

DNA barcoding of ectotherm blood parasites from Southern Africa to provide a genetic and evolutionary perspective.

It is estimated that more than half of the human population and even more animals suffer from parasitic infections. However, parasites not directly associated with human or livestock disease are often understudied or have limited data available. When trying to understand the phylogenetic placement of these human or livestock infecting parasites, their relationships with other closely related taxa becomes more important. For example, gaining insights from the phylogenetic relationships of ectotherm blood parasites may provide a better perspective of why certain parasites do not produce the same disease severity as seen in their close relatives of mammalian and avian hosts. Research completed on ectotherms blood parasites from South Africa, strongly suggests that besides general biodiversity surveys and describing new species, molecular data specifically for mtDNA barcoding markers are lacking, as most molecular data available for ectotherm blood parasites are from the conservative nuclear 18S rRNA gene. This study aims to develop a basis for generating the first COI barcodes of complex and understudied parasite taxa of ectotherm hosts. NGS will be used to initially sequence the full mtDNA genomes for selected parasites, to provide data to develop universal barcoding primers for a broad range of parasite taxa. Furthermore, this study is a joint venture between the Biochemistry and Zoology departments of the North-West University (NWU) and the Department of Zoology and Entomology, of the University of the Free State, Qwaqwa campus.