

Linking epigenetics and biological conservation: Toward a *conservation epigenetics* perspective: Supplementary files.

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Table S1. Advantages and disadvantages of DNA methylation and metrics and components to monitor epigenetic erosion at the population level, similar to genetics.

DNA methylation sequencing assays*	Advantages of DNA methylation	Drawbacks of DNA methylation	Genomic components and measures	Epigenomic components and measures	Components to monitor	Metrics of diversity and structure (References)
Bisulfite-based methods 1. <i>MethylC-seq</i> 2. <i>Reduced representation bisulfite sequencing (RRBS)</i> 3. <i>WGBS</i>	1. Links modifications with the environment 2. Regulation of gene expression 3. Links to phenotypic plasticity 4. DNA sequence context 5. Large number of modifications due to the higher epimutation rate 6. Source of nongenetic inheritance 7. Integrating DNA methylation data with other genomic data	1. Tissue (age, condition)-specific 2. Spontaneous stochastic DNA methylation modifications 3. Influenced by nucleotide context	1. Single Nucleotide Polymorphism 2. Number of polymorphic sites 3. Genetic variation 4. Haplotype diversity 5. Selection-based analyses 6. Introgression 7. Functional enrichment 8. Gene annotation	1. Single Methylation Polymorphism 2. Number of methylated sites (i.e., methylation levels) 3. Epigenetic variation 4. Haplotype diversity 5. Selection-based analyses 6. Introgression 7. Functional enrichment 8. Gene annotation 9. Differentially methylation analysis	1. Infer ancestry information and describe the ancestral allele methylation status 2. Levels of isolation and differentiation between populations 3. Haplotype diversity 4. Detect selection forces on DNA methylation	ADMIXTURE (Heyn et al. 2013; Rahmani et al. 2017) EPISTRUCTURE (Heyn et al. 2013; Rahmani et al. 2017) <i>epi-F</i> statistics (Mahajan et al. 2015; Liebl et al. 2013; Herrera et al. 2017; Sheldon et al. 2018) <i>epi-F</i> metrics (Mahajan et al. 2015; Liebl et al. 2013; Herrera et al. 2017; Sheldon et al. 2018) G_{ST} (Liu et al. 2012) <i>epi-h</i> metrics (Liu et al. 2012; Sheldon et al. 2018) Epiallele richness Percentage of polymorphic loci (%Poly) (Sheldon et al. 2018) D^m (Wang et al. 2015)
Enrichment-based methods 1. <i>Methylated DNA immunoprecipitation sequencing (MeDIP-seq)</i> 2. <i>Methylated DNA binding domain sequencing (MBD-seq)</i> 3. <i>Methylated DNA capture (MethylCap-seq)</i>						
Methyl-sensitive restriction enzyme-based methods						

*This table is not aim to cover all possible methods that profile DNA methylation but to focus on those that are most frequently used. Assays for sequencing DNA methylation are classified into three categories: bisulfate-based, enrichment-based and restriction enzymes-based methods. More comprehensive reviews of available techniques have been written by other authors (Kurdyukov and Bullock 2016; Olkhov-Mitsel and Bapat 2012)

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