Accurate determination of species is important for fields that rely on an accurate measures of biodiversity such as systematics, ecology, and conservation. Morphological data has dominated systematics for centuries but its exclusive use in delimiting species can be problematic. This is especially so in insects, the most diverse group of multicellular organisms on earth. Despite the rapid development of molecular methods, morphological criteria remain the main tool for species delimitation in insects. Reliance on morphological traits, however, can limit or obscure evidence of the evolutionary processes (e.g. convergence, cryptic diversity) that generate and maintain species boundaries. Recently, methods based on population genetic/coalescent models have been applied for identifying independently evolving species-level lineages. In addition, molecular identification based on easy-to-obtain genetic markers (DNA barcoding) is widely used. In this project, we will test whether morphological and coalescent methods provide congruent results and compare these with species delimitation based on DNA barcode sequences. These issues will be tested in the miltogramminae flies --nest-parasites of digging wasps and bees belonging to the large family known as 'flesh flies' (Sarcophagidae). These flies are an example of a recent rapid radiation in which many distinct, but difficult to recognize, species originated over a very short evolutionary period. The members of Miltogramminae are defined exclusively based on morphology; species among and between genera differ by subtle characters, likely under strong natural selection. The exclusively morphology-oriented approach to taxonomy in this group has resulted in alternative taxonomic systems, each with different species concepts. The highest species diversity of our chosen genera is in Middle East and Central Asia, where dozens of morpho-species occur sympatrically. Hence, this area is an ideal natural laboratory for testing species boundaries and gene flow between different morphotypes. In this project we will answer the following specific questions: Is coalescent-based species delimitation congruent with standard morphological delimitation of species? Is there cryptic diversity in Miltogrammine genera which can be detected by morphological markers? Is the COI barcode inference concordant with results based on the nuDNA species tree and comparative morphology?

Material for our research will be collected in Iran, a country with an outstanding diversity of Miltogramminae. Morphological characters will be documented using stereomicroscope with integrated system for digital imaging. For molecular research we will use innovative laboratory methods that employ Next Generation Sequencing (NGS). Molecular and morphological data will be compared using new bioinformatic software that includes coalescent-based methods and statistics. The project involves collaboration among a talented team of local and international experts in taxonomy, molecular evolution and bioinformatics, including important Iranian scientists and students.

Through direct comparison of new and traditional approaches to a major problem in biodiversity research, this project will establish a more complete framework for modern taxonomy of our model-group, and will provide a serious step towards using these approaches for construction of a uniform taxonomic system for the vast and complex species diversity of Diptera and other insects.