

## Multilocus Sequence Typing (MLST) for genetic characterization of *Trichomonas gallinae* isolates

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### Abstract:

*Trichomonas gallinae* is a flagellated protozoan parasite responsible for avian trichomonosis. *T. gallinae* commonly infects many species of birds in the world, while previously it was mainly restricted to pigeons and their avian predators. The rock pigeon *Columbia livia* is considered the primary host of *T. gallinae*. Multilocus sequence typing (MLST) is a powerful and highly discriminatory method for analysing pathogen population structure and epidemiology. We have described the whole genome sequence of the *T. gallinae* (the British finch epidemic strain) was mined for the single-copy of housekeeping genes for MLST genotyping (Abdulwahed *et al.*, unpubl.). MLST scheme has been developed and used for the first time to investigate the population structure, genetic diversity and epidemiology of *T. gallinae*. We discovered a MLST scheme, comprised of twenty single-copy housekeeping genes, to genetically characterize *T. gallinae*, and these genes fragments were successfully amplified with PCR and sequenced. All different strains that typed as isolates of *T. gallinae* were selected for MLST. Seven isolates of *T. gallinae* were sampled and characterized for the twenty gene MLST scheme, along with their strain, year found, location, evidence of upper alimentary tract lesions consistent with trichomonosis and type of culture extract. All sequences obtained for a single locus were aligned without gaps. The PCR amplification product of a single copy gene also led towards a single sequence, based on the presence of single loci found in the *T. gallinae* genome.