

Editorial

Integrative Taxonomy and Parasite Identification in the Molecular Era

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Parasite identification remains one of the most important areas of parasitological research. Accurate parasite identification underpins biodiversity studies, disease surveillance, epidemiology, host–parasite interactions, and disease control. For decades, parasite taxonomy relied primarily on morphological observations, including anatomical structures, developmental stages, and host associations. While morphology continues to provide the foundation for species descriptions, recent advances in molecular biology have transformed our ability to recognize parasite diversity and investigate evolutionary relationships.

Integrative taxonomy combines morphological, molecular, ecological, biogeographical, and evolutionary evidence to delimit and identify species more robustly than any single source of information alone. Several recent articles published in *Parasitologia* illustrate this ongoing transition from traditional taxonomy toward integrative approaches that combine morphology, molecular biology, pathology, and epidemiology. For example, McAllister et al. described a new species of *Eimeria* from a North American watersnake using classical oocyst morphology supported by molecular evidence [1]. Similarly, Rindoria et al. combined scanning electron microscopy with analyses of multiple genetic markers to characterize *Lamproglena barbicola*, demonstrating the value of integrating morphological and molecular datasets for species delimitation [2]. Museum-based taxonomic revisions also continue to contribute to our understanding of parasite biodiversity and host associations, as demonstrated by the revision of *Gyrodactylus* species from freshwater fishes in Bulgaria [3].

The importance of combining multiple diagnostic approaches is also highlighted beyond species descriptions. In their scoping review of naturally occurring xenomas in fish, Mariacher et al. showed that microscopy remains central to diagnosis but emphasized the increasing need for standardized workflows that incorporate molecular tools [4]. Likewise, De Vivero et al. reviewed recent advances in molecular detection of helminths, demonstrating how PCR-based methods, sequencing technologies, and emerging genomic approaches are expanding opportunities for parasite surveillance and epidemiological investigations [5]. Diagnostic innovation is further illustrated by the evaluation of touchdown loop-mediated isothermal amplification (LAMP) for the detection of *Giardia duodenalis*, emphasizing the growing potential of rapid molecular assays for parasite diagnosis [6].

Molecular approaches are also contributing to a broader understanding of parasite transmission and disease ecology. Mugasa et al. used molecular methods to investigate *Cryptosporidium* species circulating at the wildlife–human interface in Uganda, highlighting the importance of One Health perspectives in modern parasitology [7]. Similar advances have improved our understanding of parasite diversity and transmission in wildlife hosts, including recent molecular investigations of *Sarcocystis* and *Hepatozoon* infections in bobcats from the United States [8]. Molecular diagnostics have also improved the detection of oppor-



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tunistic and zoonotic infections in humans, as illustrated by the molecular characterization of co-infections involving *Cryptosporidium meleagridis* and *Enterocytozoon bienersi* [9].

Among the most transformative recent developments in parasite diagnostics is the application of nanopore sequencing—a portable, long-read third-generation sequencing technology capable of generating real-time sequence data with minimal laboratory infrastructure. The MinION platform and related devices have demonstrated promise for field-deployable parasite identification, enabling whole-genome sequencing of *Plasmodium* from finger-prick blood samples and real-time tracking of drug resistance alleles in endemic settings [10]. Building on this, Sugi et al. developed a targeted 18S rDNA barcoding strategy using portable nanopore sequencing for accurate blood parasite identification in resource-limited settings, demonstrating superior species-level resolution compared to conventional microscopy [11]. At the same time, nanopore-based amplicon methods have been successfully applied to detect microsporidian and protist parasites in reared insects, generating novel phylogenetic data that improve understanding of entomopathogen diversity [12]. A comprehensive review by Dufourni et al. further consolidates the evidence base for nanopore sequencing in veterinary parasite and pathogen detection, providing practical workflow guidance relevant to One Health surveillance contexts [13]. suggest that long-read sequencing may become an increasingly valuable complement to morphological identification, particularly for cryptic taxa or multi-species infections that conventional short-read platforms struggle to resolve.

A second frontier of considerable promise is the detection of parasites through environmental DNA (eDNA), genetic material shed by organisms into their surroundings and recoverable directly from water, soil, or sediment. Johnson et al. demonstrated that eDNA-based approaches can be as sensitive as or outperform traditional sampling methods for freshwater parasite surveillance and compared the relative utility of qPCR and metabarcoding workflows [14]. For disease monitoring on a community scale, Bautista et al. refined a multiplex eDNA qPCR assay for simultaneous detection of *Schistosoma japonicum* and its snail intermediate host, enabling cost-effective spatiotemporal mapping of schistosomiasis transmission risk [15]. The eDNA approach has also been explored for zoonotic parasites of public health importance: eDNA detected from river water has been suggested as a surveillance tool for *Echinococcus multilocularis*, opening avenues for early warning monitoring in newly indigenous regions [16]. In general, the pairing of eDNA with high-throughput metabarcoding enables simultaneous screening of diverse parasite communities across ecosystems, making it a potentially powerful tool for biodiversity-based One Health surveillance [17]. A key restriction, however, remains the difficulty of discriminating between viable infectious stages and degraded environmental DNA, highlighting the need to integrate eDNA findings with host surveillance and morphological confirmation [18].

At the frontier of molecular parasitology, single-cell RNA sequencing (scRNA-seq) is opening fundamentally new windows into parasite biology and host–parasite interactions. Early applications to *Plasmodium falciparum* revealed previously hidden transcriptional heterogeneity among individual parasites across asexual and sexual life-cycle stages, challenging assumptions of transcriptional continuity through the intraerythrocytic developmental cycle [19]. The approach has since been extended to construct comprehensive single-parasite transcriptional atlases for *Toxoplasma gondii*, identifying novel transcription factors controlling antigenic switching and revealing concerted patterns of gene expression shared with *Plasmodium* despite fundamental differences in cell division biology [20]. For multicellular helminths, scRNA-seq has enabled the construction of whole-organism cell atlases that map developmental trajectories and identify candidate drug targets, while at the same time profiling host immune cell populations responding to infection [21]. Advances

in sample preservation and sequencing chemistry are now extending these approaches to field settings, with new protocols enabling scRNA-seq of *Plasmodium knowlesi* from clinical isolates collected in low-resource environments [22]. With single-cell transcriptomics becoming more accessible in cost and infrastructure, it is poised to significantly accelerate our understanding of stage-specific biology, immune evasion mechanisms, and host–parasite co-evolutionary dynamics across diverse parasite taxa.

Technological innovation continues to advance parasite diagnostics more broadly. Molecular methods have enabled the detection of previously unrecognized host–parasite associations, such as the identification of *Histomonas meleagridis* in poultry red mites [23]. At the same time, artificial intelligence-assisted microscopy is emerging as a valuable diagnostic tool. Shin et al. demonstrated the potential of automated image analysis for the detection of trematode eggs, illustrating how computational approaches may complement traditional diagnostic methods [24]. These developments reflect a broader trend toward increasingly integrated diagnostic frameworks that combine morphology, molecular biology, epidemiology, and data science.

As highlighted by Hide when introducing the recent Special Issue on *Molecular Epidemiology* [25], modern parasitology is entering an era characterized by rapidly expanding molecular and genomic potentials. The emergence of nanopore sequencing, eDNA surveillance, and single-cell transcriptomics represent the leading edge of this expansion. Nevertheless, molecular data cannot replace taxonomy; rather, they depend upon robust taxonomic foundations for interpretation. Accurate parasite identification will continue to require well-characterized voucher specimens, careful morphological observation, and sound biological understanding.

The future of parasite identification lies not in choosing between morphology and molecular biology, but in integrating both approaches across multiple scales from individual cell transcriptomes to landscape-level eDNA surveys. The recent contributions published in *Parasitologia*, combined with the advances summarized here, demonstrate that integrative taxonomy is becoming the standard framework for understanding parasite diversity, evolution, and transmission. Such approaches will be increasingly important as parasitologists address emerging challenges associated with biodiversity conservation, wildlife health, food security, and One Health initiatives.

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