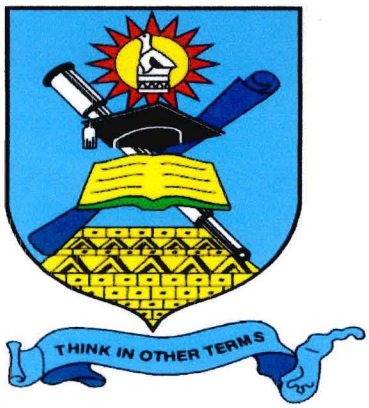

NATIONAL UNIVERSITY OF SCIENCE AND TECHNOLOGY

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MORPHOLOGICAL AND MOLECULAR (RAPD PCR) CHARACTERISATION OF CICHLID SPECIES (*Oreochromis niloticus, Tilapia rendall* and *Tilapia sparmanii*) FROM ANCHOR YEAST DAM, GWERU, ZIMBABWE.

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A DISSERTATION SUBMITTED IN PARTIAL FULFILMENT OF THE REQUIREMENTS FOR A MASTERS DEGREE IN APPLIED MICROBIOLOGY AND BIOTECHNOLOGY.

2013

ABSTRACT

The group of cichlids is divided into three genera, *Oreochromis*, *Tilapia* and *Danakilia.* Classification into these three genera is primarily on the basis of breeding habits and identification can be very difficult due to similar morphological features between species and the large intra species morphological variation. Morphological and genetic characterization was done on *O. niloticus, T. rendalli and T sparmanii*. 5 samples of each species were collected from Anchor yeast dam in Gweru and caudal fin clips immediately excised and preserved at -20°C for subsequent DNA extraction. Morphological analysis was done on formalin fixed samples. Morphometric measurements did not yield any analyzable data, which is very common in fish analysis, while meristic counts clearly separated the three species on the basis of number of lateral line scales and number of gill rakers. Molecular analysis was done on DNA extracted from caudal fins using a lysis buffer with 4M urea. Twelve RAPD primers were screened for their ability to amplify polymorphic bands between the three species. Of the 12 RAPD primers that were used, 10 showed polymorphism of 88.2%. High genetic similarity indices were recorded between samples from the same species (*O. niloticus*; 0.71, *T rendalli;* 0.67, *T sparmanii;* 0.71). As expected, the highest genetic distant value was recorded between *T. rendalli* and *O. niloticus* (0.934) which makes biological sense since they are in different genera. Meristic and genetic data both produced similar clustering patterns of a dendrogram with two clusters that further branch into species specific clusters. However, the meristic dendrogram further divided species *O. niloticus* and *T rendalli* into two further clusters each, a sign of possible hybridization. The genetic dendrogram did not show this because of the reduced number of samples, that were taken for further DNA analysis due to failure to amplify and so less variation was detected. The results support the classification system according to Trewavas, 1983. The results show that morphological and genetic analysis can be used concurrently in fish characterization as confirmation of each other.