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Runs of homozygosity analyses on reduced genomic data allow correct ranking of inbreeding estimates

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Runs of homozygosity (ROHs) are proxy for genomic Identical-by-Descent segments and increasingly used as a measure for individual inbreeding. ROHs analyses are mostly applied to SNPs-arrays and whole-genome-sequencing data. Softwares used for their detection assume that non-genotyped genomic positions are non-variant. This assumption might be true for whole-genome-sequencing data, but not for reduced genomic representations and can lead to spurious ROHs detection. We simulated the outputs of whole-genome-sequencing, SNP-arrays and RAD-sequencing for populations of different sizes. We compared the results of ROHs calling with two softwares: *PLINK* and *RZooRoH*. We show that, when a sufficient fraction of genome is sequenced, ranks of ROHs-based inbreeding coefficients are conserved among individuals and most of the genome is correctly assigned within and outside ROHs. We show that SNP density can be used as a proxy for the suitability of the reduced-genomic data for ROHs analyses: *RZooRoH* required a minimum of 3,000 SNPs/Gb while *PLINK* required a minimum of 20,000 SNPs/Gb to conserve the ranks of inbreeding between WGS and RAD-sequencing. With reduced representation, we find ROHs distribution are consistently biased towards an underestimation of the total numbers of small ROHs and an overestimation of the total numbers of large ROHs. Finally, we discuss the relevance of using ROHs vs SNP-independent-based measures of inbreeding coefficients with reduced genomic representations.

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Monitoring within-species genetic diversity of amphibians with eDNA metabarcoding

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Ongoing habitat alterations and climate change can lead to a dramatic decline in local populations, and cost-efficient tools to rapidly estimate population genetic diversity in space and time are urgently needed. Here we used the common frog *Rana temporaria* (Linnaeus, 1758) from 10 wetland sites in the Italian Alps to: i) develop and test a standardized eDNA metabarcoding protocol for the monitoring of within-species genetic diversity (targeting a short fragment of the COI barcode region); and ii) critically compare the results of eDNA metabarcoding with those obtained from traditional genetic

sampling. Our results showed that a single temporal sampling replicate performed after spawning (and when egg clutches and/or larval stages are still present in the water) is sufficient to successfully characterize haplotype richness, but two temporal replicates are needed to obtain more accurate information on haplotype frequencies. We then demonstrated that standard genetic variability estimates (haplotype and nucleotide diversity) derived from eDNA metabarcoding are strongly correlated with those derived from traditional genetic data. Similarly, we also found a moderate but yet significant correlation between the population structures inferred from the two considered methods. Thus, our protocol proved to be a fast and effective tool that could be used for the establishment of a surveillance network, with the ultimate goal of monitoring temporal trends in the genetic diversity of pond-breeding amphibians.

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The origin of meiosis from eukaryogenesis

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The origin of sexual reproduction in eukaryotes is an evolutionary mystery. Sexual recombination can promote purifying selection and reduce selective interference, but similar advantages are achieved in prokaryotes through lateral gene transfer (LGT). The selective pressures behind the evolution of a novel mechanism of genetic exchange in eukaryotes – sexual reproduction – are still obscure. In this talk, I discuss how the origin of meiotic sex is tightly linked to the process of eukaryogenesis. The transition from prokaryotes to eukaryotes involved an expansion in genome size, together with the proliferation of genomic repeats. Using computational models, I show that large genomes are vulnerable to the progressive accumulation of deleterious mutations through Muller's ratchet, whilst limiting LGT's ability to purge deleterious mutations. A high repeat density introduces an additional cost to LGT, because of the increased genomic instability arising from ectopic recombination. The way of avoiding catastrophic gene loss is to combine increased recombination length with the requirement for sequence homology – a first step towards meiotic homolog pairing. Homology along extended sequences of DNA allows recombination to take place across a considerable fraction of each chromosome, which is sufficient to halt the decay of eukaryotic-sized genomes through Muller's ratchet. The transition to linear chromosomes and homolog pairing minimises the risk of ectopic recombination and the associated loss of genetic information, allowing the evolution of larger and more complex eukaryotic genomes.

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Adaptive evolution under rewired genetic codes

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The standard genetic code is extremely robust to the effects of point mutations: the missense mutations it allows are conservative with respect to key physicochemical properties of amino acids. Recent advances in synthetic biology enable the engineering of organisms with rewired genetic codes, making the rational design of non-standard