

Biographic Information: (4 100 characters)

After my PhD, I took over the Population Genetics laboratory. My initial (and still predominant) research is on fish. However, I had to do project-driven research that was popular (e.g. on elephants to worms) in order to be able to secure funding. During this time, I also majored in B.Sc. (Information Technology) with distinctions in: Information Technology I, II and III. This enabled me to write relevant programs for my research, such as calculating the condition factor of organisms from length and mass values, models to estimate the production potential of rainbow trout and Atlantic salmon in southern Africa, fertilization success determination of fishes by hypothesis testing for two proportional values, average heterozygosity estimation and modified genetic distance calculation, conversion of F_{st} to N_{em} values and catfish production system. The latter program was awarded the 2nd prize at the BankorpData National Computer Competition.

I completed a course successfully on DNA Barcoding (7-11 April 2008) presented by Dr Powell (Imperial College, London), and used my sabbatical leave during 2010 to study DNA barcoding as an additional method of genetic analysis and to obtain samples (see on-going and planned future research) for it. This, and the fact that I teach four modules [there are a maximum of four/year] every year, restricted my research outputs. Nevertheless, I have presented DNA barcoding results at three occasions (seven in total by my students, collaborators and I) during the last two years.

In 2011, the African Centre for DNA barcoding (ACDB; www.acdb.co.za) was established at the University of Johannesburg. I am heading the section on animal research. Presently I have 2 MSc students and 3 PhD students. My most recent (registered) two international projects are: 1) Marine Fishes of Namibia and 2) An Inventory of Namibian Aquatic Biodiversity: Ecological, Morphological and Genetic Analyses (together with three principal Namibian investigators). These international collaborators, as well as others from Germany (Prof Wink: Univ. Heidelberg and Prof Kramer: Univ. Regensburg), and I are actively researching biodiversity as part of various projects and at different levels (e.g. see completed, ongoing and planned future research sections).

Not only is my work recognized internationally (see paragraph 1 of self-assessment), but also by the national community. For example, I am the invited judge for the international Swaziland Angling Association this year between the Kingdom of Swaziland, Namibia and South Africa. Our research (as part of the regional node or the International Barcoding of Life Data, iBOLD, project) is sponsored by Toyota (www.toyotaoutreach.com); I have been active to promote our research during national TV (National Artificial Lure: Rapala ART LURE Championship Competition 2010; broadcasted on two channels 7 times; Project Aardwolf 2010) and 4 radio interviews. We also involved primary school learners (lectures, field collections, tree planting and prize-giving) at the previous Toyota Outreach 2011 project. The Toyota Outreach 2011 project was broadcasted on national TV (5 Feb. 2012; Program: Groen).

Guest/invited speaker: I was the *guest/invited speaker* at 4 international conferences on freshwater fishes and recently I was *invited* as the *guest speaker* on DNA barcoding: implications & limitations for identification of existing & new biodiversity at the South African Academy for Science and Arts, Section Biology conference on 5 October 2011. These opportunities inspired me to analyse and present results and I am in the process of preparing it for publication.

Reviewer: I am a regular reviewer for 3 international journals and a member of an international editorial advisory board: *ACTA Ichthyologica Et Piscatoria*. I have been a reviewer for 5 national and 15 international journals (e.g. *Biochemical Systematics and Ecology*; *Aquaculture Research*; *Molecular Phylogenetics and Evolution*; *Aquatic Living Resources*; *Journal of Fish Biology*; *Biological Journal of the Linnean Society*; *Molecular Ecology*; *Heredity*).

Completed research (6 600 characters):

Genetic diversity is one of three levels of diversity that is explicitly mentioned in the Convention on Biological Diversity (CBD). A better understanding of genetic diversity at population and species levels contribute to numerous taxonomic problems relating to circumscription and rank, particularly of cryptic species and poorly understood species complexes of plants and animals. As such, these studies contribute to the inventory of biodiversity in Africa (a national obligation since S.A. is a signatory of the CBD). This leads to deeper insight into the process of speciation in southern Africa, with obvious theoretical and practical value for biodiversity management and conservation. Not only do I mainly focus on genetics, but also include studies (as can be seen in my cv) on the other pillars/levels on which the CBD is based upon (species and ecological diversity).

A unique feature of my work is that the genetic variability and patterns of divergence in animals and plants can directly be compared to give a better view of population dynamics in African ecosystems (see completed, on-going and planned future research). My research mainly focussed on morphology, allozyme studies and DNA barcoding of southern African animal and plant species. The emphasis of my studies is on the

determination of genetic variation within populations, selection of individuals with favourable phenotypes from gene pools, gene flow between populations, identification of hybrids, and evolutionary (phylogenetic) relationships between taxa. Such studies relate to several fields including conservation biology, population dynamics and systematics, and I have contributed in all of these fields over the years. My extensive experience enabled me to publish reviews on the use of allozyme electrophoresis: 1) in plant systematics and 2) of gene nomenclature for enzyme-coding loci generally used in plant and animal studies.

The following information has relevance to the section on on-going and future planned research as well but is presented here because of the limits to the numbers of characters allowed by the NRF for that section. Completed, on-going and future research has and will also focus on the applications of DNA barcoding for BIOSECURITY, especially in the fields of marketplace surveillance, invasive species, and agriculture.

Market place surveillance: e.g. the Namibia project. The Namibian coastline of approximately 1 500km falls within the Benguela Current system, which is rich in pelagic and demersal fish, supported by plankton production driven by intense coastal upwelling. The demersal (deep-water) fishery is the most valuable in Namibia, and almost the entire catch is exported. Currently economic fraud and food safety concerns are pushing the need for accurately labelled food products and full disclosure of product composition. In this regard, seafood is gaining increasing attention due to the potential health-related risks associated with misbranding species. One challenge faced by both consumers and regulators is the detection of "seafood substitution" in the marketplace - where low value species or a species with a potential food safety hazard are mislabelled and substituted in whole or in part for a more expensive, or for a species with no potential food safety hazard. It is not always possible to tell just by simple inspection of an aquatic product that misbranding has occurred. Processing often removes or damages diagnostic characteristics crucial for the identification of species by conventional taxonomic means. Therefore, traditional morphological methods are often insufficient to provide for species resolution identification. This is highlighted in the literature, which showed for example that 77% of Red Snapper fillets sold in the eastern USA were mislabelled. Because of these limitations, the development of a genetic-based tool for fish species identification would provide an unparalleled level of opportunity for scientists and consumers. DNA barcoding is one such technique that is relatively simple to apply and yet can distinguish even between closely related species or strains. DNA barcoding works by comparing the sequence of DNA bases from a short part of the genome that is standardized between taxa. According to highly esteemed international scientists, the prospect for barcoding as a regulatory tool is positive, allowing future practices to better address issues of market cost, safety, and environmental impact. I have discovered incorrect species identifications, new distributions, species allocated to incorrect families in the marine fish projects, and possible new species in the extended project on freshwater fish in the Namibian Aquatic Biodiversity project.

Invasive species: We (ACDB) have been and are involved in a collaborative project with the Early Detection and Rapid Response Programme of the Working for Water Programme at the South African National Biodiversity Institute. Here we will address one of the biggest ecological challenges in Africa, and globally: the invasion and spread of exotic species. My focus is on fish and molluscs in this project. For additional information (to those presented in the other sections), please refer to the webadres: <http://acdb.co.za/index.php/sa-invasive-project-new/project-presentation-2.html>

Economic importance: e.g. the scale insect project in **agriculture**. This project (in which optimal barcoding genes are evaluated) is in collaboration with the Agricultural Research Council and funded by the National Department of Agriculture. It focusses on DNA barcoding of plant scale insects of economic importance to South Africa and its trading partners. Scale insects are a major pest, associated with plant tissue, making them a major quarantine risk and one of the world's most invasive groups of animals. Identification is challenging even with the help of expert taxonomists. Here we build a DNA barcode database for approximately 190 scale insect species that are important for either importation or exportation of agricultural goods in Africa. This database is the first essential step in implementation of quarantine inspection services, which has been requested urgently, and **will become the status quo** among trading partners. Although much of the work has been completed, some are also on-going (it is presented here because of the limits to the numbers of characters allowed by the NRF for different sections).

Summary: A summary of my accomplished research include the supervision of 36 postgraduate students, best senior RAU/UJ researcher award, best publication published in a local journal award, best student awards, peer-reviewed published conference proceedings, national and international conference contributions, workshops attended and/or contributions made, and peer reviewed publications.

Self-Assessment: (3 250 characters)

My h-index is 13; 89 of my 109 publications were cited 563 times in the ISI Web of Science: 426 times by others in 385 articles. I strive to support national journals for localised research, but also international journals with higher impact factors (IF) such as *Small Ruminant Research* (IF=1.395) to *Zoologica Scripta* (IF=3.091) for animal science, and *Taxon* (IF=2.36) to *The Botanical Review*, (IF=2.657) for botanical studies. I have received reprint requests from scientists in Argentine, Australia, Belgium, Botswana, Brazil, Canada, Czech Republic, Chile, Colombia, Croatia, Denmark, France, Germany, Hungary, Iraq, Japan, Kenya, Lithuania, Namibia, Nigeria, Pakistan, Philippines, Poland, Portugal, South Africa, Spain, Taiwan, The Netherlands, U.K., USA, Uruguay, and Zimbabwe.

No 1 of top ten articles downloaded: FH van der Bank *et al.* (2009) were our 1st results published that included barcoding and it was **no 1** of the “**Top ten articles downloaded via InformaWorld in 2010**” (communication from the Editor, African Journal of Aquatic Science, 2011/07/27). My contribution: I designed the research, generated the DNA barcodes, analysed the data and wrote most of the paper. My student (Soekoe) generated the allozyme data under my supervision. The study was done with international collaboration (Prof Wink) and was based on a multi-disciplinary approach (ecological data, morphometrics, meristics, allozymes, genomic fingerprints — generated with six Inter-Simple Sequence Repeat (ISSR) analyses and DNA barcoding).

International collaboration led to the description/resurrection of **eight new** fish species. This is an outstanding accomplishment. Other researchers also recognize my input (e.g. Hadfield *et al.* (2011)) named a new species of isopod, which I collected for them, after me: *Cymothoa hermani* sp. nov.

Our research not only has theoretical, economic and socio-economic, but also practical value. For economic and socio-economic value, please see completed, on-going and planned future research section.

Practical value: For example, our 62 page publication on Bulldogs (i.e. fish sold in the aquarium trade as “freshwater dolphins” because of the anatomical similarities with dolphins) showed that 4 other species were included in this species complex before our study (Kramer *et al.*, 2007). This result is important to limit invasive/alien fish trade in the many countries from which they originate. In addition, studies by Van der Bank & Deacon (2007) reported that increased backcrossing has reduced the usefulness of morphological and genetic data for identifying *Oreochromis niloticus*, *O. mossambicus* and their hybrids in a major South Africa river. The emphasis of this (and similar studies by us; see below) is to highlight the effect of alien species on our fauna for conservation. The introduction of the alien species resulted in the loss of 2 species and the creation of a hybrid one. Other impacts, such as the linking of river systems and building of dam walls also impact negatively on our fishes as shown in the multidisciplinary investigation of differentiation and potential hybridization between two yellowfish species *Labeobarbus kimberleyensis* and *L. aeneus* from the Orange-Vaal System.

On-going and Planned and Future Research: (4 000 characters)

This section should be reviewed together with the one on completed research because neither section can be regarded as separate entities (i.e. completed research leads to on-going research and while some parts are completed, others are still on-going). In addition, there are limits to the numbers of characters allowed by the NRF for this section, hence the cross-referencing.

Since my previous rating, I deliberately focussed my research to increase depth and relevance. Because morphology-based identifications has limits, and there is a limited pool of taxonomists in this field, molecular diagnostic tools such as DNA barcoding for effective species identification was proposed by world-renowned scientists. I decided to invest time and efforts in DNA barcoding as additional technique because it is a very useful tool to accelerate species recognition, for the discrimination of biodiversity, and to facilitate conservation efforts, stock management, and ecosystem monitoring, phylogeographic and speciation patterns. Barcodes have many advantages, ranging from population genetic and phylogenetic analyses, identification of prey in gut contents, forensic and food safety, to delimit species boundaries, reveal cryptic species, to discover new species, and to detect invasive species. The use of barcodes facilitates identification to a high degree of certainty of most biodiversity, including larvae, carcass fragments, illegal trade in protected species and damaged specimens. It is used for rapid, high-throughput and mostly automated assessments. However, the starting point for understanding and conservation of biodiversity is the establishment of what species are present and where.

To date, most barcoding research at ACDB has focussed on building the reference library of DNA barcodes for animals, an essential and critical part of the project. As a result I have collected samples of fish, molluscs, crustaceans and spiders from more than: 25 orders, 83 families, 107 genera, 432 species and 2261 individuals in c 20 months. Approximately 76% thereof is already barcoded. I now have enough data for at least seven publications and I am looking forward to analyse and publish it. The outstanding 24% to be barcoded will

undoubtedly present more opportunities for additional publications (some of our sampled species are still undescribed).

International collaboration & student supervision: I absolutely believe that collaborative research and student supervision outweigh single author publications. I prefer to publish as often as I can with highly rated international collaborators (e.g. from Germany and Namibia). Our collaboration using the multi-disciplinary approaches (ecological data, morphometrics, meristics, allozymes, ISSR analyses, and DNA barcoding) is a novel approach, producing ground-breaking results (i.e. the description of new species). Because I am involved in the iBOLD project: samples, dates of collections, localities, museum voucher numbers, images, measurements and barcodes for the specimens are freely accessible from the iBOLD system (www.barcodinglife.org). This is intended to limit future bio-prospecting (specimens and DNA could be made available to other scientists to analyse it for a very long time); another goal and advantage of the iBOLD project.

Socio-economic value: We are currently preparing the following manuscripts for publication. A study that focuses on DNA barcodes of African silver catfish, *Schilbe intermedius*, which also indicate the presence of undescribed species/subspecies and, so far, provided river system-level phylogeographic resolution of populations. The above-mentioned study is **socio-economically** extremely important because *S. intermedius* is the most abundant fish species in African river systems and also a healthy (because of the omega three oils it contains) protein source for many subsistence fishermen and their families. For example, silver catfishes are the most abundant in numbers and weight (e.g. in Lake Tzaneen, SA) and in catch per unit efforts in the Pendjari River (Benin). Translocation of individuals from this species complex between river systems can also have adverse alien/invasive consequences. Another study is on DNA barcoding of the endemic southern African marine gastropod genus *Oxystele*, which reveals doubtful identifications in two taxa. *Oxystele* constitute some of the most abundant molluscs on southern African shores.

In conclusion, the DNA barcoding and other multidisciplinary approaches have and will contribute to the global information on animal biodiversity, adding practical (e.g. biosecurity, rapid and accurate identification, socio-economic and economic importance) as well as theoretical value (e.g. phylogenetic, phylogeographic relationships and species boundary determinations).