



## WHITHER GENOME SEQUENCING OF PASSER?

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*Passer domesticus* or the common house sparrow is a passerine with a world-wide distribution. The species do not show an obligatory commensal relationship with human beings. House sparrows have lived successfully around human beings for a long time, often competing well with other birds. In fact, these birds were considered a menace in the past, particularly in the USA. House sparrows may be occasional pollinators of flowers and edible crops, and despite being perceived as anti-farmers, they might actually be assisting in pest control. But in the recent times, the numbers of this bird have been declining in many urban areas because of electromagnetic radiations and other anthropogenic activities. *Passer domesticus* may suite as one of the models for studies influencing human technological advances on life and commensal life-forms in human habitats. Keeping in view of the good level of interest of obtaining better insights into evolutionary lineages of these birds and in particular understanding the genetics in various contexts (such as MHCs, SNPs, microsatellites, gene expressions and epigenetics), we discuss the challenges in genome sequencing of this bird.

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### Introduction

*Passer domesticus* or the common house sparrow is a passerine with a world-wide distribution. The species does not show an obligatory commensal relationship with human beings. It is rare in grasslands, forests and woodlands. House sparrows have lived successfully around human beings for a long time, often competing well with other birds. In fact, these birds have been considered a menace in the past, particularly in the USA. House sparrows may be occasional pollinators of flowers and edible crops, and despite being perceived as anti-farmers, they might actually be assisting in pest control. But in the recent times, the numbers of this bird have been declining in many urban areas owing to reduction in population-sizes that may be associated with electromagnetic radiations besides other recent anthropogenic activities.<sup>1,2</sup> In the recent-past, there have been a few efforts initiated to conserve this species.<sup>3</sup> *Passer domesticus* may suite as one of the models for studies on the influence of human technological advances on life in general and commensal life-forms in human habitats in particular.

### Discussion

House sparrows have already been used for research on various other topics. Information from this species may provide clues for the fight against infectious diseases including avian influenza virus and west Nile virus. The bird has been used for studying digestive flexibility, senescence,

avian circadian system and anthropogenic pollution effects on wildlife. *Passer domesticus* may also offer a chance to study the *ecological* and *evolutionary* aspects of species invasions.<sup>4</sup> Thus, the species might in fact form a perfect model to study the interplay between multiple aspects such as the infectious diseases in birds around human settlements, inter-bird-species conflicts, population dynamics, and sensitivity of wildlife and adaptation to the rapidly changing parameters within human-made habitats. There is also a lot that needs to be understood about the genetics and genomics of this species. Research in all such directions would be accelerated if the house sparrow genome sequence is established.

There is already a good level of interest in the genetics of *Passer domesticus* in various contexts such as MHCs, SNPs, microsatellites, gene expressions and epigenetics.<sup>5-9</sup> For example, a few attempts have been to study the some of the transcriptomes and SNPs using the next generation sequencing technologies. Transcriptome of bursa, blood and spleen have been deposited in SRA in 2012. Some genomic sequences derived using the Roche 454 machine is also available but the total amount of read regions is minimal. Thus, unfortunately this species needs a dedicated project for obtaining a reliable reference sequence to begin with! A few avian genomes have also been sequenced allowing us to speculate the features of the genome of the related species to some extent.<sup>10</sup> Studies on mitochondrial DNA suggest that speciation in the *Passer* genus might have occurred even before Pleistocene era.<sup>11</sup> While similar proportions of the genes have been predicted in zebra finch and chickens,<sup>12,13</sup> possibly the *P. domesticus* genome is comparable to the genome biology of Chicken, where an approximate 23000 genes seem to translate the entire repertoire of proteins.<sup>14</sup> Thus, an approximate one billion base pairs of nuclear genome and about 20,000 genes may be present in Passerines.

After sequencing the sparrow genome, it would be possible to address issues related to its genome structure. It should be interesting to compare genomes of house sparrows, zebra finch and chicken using sequence analysis and experiments. For example, evolutionary distances

among these bird species can be quantified, including variations across the coding and non-coding regions. The distinctive properties of avian micro-chromosomes can also be better inferred eventually, and crosschecked towards syntenic conservation, after the house sparrow genome is sequenced. Song bird genomics and comparison with other birds indeed form essential challenges that must be confronted to identify potential genetic limitations associated with their recent and sudden debility. The comparative genomics analysis nevertheless can be the foundation for further studies to explore specific questions. For example, it is worth attempting to discern what genetic aspects might have earlier helped some of the species to dominate other birds and whether or not any aspects of these dominating species would be causing sudden endangerment in multiple places. For biologists concerned with faunal biodiversity, it would be a special impetus to investigate the loss or gain of genes, or sequence changes in specific regions; this may have resulted in unique responses to recent environmental changes. Furthermore, the house sparrow genome sequence can also assist research on many other fronts including comparative genomics, structural and gene dynamic studies for many bird species. We firmly believe that the chances of obtaining better insights into evolutionary lineages would increase with every new genome sequence known and studied. In conclusion, there is a need to establish reliable nuclear and mitochondrial reference genomes of birds, particularly the house sparrow, by employing high depth and good quality sequencing from multiple individuals is the key for multiple active research areas.

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