

## Whole genome sequence of CARI- KADAMBARI

Whole genome sequence of improved variety of Guinea Fowl (*Numida meleagris*) CARI-KADAMBARI completed and identified the genes which may define the uniqueness of guinea fowl as this species is known for hardiness, more thermo-tolerant, disease resistant and good adaptability. CARI- KADAMBARI variety of guinea fowl reared at the Institute farm was used for detecting selection signatures / beneficial mutations for tropical adaptability, disease resistance and understanding population history & mechanisms. Blood samples from adult guinea fowl were collected and whole genome sequence data was generated using next generation sequence technology (NGS) and analysed for high informative SNPs throughout the genome. Whole genome sequence of guinea fowl was aligned with available reference genome of *Gallus gallus domestics and* showed average genome mapping percentage of 74.26%. Across the genome an average of 13,514,261 SNPs. Whole genome SNP calling was 2.53, indicative of better SNP calling. Potential genomic regions under selection in Guinea fowl revealed 420 genes governing cellular response to stress of which 35 genes were detected as candidates for thermo-tolerant. In addition, 18 putative genes identified which are associated with immune response. Several genes were found to be potential candidates for stress tolerance and heat adaptability. The building blocks of genetic adaptation to hot environmental climates may be evolved by these candidate genes as functional genomic targets. Our strategic findings would provide vital insights into unique candidate genes which would lay the foundation of future molecular breeding aimed at achieving rapid and sustainable improvements in thermo-tolerance and disease resistance of bird.