Steinfartz, S. (2021). Context-dependent dispersal determines relatedness and genetic structure in a patchy amphibian population. *Molecular Ecology*, 30(20), 5009-5028. <https://doi.org/10.1111/mec.16114>

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