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Abstract



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S2. C19 Genes timing avian phenology in a changing climate: lessons from long-distance migratory birds

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The timing of life-history events of migratory birds is at least partly under genetic control, but the identification of candidate genes has lagged behind. It has been proposed photoperiodic response genes, such as those of the *Clock* family, show latitudinal variation and may be modulating avian timing of reproduction, reflecting seasonal and geographic variation in selective pressures. However, the extent to which those genes affects other avian life-cycle events is poorly known. Recently, we have investigated whether the timing of major life-history events, such as moult and migration timing, is controlled by *Clock* genes in long-distance passerine migrants. We first showed that a rare *Clock* genotype is associated with late breeding of barn swallow (*Hirundo rustica*) females and with delayed moult of wing feathers in the African winter quarters. Moreover, the analysis of a large dataset of four species of trans-Saharan migrants sampled while crossing the central Mediterranean (*Anthus trivialis*, *Saxicola rubetra*, *Luscinia megarhynchos*, *Ficedula hypoleuca*) highlighted that timing of spring migration was associated with *Clock* allele size, with individuals characterized by “longer” alleles (alleles with larger polyglutamine stretches) migrating later than those with “shorter” alleles. Our novel findings suggest that *Clock* genes may control the entire life-cycle of migratory birds. Importantly, since avian migration phenology is rapidly responding to global warming, with birds now migrating several days earlier than only a few decades ago, our findings suggest that directional selection on genes controlling migration phenology may be ongoing, and may allow to quantitatively predict the extent of genetic “signatures” of climate change.

S2. C20 From species to strains: production of toxins in populations of cyanobacteria and implications for water management

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Cyanobacteria are able to colonize virtually every type of water bodies, developing with higher biomasses in nutrient enriched and thermally stable lakes. This group of microalgae also produces an impressive range of secondary metabolites, including a wide range of powerful toxins, with important implications for health risks associated with the human exploitation of recreational and drinking waters. The ability to synthesize toxins is controlled at the level of strain, and the selection of toxic and non-toxic genotypes in different cyanobacterial species is the major source of variations in the toxins quota (the content of toxins per unit biomass). In this contribution we will report a case study of two populations of *Planktothrix rubescens* colonizing two connected lakes of different size and hydrology (lakes Garda and Ledro, NE-Italy). The lakes were characterized by significant and comparable relationships between the concentrations of microcystins (MCs, hepatotoxins) and the biomass of *P. rubescens* (B_{Pr}), with a limited variability in the MC quota. These findings were consistent with the development of specific genotypes, possibly common to the two lakes. The results will be discussed taking into account i) the wide range of variability in the MC quota reported in different European water bodies colonized by different strains of *Planktothrix*; ii) the implications for water management when the risk assessment is due to the adoption of fixed cyanobacterial density and biomass limits; iii) the weaknesses of the models relating MCs and biomasses when the lakes are dominated by mixed cyanobacterial populations. The results will also be discussed in the light of the very recent discovery of new, unexpected toxic strains of Oscillatoriales in Lake Garda. In this context, a paradigm change is advocated, taking into account, in the study of toxic cyanobacteria and risk assessment, not only the level of species, but also genotypes (strains).