Urban birds must cope with environmental condition that may be extremely different from those experienced in natural habitats. They are exposed to constant human presence, disturbed photoperiod, noise and pollution. Nevertheless, many species, such as the Feral Pigeon *Columba livia forma urbana*, establish thriving urban populations. Urban-adapted individuals are characterized by life-history traits, behavior, morphological features and genetic pool different from rural conspecifics. Also, population densities are often much higher in urban than in non-urban habitats. However, living in high densities may impose certain threats, including elevated risk of pathogen infection, as pathogens and diseases spread easier in large aggregations of potential hosts. It may force urban birds to develop stronger immunocompetence. One of the key parts of native immune defense are the toll-like receptors (TLR). They are present on the surface of leukocytes and their role is to identify pathogens. But not all microorganisms impose direct threat on the host. Diverse microbiota inhabit gastro-intestinal tract and some of its components have beneficial influence, while the others can be potentially virulent. Modern genetic methods allow to identify full taxonomic composition of hosted microbiota, basing on sequencing and profiling specific fragments of their genome. The aim of the study is to investigate associations between TLR genes and gut micorbiota in the Feral Pigeon, as well as to analyze the influence of population density on composition and diversity of TLR genes and the microbiota profile.