INSIGHTS

PERSPECTIVES

The majority of Earth's species diversity remains to be discovered and described, particularly from its most remote regions (such as the Andes Mountains in Ecuador).

PHOTO: GLENN R. SPECHT-GRS PHOTO/SHUTTERSTOCK

BIODIVERSITY

Completing Wallace's journey

A global inventory of species diversity is critical for understanding the evolution of life on Earth

By **Jonathan D. Kennedy**[1] *and* **Jon Fjeldså**[2,3]

British naturalist Alfred Russel Wallace developed the theory of evolution as a consequence of the taxonomic discoveries made during his expeditions across the Indonesian archipelago in the 19th century. From his collections, thousands of new species have been described, including around 2% of all living bird species. Birds are one of the most comprehensively documented organismal groups, but multiple new species continue to be described yearly, and at an increasing rate. Nearly all recent avian species discoveries come from disjunct geographic locations. However, on page 167 of this issue, Rheindt *et al.* (*1*) describe five new species and five subspecies from three islands off the eastern coast of Sulawesi, Indonesia. This is the largest number of new species descriptions from a restricted geographic locality in over a century and highlights the importance of documenting biodiversity today, given the environmental threats that could condemn many as yet unidentified taxa to extinction.

Knowing how many species are present on Earth remains a fundamental scientific question whose answer is essential to generating a reliable benchmark from which current and future biodiversity losses can be gauged. Currently, as much as 86% of the world's overall species diversity is undescribed (*2*). Even for a well-known group such as birds, some estimates suggest that overall numbers could be substantially higher than the ~10,500 presently recognized species (*3*). The taxonomic description of bird species has benefited from their relative ease of observation. In addition, numerous clearly defined characters signify that lineages are evolving independently from one another [e.g., differentiation in plumage coloration, acoustic signaling, and genomic characters (*4*)]. Because of this progress, present-day avian species discoveries tend to represent relatively shallow levels of evolutionary distinctiveness. Although phenotypic and genetic evidence convincingly suggests that all 10 forms described by Rheindt *et al.* are independently evolving populations, these data also indicate that they represent lineages that are members of well-known genera, with close relatives distributed on nearby islands. Descriptions of deeper and more distinctive evolutionary branches of the avian tree

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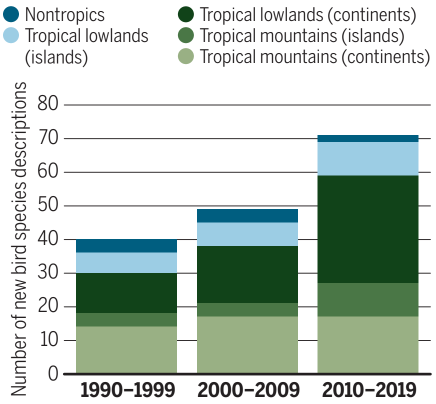
of life are rare, the most recent noteworthy example being the *Xenoperdix* forest partridges discovered in the mid-1990s (*5*).

Between 1990 and 2019, approximately 160 new bird species descriptions were made worldwide (see the figure), so the discovery of five bird species from a relatively small geographic locality is impressive, driven by the local aggregation of small-ranged species. This suggests that many biologically underexplored places likely still exist across Earth. Formal species descriptions, such as those by Rheindt *et al.*, are a necessary step toward initiating conservation actions that aim to preserve these little-known biotas.

New bird species descriptions

The total number of new species descriptions increased over the past three decades (*9*, *10*).



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In comparison to birds, global knowledge of other vertebrate, invertebrate, plant, fungal, and microorganismal life is far more limited, particularly in tropical regions. Millions of unknown species, likely representing more distinctive portions of the tree of life, remain to be discovered (*2*, *6*). To discover these taxa most efficiently, geographic areas with high promise should first be targeted. It is thus notable that most new bird species discoveries in the past 30 years have been from localities that reside in tropical or subtropical latitudes. These areas tend to have complex landscapes, geologies, soil conditions (such as ultramafic soils), and topographic or aquatic barriers (such as mountains and river systems, respectively). Most problematically, these locations are poorly accessible, resulting in historically limited biological exploration. Limited access reflects not only geographic barriers but also political and commercial obstacles. Mountainous areas in the tropics, both in island and continental settings, hold great promise for discovering new species because they are environments that tend to harbor little-studied biological communities, where range-restricted species can evolve (endemism) (*7*). Bird descriptions arising from these areas (especially in Indochina, Malesia, eastern Africa, Brazil, and the tropical Andes) are highly indicative of generally poorly known terrestrial biotas.

Extensive population growth and human consumption over the past century have caused substantial habitat degradation, primarily due to urban development, logging, mining, and wildlife trade and exploitation. These combined threats continue unabated and are driving the global extinction crisis, with current rates of extinction estimated to exceed background rates by a factor of 100 to 1000 (*8*). Much of the world's biodiversity is under considerable risk of being lost before it is ever scientifically known. For these reasons, Wallace's journey to find, describe, and study taxonomic diversity should continue today with increased vigor and resources, as this will ultimately increase knowledge about the most effective way to preserve nature. Achieving this will require more extensive international collaborative efforts by governments, academics, and local communities. To thoroughly explore and describe the poorly known parts of the terrestrial, subterranean, and aquatic world will also necessitate increased recognition of the value that taxonomic discovery has toward our general understanding of the natural world. To secure increased funding, scientists must better explain to their colleagues, the public, policy-makers, and funding agencies why biological exploration should be seen as a pressing issue today, not just a historical activity of Wallace's time. Without knowing how many species there are in the world, and their distributions, our understanding of how ecological and evolutionary processes have generated the full diversity of life on Earth is incomplete, limiting our capacity to successfully maintain biodiversity into the future. ■

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INFECTIOUS DISEASE

Tolerance to antibiotics affects response

Bacterial tolerance to antibiotics reduces the ability to prevent resistance

By **Andrew D. Berti**[1] *and* **Elizabeth B. Hirsch**[2]

Antimicrobial resistance is increasing worldwide (*1*). More than 2.8 million antibiotic-resistant infections were identified in the United States in 2019, resulting in more than 35,000 deaths (*2*). Prior to the development of antimicrobial resistance, bacteria frequently develop enhanced antimicrobial tolerance (*3*). Antimicrobial resistance is the ability of a microbe to grow in an inhibitory concentration of an antibiotic, whereas tolerance is a reduced rate of antimicrobial killing (*4*). Antibiotic combinations are often used to improve efficacy (*5*) and to prevent the emergence of antibiotic resistance (*6*). However, it is unclear if antibiotic combinations prevent the emergence of tolerance. On page 200 of this issue, Liu *et al.* (*7*) examine sequential *Staphylococcus aureus* isolates from patients treated with daptomycin plus rifampin. Although this combination of antibiotics delayed the emergence of tolerant populations, once tolerance was established, the benefits of combination therapy in preventing resistance were lost.

Antibiotic tolerance is a natural phenomenon that occurs as a spontaneous "hibernation-mode" phenotypic switch within a small subset of a microbial population. Transient microbial growth arrest is induced by stressful conditions, such as a sudden decrease in nutrient availability, when continued rapid growth would threaten viability. Once the insult is removed, bacteria can resume typical microbial growth (*8*). Phenotypically tolerant microbes are genetically indistinguishable from other nontolerant, growing bacteria. However, mutations in one of sev-

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