

**Daria Shipilina****Peer-reviewed Journal Papers**

1. Talla, V., Kalsoom, F., Shipilina, D., Marova, I., Backström, N. (2017). Heterogeneous patterns of genetic diversity and differentiation in European and Siberian chiffchaff (*Phylloscopus collybita abietinus* / *P. tristis*). *G3: Genes, Genomes, Genetics* 7: 3983-3998. doi:10.1534/g3.117.300152
2. Shipilina, D., Serbyn, M., Ivanitskii, V., Marova, I., Backström, N. (2017) Patterns of genetic, phenotypic and acoustic variation across a chiffchaff (*Phylloscopus collybita abietinus/tristis*) hybrid zone. *Ecology and evolution* 7: 2169–2180. doi: 10.1002/ece3.2782
3. Marova, I., Shipilina, D., Fedorov, V., Alekseev, V., Ivanitskii, V. (2017) Interaction between Common and Siberian Chiffchaff in a contact zone, *Ornis Fennica* 94: 66–81. ISSN: 0030-5685
4. Marova, I., Shipilina, D., Alekseev, V., Fedorov, V., Ivanitskii, V. (2016) Hybridisation of Eastern European and Siberian chiffchaffs (*Phylloscopus collybita abietinus* - *P.c. tristis*): complex analysis of the sympatry zone on Southern Ural. *Ornitologia* 40: 27–45. (In Russian) ISSN-0474-7313

**Nicholas Barton****Peer-reviewed Journal Papers**

1. Pickup, M., Barton, N. H., Brandvain, Y., Fraise, C., Yakimowski, S., Dixit, T., Field, D. (2019). Mating system variation in hybrid zones: Facilitation, barriers and asymmetries to gene flow. *New Phytologist*, 224(3), 1035–1047. doi:10.1111/nph.16180
2. Castro, J. P., Yancoskie, M. N., Marchini, M., Belohlavy, S., Hiramatsu, L., Kudka, M., Chan, Y. F. (2019). An integrative genomic analysis of the Longshanks selection experiment for longer limbs in mice. *eLife*, 8. doi:10.7554/eLife.42014
3. Barton, N. H. (2019). Is speciation driven by cycles of mixing and isolation? *National Science Review*, 6(2), 291–292. doi:10.1093/nsr/nwy113
4. Barton, N. H., Hermisson, J., Nordborg, M. (2019). Why structure matters. *ELife*, 8, e45380. doi:10.7554/eLife.45380
5. Sella, G., Barton, N. H. (2019). Thinking about the evolution of complex traits in the era of genome-wide association studies. *Annual Review of Genomics and Human Genetics*, 20, 461–493. doi:10.1146/annurev-genom-083115-022316
6. Barton, N. H., Etheridge, A. M. (2018). Establishment in a new habitat by polygenic adaptation. *Theoretical Population Biology*. 122(7), 110–127. DOI: 10.1016/j.tpb.2017.11.007
7. Charlesworth, B., Barton, N. H. (2018). The spread of an inversion with migration and selection. *Genetics* 208(1):377-382. doi:10.1534/genetics.117.300426
8. Novembre, J., Barton, N. H. (2018). Tread lightly interpreting polygenic tests of selection. *Genetics*, 208(4), 1351-1355. doi:10.1534/genetics.118.300786
9. Payne, P., Geyrhofer, L., Barton, N. H., Bollback, J. P. (2018). CRISPR-based herd immunity can limit phage epidemics in bacterial populations. *eLife*, 7. DOI: 10.7554/eLife.32035
10. Ringbauer, H., Kolesnikov, A., Field, D., Barton, N. H. (2018). Estimating barriers to gene flow from distorted isolation-by-distance patterns. *Genetics* 208(3):1231-1245 doi:10.1534/genetics.117.300638.
11. Sachdeva, H., Barton, N. H. (2018). Introgression of a block of genome under infinitesimal selection. *Genetics*, 209(4), 1279–1303. DOI: 10.1534/genetics.118.301018

12. Ellis, T., Field, D., Barton, N. H. (2018). Inference from paternity and sibships accounting for uncertainty in genealogy. *Molecular Ecology Resources*, 18(5), 988–999. DOI: [10.1111/1755-0998.12782](https://doi.org/10.1111/1755-0998.12782)
13. Bodova, K., Priklopil, T., Field, D., Barton, N. H., Pickup, M. (2018). Evolutionary pathways for the generation of new self-incompatibility haplotypes in a non-self recognition system. *Genetics*, 209(3), 861–883. DOI: [10.1534/genetics.118.300748](https://doi.org/10.1534/genetics.118.300748)
14. Tavares, H., Whitley, A., Field, D., Bradley, D., Couchman, M., Copsey, L., Coen, E. (2018). Selection and gene flow shape genomic islands that control floral guides. *PNAS*, 115(43), 11006–11011. DOI: [10.1073/pnas.1801832115](https://doi.org/10.1073/pnas.1801832115)
15. Barton, N. H. (2018). The consequences of an introgression event. *Molecular Ecology*, 27(24), 4973–4975. DOI: [10.1111/mec.14950](https://doi.org/10.1111/mec.14950)
16. Barton, N. H. (2017). How does epistasis influence the response to selection? *Heredity* 118(1):96-109 doi:[10.1038/hdy.2016.109](https://doi.org/10.1038/hdy.2016.109)
17. Barton, N. H., Etheridge, A. M., Veber, A. (2017). The infinitesimal model: Definition derivation and implications. *Theoretical Population Biology* 118:50-73 doi:[10.1016/j.tpb.2017.06.001](https://doi.org/10.1016/j.tpb.2017.06.001)
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19. Friedlander, T., Prizak, R., Barton, N. H., Tkacik, G. (2017). Evolution of new regulatory functions on biophysically realistic fitness landscapes. *Nature Communications*, 8(1), 216. DOI: [10.1038/s41467-017-00238-8](https://doi.org/10.1038/s41467-017-00238-8)
20. Lagator, M., Paixao, T., Barton, N. H., Bollback, J. P., Guet, C. (2017). On the mechanistic nature of epistasis in a canonical cis-regulatory element. *eLife*, 6. DOI: [10.7554/eLife.25192](https://doi.org/10.7554/eLife.25192)
21. Novak, S., Barton, N. H. (2017). When does frequency-independent selection maintain genetic variation? *Genetics* 207(2):653-668. doi:[10.1534/genetics.117.300129](https://doi.org/10.1534/genetics.117.300129)
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23. Sachdeva, H., Barton, N. H. (2017). Divergence and evolution of assortative mating in a polygenic trait model of speciation with gene flow. *Evolution* 71(6):1478-1493 doi:[10.1111/evo.13252](https://doi.org/10.1111/evo.13252)
24. Schmidt, T. L., Barton, N. H., Rasic, G., Turley, A. P., Montgomery, B. L., Iturbe-Ormaetxe, I., Cook, P. E., Ryan, P. A., Ritchie, S. A., Hoffmann, A. A., O'Neill, S., Turelli, M. (2017). Successful local introduction and heterogeneous spatial spread of dengue-suppressing *Wolbachia* through an urban population of *Aedes aegypti*. *PLoS Biology*, 15(5). DOI: [10.1371/journal.pbio.2001894](https://doi.org/10.1371/journal.pbio.2001894)
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27. Barton, N. H. (2016). Sewall Wright on evolution in Mendelian populations and the “Shifting Balance”. *Genetics* 25(11):2325-32 doi:[10.1534/genetics.115.184796](https://doi.org/10.1534/genetics.115.184796)
28. Barton, N. H. (2016). Richard Hudson and Norman Kaplan on the coalescent process. *Genetics* 202(3):865-6 doi:[10.1534/genetics.116.187542](https://doi.org/10.1534/genetics.116.187542)
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33. Lohse, K., Chmelik, M., Martin, S. H., Barton, N. H. (2016). Efficient strategies for calculating block-wise likelihoods under the coalescent. *Genetics* 202(2):775-86 doi:[10.1534/genetics.115.183814](https://doi.org/10.1534/genetics.115.183814)
34. Paixao, T., Barton, N. H. (2016). The effect of gene interactions on the long-term response to selection. *PNAS*, 113(16), 4422–4427. DOI: [10.1073/pnas.1518830113](https://doi.org/10.1073/pnas.1518830113)
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37. Polechova, J., Barton, N. H. (2015). Limits to adaptation along environmental gradients. *PNAS*, 112(20), 6401–6406. DOI: [10.1073/pnas.1421515111](https://doi.org/10.1073/pnas.1421515111)
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