**Name: Gyamfua Afriyie**

**Title: Genetic parameters of selected quantitative traits of common carp farmed in Pond-RAS-Pond conditions**

**Abstract**

Common carp (*Cyprinus carpio*) is one of the most widely farmed fish species globally. It is prized for its adaptability to diverse aquaculture systems and its importance in food security and economic development. Different selective breeding techniques have been applied to farmed animals to enhance desirable traits. Presently, crossbreeding and selection are the most popular methods used.

This study will be based on the processing and analysis of data obtained through a new approach in a selective breeding program of common carp provided under fishpond management to shorten the generation interval (GI) of the Amur mirror carp (AMC). Here, fish were farmed during the first growing season in traditional ponds, in recirculating aquaculture systems (RAS) during the winter, and during the second summer, again in ponds. This ensured that fish continued growing during the cold season and that they should achieve earlier gonadal maturation. However, the fusion of the two culturing systems before the selection challenge could be affected by a genotype by environment interactions (G×E) effect, and different genotypes (families, individuals) could yield from culturing in different rearing systems. The true values (phenotypes) of important quantitative traits play a critical role in determining the best individuals to be selected for establishing the next generation of a selective breeding program. Currently, scarce information, limited to no research, is available on the strength of genotype by environment (G×E) interactions when RAS is included before the selection challenge within a selective breeding program focused on genetic improvement of carp for fishpond management.

The study aims to investigate the heritability of important quantitative traits (weight, FC, muscle fat content, fillet yield predictors, etc.) in different rearing stages of an AMC stock, genetic correlations between the rearing stages, and evaluating of G×E interactions for the traits. The analyses will be done using already collected phenotype data for quantitative traits during the three rearing stages using pedigree and/or genomic information assessed from a low-density SNP panel. The statistical analyses will be performed using DMU, RStudio, and other appropriate software. Results will i) provide exact insight into how different rearing technologies may influence the genotype dominance within a stock; ii) determine the possibility of using Pond-RAS-Pond systems before the selection challenge; and iii) contribute to the further development of the effective selective breeding program in common carp.