

## GUIDELINE MATERIALS AND DOCUMENTATION FOR THE GENETIC DIVERSITY INDICATORS OF THE MONITORING FRAMEWORK FOR THE KUNMING-MONTREAL GLOBAL BIODIVERSITY FRAMEWORK

ALICIA MASTRETTA-YANES<sup>1,2</sup>, SOFÍA SUÁREZ<sup>3</sup>, REBECCA JORDAN<sup>4</sup>, SEAN HOBAN<sup>5,6</sup>, JESSICA M. DA SILVA<sup>7,8</sup>, LUIS CASTILLO-REINA<sup>9</sup>, MYRIAM HEUERTZ<sup>10</sup>, FUMIKO ISHIHAMA<sup>11</sup>, VIKTORIA KÖPPÄ<sup>12</sup>, LINDA LAIKRE<sup>12</sup>, ANNA J. MACDONALD<sup>13</sup>, JOACHIM MERGEAY<sup>14,15</sup>, IVAN PAZ-VINAS<sup>16</sup>, GERNOT SEGELBACHER<sup>17</sup>, ALICIA KNAPPS<sup>17</sup>, HENRY RAKOCZY<sup>17</sup>, AMELIE WEILER<sup>17</sup>, ANGELICA ATSAVES<sup>17</sup>, KIRA CULLMANN<sup>17</sup>, SIMONE BAGNATO<sup>17</sup>, BRENNAN R. FORESTER<sup>18</sup>

- <sup>1</sup> Consejo Nacional de Humanidades Ciencias y Tecnología (CONAHCYT), Avenida Insurgentes Sur 1582, Crédito Constructor, Benito Juárez, Ciudad de México. C.P. 03940. Mexico. \*
- <sup>2</sup> Departamento de Ecología de la Biodiversidad, Instituto de Ecología, Universidad Nacional Autónoma de México. Av. Ciudad Universitaria 3000, 04510, Coyoacán, Ciudad de México, Mexico
- <sup>3</sup> Laboratorio de Genética de la Conservación, Jardín Botánico, Instituto de Biología, Universidad Nacional Autónoma de México. Ciudad de México, Mexico
- <sup>4</sup> CSIRO Environment, 15 College Rd, Sandy Bay 7005, Tasmania, Australia
- <sup>5</sup> Center for Tree Science, The Morton Arboretum, Lisle, USA
- <sup>6</sup> Committee on Evolutionary Biology, The University of Chicago, Chicago, USA
- <sup>7</sup> South African National Biodiversity Institute, Kirstenbosch Research Centre, Private Bag X7 Claremont 7735, Cape Town, South Africa
- <sup>8</sup> Centre for Ecological Genomics and Wildlife Conservation, Department of Zoology, University of Johannesburg, Auckland Park 2006, Johannesburg, South Africa
- <sup>9</sup> Department of Biology, Faculty of Science, KU Leuven, Leuven, Belgium
- <sup>10</sup> Univ. Bordeaux, INRAE, BIOGECO, F-33610 Cestas, France
- <sup>11</sup> National Institute for Environmental Studies, Onogawa16-2, Tsukuba, Ibaraki, Japan
- <sup>12</sup> Department of Zoology, Stockholm University, SE10691 Stockholm, Sweden
- <sup>13</sup> Australian Antarctic Division, Department of Climate Change, Energy, the Environment and Water, Kingston, Tasmania 7050, Australia
- <sup>14</sup> Research Institute for Nature and Forest, Gaverstraat 4, 9500 Geraardsbergen, Belgium
- <sup>15</sup> Ecology, Evolution and Biodiversity Conservation, KU Leuven, Charles Deberiotstraat <sup>32</sup>, Box 2439, Leuven, Belgium
- <sup>16</sup> Université Claude Bernard Lyon 1, LEHNA UMR 5023, CNRS, ENTPE, F-69622, Villeurbanne, France
- <sup>17</sup> University of Freiburg, Wildlife Ecology and Management, 79106 Freiburg im Breisgau, Germany
- <sup>18</sup> U.S. Fish and Wildlife Service, Fort Collins, CO, USA

\*Corresponding author: Alicia Mastretta-Yanes, Email: amastretta@iecologia.unam.mx

*Abstract.* Genetic diversity is fundamental to biological diversity, vital for species' health and adaptation to environmental change. Under the recently adopted Kunming-Montreal Global Biodiversity Framework (GBF), 196 Parties committed to report the status of genetic diversity for both wild and domesticated species. For this, three genetic diversity indicators were developed, two of which focus on processes contributing to genetic diversity conservation: ensuring that populations are large enough to maintain genetic diversity (effective population size  $N_e$  500 indicator) and maintaining genetically distinct populations (populations maintained, PM indicator). A third indicator focuses on the number of species being monitored using DNA-based methods. Adopted by 196 CBD Parties in December 2022, GBF integrated  $N_e$  500 and PM as headline and complementary indicators, respectively. To aid nations in quantifying these indicators, a detailed set of guideline materials was developed, encompassing species selection, data compilation, and indicator computation. These guidelines draw from the collaborative efforts of the first multinational assessment of genetic diver-

sity indicators that was recently completed and that will be refined continually through a versioning system, as more experience is gained and shared. The materials aim to support the global monitoring framework established by the CBD and are accessible online for utilization and updates. The guidelines are available at <https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/>

*Key words:* biodiversity indicators, Kunming Montreal Global Biodiversity Framework, biodiversity monitoring, COP15, effective population size, population maintained, populations.

Genetic diversity is the foundation of all biological diversity. It is necessary for populations of both wild and domesticated species to remain healthy and be able to adapt to environmental change, and for conserving nature's contributions to people (Des Roches et al., 2021). Starting in 2020, during preparation of what would become the Kunming Montreal Global Biodiversity Framework (GBF), three genetic diversity indicators were developed (Hoban et al., 2020, 2021; Laikre et al., 2020): (1) effective population size ( $N_e$ ) 500 indicator, which measures the proportion of populations within a species that are of sufficient size ( $N_e > 500$ ) to maintain genetic diversity and adaptive potential within that species; (2) populations maintained (PM) indicator, which measures the proportion of populations that still exists compared to the total number of populations that used to occur; and (3) a DNA-based monitoring indicator, which is a count of the number of species in which genetic diversity has been or is being monitored using DNA-based methods. The first two indicators focus on processes contributing to genetic diversity conservation: ensuring that populations are large enough to maintain genetic diversity ( $N_e$  500 indicator) and maintaining genetically distinct populations (PM indicator). These two indicators were adopted in 2022 by GBF as headline A4 and complementary indicators, respectively, which means that GBF parties will use these indicators to report on their progress over the next decade (CBD, 2022b, 2022a). They also cover two key aspects of the GBF: conserving genetic diversity both within populations and between populations.

The GBF commitment to monitoring genetic diversity for all species, instead of only socioeconomically and culturally valuable taxa (as was required in 2010-2020), represents a significant milestone for conservation genetics, but comes with new challenges. By focusing on processes underlying the generation and maintenance of genetic diversity, the PM and  $N_e$  500 indicators alleviate some of these challenges because they can be estimated using both genetic and non-genetic data (Hoban et al., 2020; Laikre et al.,

2020). Genetic data include DNA-based molecular markers to estimate  $N_e$  or delimit population boundaries, whereas non-genetic data include census population size ( $N_c$ ), which could be transformed to  $N_e$  using a  $N_e/N_c$  ratio, as well as occurrence data and knowledge of the species' biology, history and dispersal to define populations geographically (Hoban et al., 2023, 2024). Integrating data from these diverse sources, formats and disciplines, from global databases to local knowledge, would make it possible to monitor genetic diversity across the world, much faster than is possible with genetic studies alone (Mastretta-Yanes et al., 2024). Gathering and sharing biodiversity data has its own difficulties (Blair et al., 2020; Enke et al., 2012). However, integrating the diverse data needed to estimate genetic diversity indicators also requires capacity building to integrate genetic principles to new fields, designing new data collection protocols, and mobilizing data for indicator calculation in a reliable, transparent, and inclusive way, without stretching the personnel, time, and financial resources of the agencies in charge of reporting them.

To contribute to meeting these challenges, with colleagues, we co-developed the following guideline materials, as part of the first multinational assessment of the genetic diversity indicators (Mastretta-Yanes et al., 2024). Part of the guidelines were described previously in Hoban et al. (2023), but after implementing them across nine countries (Australia, Belgium, Colombia, France, Japan, Mexico, South Africa, Sweden, and the United States of America), several improvements were made. These improvements incorporate feedback from around 80 participants (students, practitioners and researchers) who gathered data for the indicators, as well as feedback from 13 international webinars & seminars with hundreds of participants. This publication leverages our shared experience, with more detailed guidelines in an online documentation format, that will be kept updated through a versioning system as more teams share insights. The materials are intended to assist nations in quantifying genetic indicator values

at every stage of the process: from species selection to data compilation to indicator calculation. We hope they become useful as a reference point, from which countries can adjust their protocols to their own needs and preferences.

The guidelines are available as an online documentation at

<https://ccgenetics.github.io/guidelines-genetic-diversity-indicators/>

The online documentation consists of eight content sections, as follows: (1) **Background** on the population genetics rationale behind the genetic diversity indicators, (2) **Quickstart guide** summarizing steps needed to estimate the indicators, (3) Discussion on how many and which species to include in the **species list** to evaluate the indicators, (4) **How-to guides** with practical examples showing how to perform the most common tasks involved in assessing the genetic diversity indicators, (5) **Example assessments** of real-life species, (6) **Data collection** advice with a ready-to-use template for a web tool for data collection using KoboToolBox, (7) Equations, scripts and examples for **calculations and reporting** of the indicators, and (8) **Glossary**.

#### ACKNOWLEDGMENTS

These materials are based on the co-creation experience of the first pilot multinational assessment of the genetic diversity indicators, and on interactions with practitioners, researchers and students of several institutions across the world. We are particularly grateful to the Swedish Environmental Protection Agency, the Ad Hoc Technical Expert Group on Indicators for the Kunming-Montreal Global Biodiversity Framework, and to the following people for providing feedback and ideas: Akio Takenaka, Alejandra Domínguez Álvarez, Alexander Llanes-Quevedo, Alice Hughes, Ana Wegier, Ashley Hamilton, Atsaves Angelica, Austin Koontz, Bastian Silva, Belma Kalamujić Stroil, Caitlin Miller, Catherine E Grueber, W Chris Funk, Emma Suzuki Spence, Erica Robertson, Eugenia Zarza, Fleur Visser, Gaëlle Brahy, Georgina Wood, Glenn M Shea, Henrik Thurfjell, Hesiquio Benitez, Irene Ramos, Iris Lang, Isa-Rita Russo, Juan Francisco Ornelas, Katie Millette, Keiichi Fukaya, Kira Cullmann, Libertad Arredondo-Amezcuca, Lily Durkee, Lucía Ruíz, Luke Dedecke, Malte Julius Benedikt Lehmann, Malte Lehmann, Margaret E. Hunter, Maria Alejandra Rodriguez-Morales, María Camila Latorre, Marlien van

der Merwe, Matt DeSaix, Meg Mahoney, Metztlí Arcila Santiago, Mónica Alegre, Paulette Bloomer, Per Sjögren-Gulve, Philipp Ungar, Robyn E. Shaw, Santiago Ramírez-Barahona, Sheela Turbek, Simone Bagnato, Sofía Treviño, Tanya Latty, Taylor Stack, and Victor Julio Rincon-Parra.

#### AUTHOR CONTRIBUTIONS

AM-Y developed the Github repository and coordinated the overall project with BRF. SS and AM-Y loaded the content into the Github repository and programmed the Kobo-form. AM-Y, SS, RJ, SH, JMDS and BRF wrote most of the updated version of the guidelines and made figures. AM-Y, RJ, SH, JMDS, BRF, LC-R, MH, FI, VK, LL, AJM, JM, IP-V wrote the initial version of the guidelines and made figures. GS coordinated the testing of the guidelines and contributed to the test. AK, HR, AW, AA, KC and SG tested the guidelines and provided step-by-step examples following them. All authors contributed to the design of the guidelines, the Kobo-form and proof-read the guidelines and the manuscript.

#### COMPETING INTERESTS

The authors have declared that no competing interests exist.

#### REFERENCES

- Blair, J., Gwiazdowski, R., Borrelli, A., Hotchkiss, M., Park, C., Perrett, G., & Hanner, R. (2020). Towards a catalogue of biodiversity databases: An ontological case study. *Biodiversity Data Journal*, 8. <https://doi.org/10.3897/BDJ.8.e32765>
- CBD. (2022a). *Decision adopted by the Conference of the Parties to the Convention on Biological Diversity CBD/COP/DEC/15/4 Kunming-Montreal Global Biodiversity Framework*. CBD/COP/DEC/15/4. <https://www.cbd.int/doc/decisions/cop-15/cop-15-dec-04-en.pdf>
- CBD. (2022b). *Decision adopted by the Conference of the Parties to the Convention on Biological Diversity CBD/COP/DEC/15/5 Monitoring framework for the Kunming-Montreal Global Biodiversity Framework*. CBD/COP/DEC/15/5. <https://www.cbd.int/doc/decisions/cop-15/cop-15-dec-05-en.pdf>
- Des Roches, S., Pendleton, L. H., Shapiro, B., & Palkovacs, E. P. (2021). Conserving intraspecific variation for nature's contributions to people. *Nature Ecology & Evolution*, 1–9. <https://doi.org/10.1038/s41559-021-01403-5>
- Enke, N., Thessen, A., Bach, K., Bendix, J., Seeger, B., & Gemeinholzer, B. (2012). The user's view on biodiversity data sharing—Investigating facts of acceptance and requirements to realize a sustainable use of research data. *Ecological Informatics*, 11, 25–33. <https://doi.org/10.1016/j.ecoinf.2012.03.004>

- Hoban, S., Bruford, M., D'Urban Jackson, J., Lopes-Fernandes, M., Heuertz, M., Hohenlohe, P.A., Paz-Vinas, I., Sjögren-Gulve, P., Segelbacher, G., Vernesi, C., Aitken, S., Bertola, L.D., Bloomer, P., Breed, M., Rodríguez-Correa, H., Funk, W.C., Grueber, C.E., Hunter, M.E., Jaffé, R., Liggins, L., Mergeay, J., Moharrek, F., O'Brien, D., Ogden, R., Palma-Silva, C., Pierson, J., Ramakrishnan, U., Simo-Droissart, M., Tani, N., Waits, L., Laikre, L., (2020). Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. *Biological Conservation*, 248, 108654. <https://doi.org/10.1016/j.biocon.2020.108654>
- Hoban S, Da Silva JM, Hughes A, Hunter ME, Kalamujić Stroil B, Laikre L, Mastretta-Yanes A., Millette K, Paz-Vinas I, Ruiz Bustos L, Shaw RE, Vernesi C, the Coalition for Conservation Genetics (2024). Too simple, too complex, or just right? Advantages, challenges, and guidance for indicators of genetic diversity. *BioScience*, biae006.
- Hoban, S., da Silva, J. M., Mastretta-Yanes, A., Grueber, C. E., Heuertz, M., Hunter, M. E., Mergeay, J., Paz-Vinas, I., Fukaya, K., Ishihama, F., Jordan, R., Köppä, V., Latorre-Cárdenas, M. C., MacDonald, A. J., Rincon-Parra, V., Sjögren-Gulve, P., Tani, N., Thurfjell, H., & Laikre, L. (2023). Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment of genetic indicators in nine countries. *Conservation Letters*, 16(3), e12953. <https://doi.org/10.1111/conl.12953>
- Hoban, S., Paz-Vinas, I., Aitken, S., Bertola, L. D., Breed, M. F., Bruford, M. W., Funk, W. C., Grueber, C. E., Heuertz, M., Hohenlohe, P., Hunter, M. E., Jaffé, R., Fernandes, M. L., Mergeay, J., Moharrek, F., O'Brien, D., Segelbacher, G., Vernesi, C., Waits, L., & Laikre, L. (2021). Effective population size remains a suitable, pragmatic indicator of genetic diversity for all species, including forest trees. *Biological Conservation*, 253, 108906. <https://doi.org/10.1016/j.biocon.2020.108906>
- Laikre, L., Hoban, S., Bruford, M. W., Segelbacher, G., Allendorf, F. W., Gajardo, G., Rodríguez, A. G., Hedrick, P. W., Heuertz, M., Hohenlohe, P. A., Jaffé, R., Johannesson, K., Liggins, L., MacDonald, A. J., Orozco-terWengel, P., Reusch, T. B. H., Rodríguez-Correa, H., Russo, I.-R. M., Ryman, N., & Vernesi, C. (2020). Post-2020 goals overlook genetic diversity. *Science*, 367(6482), 1083–1085. <https://doi.org/10.1126/science.abb2748>
- Mastretta-Yanes, A., da Silva, J.M., Grueber, C.E., Castillo-Reina, L., Köppä, V., Forester, B.R., Funk, W.C., Heuertz, M., Ishihama, F., Jordan, R., Mergeay, J., Paz-Vinas, I., Rincon-Parra, V.J., Rodriguez-Morales, M.A., Arredondo-Amezcuca, L., Brahy, G., DeSaix, M., Durkee, L., Hamilton, A., Hunter, M.E., Koontz, A., Lang, I., Latorre-Cárdenas, M.C., Latty, T., Llanes-Quevedo, A., MacDonald, A.J., Mahoney, M., Miller, C., Ornelas, J.F., Ramírez-Barahona, S., Robertson, E., Russo, I.-R.M., Santiago, M.A., Shaw, R.E., Shea, G.M., Sjögren-Gulve, P., Spence, E.S., Stack, T., Suárez, S., Takenaka, A., Thurfjell, H., Turbek, S., van der Merwe, M., Visser, F., Wegier, A., Wood, G., Zarza, E., Laikre, L., Hoban, S. (2024). Multinational evaluation of genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework. *Ecology Letters*, 27(7), e14461. <https://doi.org/10.1111/ele.14461>