FACULTEIT
DIERGENEESKUNDE
accredited by EAEVE

UNIVERSITEIT
GENT

INVITATION PUBLIC DEFENSE

Titel
From Taxonomy to Emerging Infectious Diseases: Towards Holistic Approaches for the Conservation of Wild Snakes in Italy

Name
Matteo Riccardo Di Nicola

Date
Monday, 23 February 2026

PROMOTORS

Prof. dr. Frank Pasmans
Faculty of Veterinary Medicine, UGent

Prof. dr. An Martel
Faculty of Veterinary Medicine, UGent

Dr. Jean-Lou Dorne
Chief Scientist Office (CSO), European Food Safety Authority (EFSA), Parma, Italy

Curriculum Vitae

Matteo Riccardo Di Nicola was born on 23 February 1986 in Milan, Italy. He obtained his BSc (2009) and MSc (2011) in Natural Sciences from the University of Milan, with research on the ecology of *Rana latastei* and the impact of the invasive crayfish *Procambarus clarkii* on amphibians in the Po Plain. Since 2010 he has worked as a field herpetologist, photographer and author, publishing several books on Italian amphibians and reptiles, including Anfibi e rettili di Sardegna and two editions of Anfibi & Rettili d'Italia. From 2013 to 2021 he also taught mathematics and science in Italian lower secondary schools (scuola secondaria di primo grado). Between 2020 and 2024 he collaborated on European Food Safety Authority (EFSA) projects, modelling chemical toxicity in amphibians, and from 2022 to 2024 he served as the Italian herpetologist for the EU "AMPHIDEB" project. Since 2021 he has also been a research collaborator at the Unit of Dermatology, San Raffaele Hospital, Milan, focusing on medical writing, data management and confocal microscopy. In 2024 he joined the Istituto Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta as a researcher on amphibian and reptile pathogens. Matteo is author or co-author of more than 100 scientific publications and several herpetological atlases, has presented at conferences, and is a member of the Societas Herpetologica Italica.

Where?

The defense will take place on Monday, 23 February 2026 at 17.00h
Leslokaal 1.1, D6, Decanaat
Faculty of Veterinary Medicine
Ghent University, Campus Merelbeke
Salisburylaan 133, Merelbeke

Members of the Jury

Prof. dr. Kristien Van Reeth
Chairman of the Jury
Faculty of Veterinary Medicine, UGent

Prof. dr. Ward De Spiegelaere
Secretary
Faculty of Veterinary Medicine, UGent

Dr. Tom Hellebuyck
Faculty of Veterinary Medicine, UGent

Prof. dr. Luc Lens
Department of Biology, UGent

Prof. dr. Raoul Manenti
Department of Environmental Science and Policy,
Università degli Studi di Milano

Summary

Global biodiversity is declining and reptiles, including Squamata, Testudines, Crocodylia and Rhynchocephalia, are no exception. Reptiles face multiple, interacting pressures (i.e., habitat loss and fragmentation, land-use change, climate shifts, persecution and trade) while their secretive habits often lead to sparse data and underestimation of risk. Snakes, in particular, are difficult to detect and frequently viewed negatively by the public, which hampers monitoring and conservation. In Mediterranean landscapes such as Italy, challenges include fine-scale habitat fragmentation and the emergence of wildlife pathogens that can depress vulnerable populations. Robust baselines, harmonised identification tools and comparable health data are therefore essential to guide management. In this context, this thesis integrates taxonomy, genetics, ecological modelling, and monitoring of ophidiomycosis caused by *Ophidiomyces ophidiicola* (Oo) to support evidence-based conservation of wild snakes from Italy.

The thesis begins with accurate identification and the explicit delineation of population units, applying consistent genetic, morphological and geographical criteria. Revised dichotomous keys for Italian and European snakes are provided, synthesising recent systematic changes and distributional information to improve the reliability of field and museum identifications. Mitochondrial markers are then used to investigate an apparently isolated population of the Southern Smooth Snake, *Coronella girondica*, around Lake Garda, illustrating how genetics can inform both taxonomic inference and conservation planning. Overall, this research highlights that both genetic evidence and historical records indicate that Alpine and sub-Alpine occurrences north of the Po are relict and likely native rather than introduced. These results support targeted protection and continued monitoring of these small, fragmented populations, including health checks where appropriate.

Next, habitat suitability modelling is used to focus search effort for rare or hard-to-detect taxa. For the endemic Sardinian grass snake, *Natrix helvetica cetti*, formal records and verified citizen-science observations are compiled to update the distribution map and to train MaxEnt models. These models show strong discrimination and indicate that altitude and precipitation regimes are influential predictors, highlighting additional climatically suitable areas on Sardinia. Fieldwork guided by model outputs confirmed the species at new sites. Melanistic asp vipers, *Vipera aspis*, a localised black

phenotype with scattered records, are then examined. Collated data and bioclimatic models predict patchy suitability, largely in montane and temperate regions along the Alps and the southern Apennines. Subsequent surveys in predicted areas located previously unrecorded melanistic individuals. Together, these case studies show how spatial tools can refine fieldwork for elusive snakes and help prioritise populations that may be vulnerable if disease pressure increases.

The core of the thesis addresses ophidiomycosis. First, current knowledge of Oo and its disease is synthesised, covering taxonomy, phylogeny, transmission routes, clinical presentation, diagnostics, and population effects. To improve comparability across studies, a practical diagnostic workflow is outlined and a case classification scheme is refined to separate infection status from actual disease. The review also argues for greater use of museum specimens to explore historical presence and for structured use of citizen observations to flag suspect lesions in the wild. These proposals are intended to lower barriers for wildlife veterinarians and field ecologists who need consistent, workable procedures.

Building on this foundation, new data from Italy are reported. A pilot investigation near Lake Garda confirmed Oo in free-ranging *Natrix tessellata*, following citizen reports of suspicious lesions. This prompted a wider, opportunistic survey across most Italian regions. Over approximately three years, 423 snakes from 17 species were examined, obtained from field surveys and museum collections; sampling prioritised individuals with gross cutaneous lesions consistent with ophidiomycosis. Oo DNA was detected in multiple taxa, with most modern positives from northern regions and a pronounced concentration in water snakes along large lakes. *Natrix tessellata* showed higher detection rates than other species, consistent with ecological traits that may facilitate transmission, such as aquatic habitats, communal overwintering, and dense mating aggregations. Museum positives from Tuscany show that the pathogen has occurred farther south in the past. Genotyping identified two lineages in Italy. Clade I was associated mainly with older, museum material, whereas most contemporary infections belonged to Clade II, and one co-infected snake occurred at Lake Garda. These patterns raise the possibility that Clade II has recently spread or outcompeted Clade I, and they motivate targeted surveillance in central Italy where dense *Natrix* populations occur but sampling has been minimal. In sum, disease in Italian snakes is neither restricted to a single site nor a single host, and the evidence now supports sustained monitoring with standard methods.

The concluding chapter synthesises the work and integrates the findings. Good taxonomy and spatial context are prerequisites for credible wildlife health work. Early use of morphological and genetic evidence should be employed to delineate the taxa and populations to be targeted. These foundations are complemented by habitat suitability modelling and supported by standardised diagnostics and case definitions. Used together, these components enable comparable datasets and effective monitoring of Oo and ophidiomycosis in free-ranging snakes.

Ophidiomycosis should be incorporated into European snake conservation planning, with emphasis on natricid snakes in lake and wetland systems. Surveillance should combine structured sampling at sentinel sites with opportunistic inputs from museum collections and vetted citizen-science observations under shared protocols. Small and isolated or rare populations highlighted by modelling should be prioritised, as their low detectability and demographic fragility can magnify disease effects. The occurrence of distinct pathogen clades in Italy requires work on origin, routes of introduction and relative fitness, including a critical evaluation of movements through trade. Future studies should include genome-wide population genetic analyses for endemic or insular taxa with suspected low diversity, standardised longitudinal capture–mark–recapture surveys to quantify infection dynamics, clearance, survival and transmission within populations (prioritising target species such as *N. tessellata*), and behavioural studies at denning and breeding sites where transmission may concentrate.

Overall, the integrative approach applied here links taxonomy, genetic characterisation, spatial modelling and harmonised diagnostics to support conservation decisions in the face of limited and heterogeneous data, and is transferable beyond Italy to other regions and taxa experiencing habitat change and emerging pathogens.