

Molecular Genetic Characterization of the Species *Vespa crabro* and *Vespa orientalis* Belonging to the Genus *Vespa*

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Abstract This study presents a molecular-genetic characterization of two hornet species, *Vespa crabro* and *Vespa orientalis*, collected from the Qashqadaryo Region of Uzbekistan. Specimens were identified morphologically and analyzed using mitochondrial cytochrome oxidase I (COI) gene sequences to assess genetic differentiation within the genus *Vespa*. A 623 bp fragment of the COI gene was successfully amplified and sequenced from both species and compared with reference sequences available in GenBank (*V. crabro* MT444756; *V. orientalis* KF933083). The results revealed low levels of intraspecific variation, with Uzbek *V. crabro* and *V. orientalis* differing from their respective reference sequences by 0.2% and 0.3%, respectively. In contrast, interspecific comparisons showed clear genetic divergence, with COI sequence differences ranging from 2.7% to 3.04%. These values fall within the accepted thresholds for species-level discrimination in Vespidae and demonstrate consistent nucleotide polymorphisms distinguishing the two species. The findings confirm the effectiveness of COI barcoding for reliable identification and differentiation of *V. crabro* and *V. orientalis* and provide the first molecular genetic data for these species from Uzbekistan. This study contributes to filling a geographic gap in the molecular taxonomy of the genus *Vespa* and establishes a baseline for future phylogeographic and biodiversity studies in Central Asia.

Keywords *Vespa crabro*, *Vespa orientalis*, Mitochondrial COI, Nucleotide sequence, Uzbekistan

1. Introduction

The European hornet, *Vespa crabro*, is the largest social wasp in Europe, with workers measuring up to 23 mm and queens up to 30 mm [1]. It is widespread across the Palearctic region, including England and Wales, and has been introduced into North America [2]. *Vespa crabro* occupies diverse habitats, but it is particularly associated with mature deciduous woodlands and urban environments. Morphologically, the head and most of the metasoma are predominantly yellow, whereas the mesosoma, anterior metasomal segments, and legs are reddish-brown with variable black markings.

This species is eusocial, forming colonies with a queen, workers, and males [3]. Colony founding typically begins in early spring, and nests are constructed from a paper-like material produced by mixing decayed wood pulp with saliva [4,5]. Nests may contain multiple combs enclosed by an envelope and are usually located in hollow trees and, frequently, in human structures such as attics and outbuildings; nest relocation may occur when space becomes limiting [6,7].

Female hornets are generalist predators that capture a broad range of arthropod prey, including other social wasps, honeybees, flies, lepidopterans, and spiders [7-10]. They may also feed on plant exudates at sap runs and visit flowering plants for nectar [4,7,11]. Where *V. crabro* co-occurs with the invasive *Vespa velutina*, resource overlap may lead to interspecific competition [12]. Although generally not highly aggressive, stings can occur during nest defense, and comparative venomics indicates marked enrichment of major venom components in *V. crabro* relative to some congeners [13].

The Oriental hornet, *Vespa orientalis*, is distributed across the Levant, Southern Europe, Northeast Africa, and Southwestern Asia, including India [14,20]. It is considered an important apicultural pest due to its strong predation pressure on honeybees and its potential to reduce foraging activity, leading to economic losses for beekeepers and decreased crop pollination [14]. In addition, it may damage fruit crops directly or indirectly, and stings can cause medically relevant reactions in sensitive individuals [14-16]. Several subspecies and regional forms have been described, often distinguished by coloration traits [17]. Previous studies have reported morphological features, including the sting apparatus and antennal chemoreceptors [18,19], and the complete mitochondrial genome of *V. orientalis* has been characterized [20].

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Despite the broad recognition and distribution of *V. crabro* [2], the taxonomic history of hornets has been complex, and subspecies delineation based on morphology—especially coloration—has been debated [21,22]. Recent taxonomic reassessments have questioned the reliability of some morphological characters and suggested that several subspecies names may represent synonyms, emphasizing the need for molecular evidence in species delimitation [23]. In this context, mitochondrial COI barcoding remains a widely applied and reliable approach for insect identification and comparative taxonomy.

Therefore, the aim of this research is to provide a combined morphological and molecular-genetic characterization of *Vespa crabro* and *Vespa orientalis* from Uzbekistan using the mitochondrial COI gene, and to assess genetic differentiation between these two species within the genus *Vespa* [23].

1.1. Zoological Description

Vespa crabro

Vespa crabro is one of the largest hornet species recorded in Uzbekistan. The body length of workers ranges from 18 to 24 mm, females measure 22–25 mm, and males 21–28 mm. The head is predominantly yellow, with the occipital and cervical regions showing a reddish hue in females, while males exhibit brighter yellow coloration. Mandibles are yellow, and antennae are reddish in females and yellow in males. The mesosoma is black with reddish markings, particularly on the pronotum. The metasoma is light yellow with distinct black spots, and the base of the first tergite is characteristically red. Legs are reddish, with the basal portions of the femora darkened.

Sexual dimorphism is evident in antennal segmentation and abdominal structure: females possess 12 antennal segments and seven visible abdominal segments, whereas males have 13 antennal segments and six abdominal segments. Diagnostic characters of *V. crabro* include its large body size, contrasting yellow-red coloration, and robust body proportions. The species is a generalist predator, feeding on a wide range of insects, including bees and wasps [24,25].

Vespa orientalis

Vespa orientalis is a large social wasp exhibiting considerable size variation, with total body length ranging from 19 to 32 mm. Females are the largest caste (25–32 mm), followed by males (20–25 mm) and workers (19–25 mm). The metasoma shows a characteristic coloration pattern, ranging from reddish-brown to dark brown, with the third (T3) and fourth (T4) tergites predominantly yellow and marked by a basal reddish-brown band extending medially, accompanied by two lateral spots. This color pattern represents a key diagnostic feature of the species.

The posterior ocelli are positioned closer to each other than to the compound eyes. The clypeus lacks a medial tooth between the broadly rounded lateral projections, and the genae are as wide as or slightly wider (up to 1.5 times) than the compound eye in lateral view. A complete pretegular

carina is present [26]. Sexual dimorphism is reflected in antennal segmentation, with males bearing 13 segments and females 12. The thorax is uniformly brown, and the wings measure 34–46 mm in length. The abdomen consists of six to seven visible segments, with males typically exhibiting seven segments.

Geometric morphometric studies have demonstrated notable variation in forewing shape within *V. orientalis*, leading to the recognition of three geographic morphogroups: AFRI (North Africa), MEDI (Northern Mediterranean), and MEAS (Middle East). The AFRI morphogroup shows pronounced wing-shape divergence, likely influenced by geographic isolation and environmental adaptation, whereas MEDI and MEAS groups exhibit more moderate differentiation corresponding to regional boundaries [27]. These morphometric differences may influence dispersal and foraging behavior but do not obscure the core diagnostic morphological traits of the species.

2. Materials and Methods

Entomological specimens were collected between 2022 and 2025 in the Kitab, Nishon, and Mirishkor districts of the Qashqadaryo Region, Uzbekistan. Adult individuals of *Vespa crabro* and *Vespa orientalis* (genus *Vespa*) were collected and preserved in 70% ethanol until further analysis.

Genomic DNA was extracted from ethanol-preserved specimens using the GeneJET Genomic DNA Purification Kit (Germany), following the manufacturer's protocol. The isolated genomic DNA was used to amplify a fragment of the mitochondrial cytochrome oxidase I (COI) gene, which is widely applied in insect molecular taxonomy. Polymerase chain reaction (PCR) amplification was performed using primers C1-J-2195 (TTGATTTTTGGTCATCCAGAAGT) and L2-N-3014 (TCCAATGCACTAATCTGCCATATTA), previously validated for insect COI barcoding (Frohlich *et al.*, 1999).

PCR reactions were carried out in a programmable thermal cycler (Touchgene Gradient, UK) under the following conditions: initial denaturation at 95 °C for 3 min; followed by 35 cycles of denaturation at 93 °C for 20 s, primer annealing at 55 °C for 30 s, and elongation at 72 °C for 2 min; with a final extension step at 72 °C for 10 min. PCR products were visualized and purified, and DNA concentrations were measured using a NanoDrop spectrophotometer prior to sequencing.

Sequencing was performed using the ABI PRISM® BigDye™ Terminator v.3.1 kit, and reaction products were analyzed on an ABI PRISM 3100-Avant automated sequencer (Core Facility “Genome”, Genotech, Moscow). Sequencing chromatograms were obtained in ABI format and initially inspected using Chromas version 1.45 [28]. Forward and reverse sequences were assembled and converted to FASTA format, after which multiple sequence alignment was conducted using Clustal X version 1.81 [29]. Ambiguous or low-quality regions were removed using GeneDoc version 2.5.000 [30]. Sequence data were converted to Nexus format

using ForCon version 1.0 for Windows.

Phylogenetic and comparative analyses were performed using MEGA11 and PAUP* version 4.0b10 [31]. All PAUP* analyses were conducted using input files in Nexus format.

3. Results

Based on molecular-genetic analyses of mitochondrial DNA, a 623 base-pair fragment of the cytochrome oxidase I (COI) gene was successfully amplified and sequenced from *Vespa crabro* and *Vespa orientalis* specimens collected in Uzbekistan. The obtained sequences were designated as *V. crabro_Uzb* and *V. orientalis_Uzb*. These sequences were compared with corresponding reference COI sequences available in GenBank, including *V. crabro* (accession number

MT444756) and *V. orientalis* (accession number KF933083).

Comparative analysis revealed clear nucleotide polymorphisms both within and between species. A total of 18 nucleotide substitutions were detected between *V. crabro_Uzb* and *V. orientalis_Uzb* across the analyzed 623 bp COI fragment. These substitutions included both transitions and transversions, with transitions occurring more frequently, which is consistent with typical mitochondrial DNA substitution patterns.

Intraspecific comparison showed minimal genetic variation. The *V. crabro_Uzb* sequence differed from the reference *V. crabro* MT444756 by a single nucleotide substitution (0.2%), indicating high genetic similarity within the species. Similarly, *V. orientalis_Uzb* exhibited low divergence from the reference *V. orientalis* KF933083 sequence, differing by only two nucleotide substitutions (0.3%).

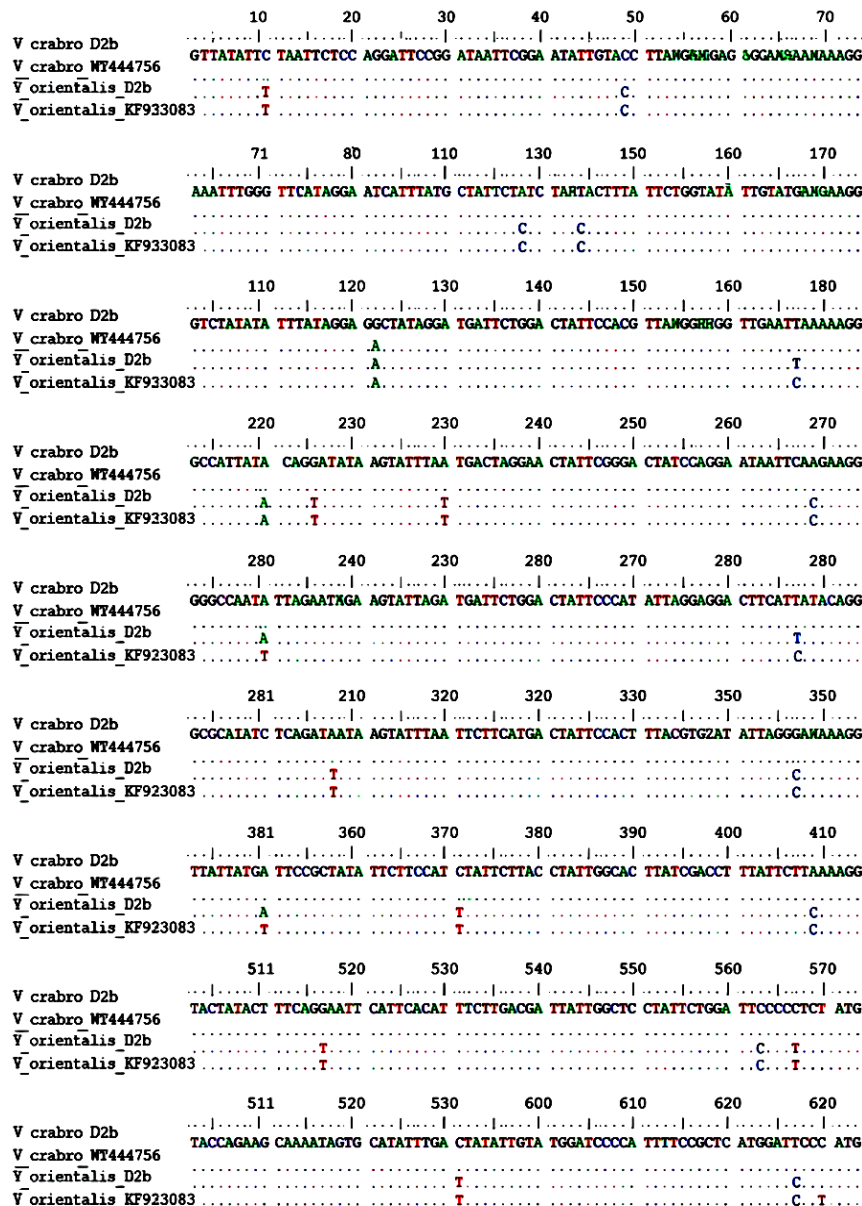


Figure 1. Comparison of nucleotide substitutions in the 623 bp COI mitochondrial DNA fragment of *Vespa crabro* and *Vespa orientalis*, including Uzbek specimens and reference sequences from GenBank

Table 1. Summary of nucleotide substitutions in the mitochondrial COI gene (623 bp) among *Vespa crabro* and *Vespa orientalis*

Comparison	Sequence length (bp)	Number of SNPs	Transitions	Transversions	Genetic divergence (%)
<i>V. crabro</i> _Uzb vs. <i>V. orientalis</i> _Uzb	623	18	11	7	2.9
<i>V. crabro</i> _Uzb vs. <i>V. crabro</i> MT444756	623	1	1	0	0.2
<i>V. crabro</i> _Uzb vs. <i>V. orientalis</i> KF933083	623	19	12	7	3.04
<i>V. orientalis</i> _Uzb vs. <i>V. orientalis</i> KF933083	623	2	2	0	0.3
<i>V. orientalis</i> _Uzb vs. <i>V. crabro</i> MT444756	623	17	10	7	2.7

In contrast, interspecific comparisons demonstrated substantially higher levels of divergence. The genetic distance between *V. crabro*_Uzb and *V. orientalis* reference sequences reached 3.04%, while *V. orientalis*_Uzb differed from *V. crabro* MT444756 by 2.7%. A summary of the number and type of nucleotide substitutions, as well as uncorrected genetic distances for all pairwise comparisons, is presented in **Table 1**.

Overall, the observed COI nucleotide polymorphisms clearly distinguish *V. crabro* from *V. orientalis* and confirm the utility of mitochondrial COI barcoding for reliable species discrimination within the genus *Vespa*. The newly generated sequences provide the first molecular genetic data for these species from Uzbekistan.

4. Discussion

The molecular-genetic analysis of the mitochondrial cytochrome oxidase I (COI) gene fragment from *Vespa crabro* and *Vespa orientalis* specimens collected in the Qashqadaryo Region of Uzbekistan revealed clear patterns of nucleotide polymorphism that contribute to understanding genetic differentiation within the genus *Vespa*. Sequencing of a 623 bp COI fragment and comparison with reference sequences from GenBank (*V. crabro* MT444756; *V. orientalis* KF933083) demonstrated distinct interspecific divergence alongside minimal intraspecific variation.

A total of 18 nucleotide substitutions were detected between the local *V. crabro*_Uzb and *V. orientalis*_Uzb sequences, resulting in an uncorrected genetic distance of approximately 2.9%. This level of divergence falls within the range commonly reported for interspecific differentiation in Vespidae based on COI barcoding and is consistent with previous molecular studies of *Vespa* species. In contrast, intraspecific comparisons showed very low levels of variation: *V. crabro*_Uzb differed from the reference MT444756 sequence by a single nucleotide substitution (0.2%), and *V. orientalis*_Uzb differed from KF933083 by only two substitutions (0.3%). These findings indicate genetic stability within species and support the reliability of COI as a species-level diagnostic marker.

The observed substitutions included both transitions and transversions, with transitions predominating, a pattern characteristic of mitochondrial DNA evolution. Several fixed nucleotide differences between *V. crabro* and *V. orientalis* were consistently detected across comparisons, providing

clear molecular signatures for species discrimination. The multiple sequence alignment (Figure 1) highlights these species-specific single nucleotide polymorphisms while demonstrating limited variation within each species, reinforcing the conclusions drawn from pairwise distance analyses (Table 1).

The genetic distinctiveness observed between the two species corresponds well with previously reported morphological and taxonomic distinctions and supports earlier conclusions that molecular data are essential for resolving species boundaries within *Vespa*, where morphological variation alone may be ambiguous. The detection of minor intraspecific variation, such as the single nucleotide difference between *V. crabro*_Uzb and the reference sequence, may reflect regional phylogeographic structure influenced by Central Asian environmental conditions.

Although molecular studies of *Vespa* species from Uzbekistan remain scarce, the present data provide the first COI-based genetic characterization of *V. crabro* and *V. orientalis* from this region. This contributes to filling a significant geographic gap in the molecular taxonomy of the genus and offers a baseline for future comparative and phylogeographic investigations.

A limitation of the present study is the reliance on a single mitochondrial marker. While COI has proven effective for species discrimination, future research incorporating nuclear genes, expanded sampling across Uzbekistan and neighboring regions, and integrative morphological analyses would allow a more detailed assessment of subspecies status, population structure, and potential hybridization. Nevertheless, the current results clearly demonstrate the utility of COI barcoding for distinguishing *Vespa* species and provide valuable molecular data relevant to biodiversity assessment, conservation, and monitoring of ecologically and economically significant hornets in Central Asia.

5. Conclusions

This study provides the first molecular-genetic characterization of *Vespa crabro* and *Vespa orientalis* from Uzbekistan based on a 623 bp fragment of the mitochondrial cytochrome oxidase I (COI) gene. Comparative analysis with reference sequences from GenBank (*V. crabro* MT444756; *V. orientalis* KF933083) revealed very low levels of intraspecific variation (0.2-0.3%), indicating genetic stability within each species.

In contrast, interspecific comparisons showed clear genetic differentiation, with uncorrected COI divergences ranging from 2.7% to 3.04%. These values fall within the commonly accepted thresholds for species-level separation in Vespidae and confirm the distinct genetic identities of *V. crabro* and *V. orientalis*. The observed nucleotide polymorphisms support the effectiveness of COI barcoding as a reliable tool for species discrimination within the genus *Vespa*.

Overall, the results contribute new molecular data for Central Asian populations of hornets and help fill a geographic gap in the molecular taxonomy of *Vespa*. These findings provide a baseline for future studies addressing population structure, phylogeography, and the ecological and economic significance of hornets in Uzbekistan and adjacent regions.

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DISCLOSURE

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