



Morphological and numerical characterization and genetic relationship detection of a number of locust species (Orthoptera: Locusta) in central Iraq

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Abstract

Objective: Phenotypic characterization of a number of locust species (Orthoptera: Locusta) in central Iraq, as well as detection of genetic similarity and difference based on the phenotypic characteristics of 12 locust samples.. **Materials and methods:** The samples were collected from different areas of the center (Al-Alam, Tikrit, Ad-Dhuluiya, Balad, Ad-Dujayl, Sharqat) using the collection kit, and the ant samples were identified at the Research Center and the Natural History Museum\University of Baghdad, and the study was conducted in the laboratories of the College of Science\University of Tikrit during the period 11/8/2023 until 12/23/2023. : The samples were collected and preserved according to the methods followed in preserving insects, and the morphological study of (50) morphological characteristics was conducted for each of the general shape of the head, thorax, abdomen, legs and wings in detail using a dissecting microscope, and the temporary sections were photographed using a digital camera and preserved until the results were studied. The numerical classification and phenotypic genetic dimension were also conducted based on the results of the studied phenotypic characteristics. **Results:** The results showed a clear difference between the species, as shown by the results of the statistical analysis of the phenotypic genetic dimension values, which ranged between (0.008-0.865), where the lowest genetic dimension was between sample No. 6 (Locusta migratoria, Balad) and No. 5 (Locusta migratoria, Tikrit), as it reached 0.008, which is considered the highest similarity rate between the two samples within the studied species. This convergence between these two species came as a result of the similarity in the largest number of studied phenotypic traits. As for the highest genetic dimension, it reached 0.0865 between sample 2 (Eypepochemis plorans, Alam) and sample 4 (Phlaeoba infamata, Sharqat), which indicates that it is the least similarity between the two species within the studied species. This divergence between these two species came as a result of the lack of matching in the traits that were studied between these two samples, while the values of the genetic dimension for the rest of the species ranged between those values.. **Conclusion:** We concluded from the research that there is a high genetic variation in the locust genome, as a result of the significant impact of environmental factors and the nature of the places where locusts live, in addition to



the multiple life cycles of locusts, which led to variation that will lead in the future to biodiversity when it reaches a certain level.

التوصيف المظهري و العددي وكشف العلاقة الوراثية لعدد من انواع الجراد

Orthroptya:Locusta المنتشر في وسط العراق

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الخلاصة:

هدف البحث الحالي الى التوصيف المظهري لعدد من انواع الجراد Orthroptya:Locusta في وسط العراق وكذلك كشف التشابه والاختلاف الوراثي اعتماداً على الصفات المظهرية لـ 12 عينة من الجراد ، تم جمع العينات من مناطق مختلفة من الوسط (العلم، تكريت، الضلوعية، بلد، الدجيل، الشرقاط) باستخدام عدة الجمع ، وشخصت عينات النمل في مركز البحوث ومتحف التاريخ الطبيعي \ جامعة بغداد، واجريت الدراسة في مختبرات كلية العلوم \جامعة تكريت في الفترة 11 / 8 / 2023 ولغاية 2023/12/23. : تم جمع العينات وحفظها حسب الطرق المتبعة في حفظ الحشرات واجريت الدراسة المظهرية لـ (50) صفة مظهرية لكل من الشكل العام الرأس والصدر والبطن والارجل والاجنحة بشكل مفصل باستخدام مجهر تشريحي وصورت المقاطع المؤقتة باستخدام الكاميرة الرقمية وحفظت لحين دراسة النتائج. كذلك اجري التصنيف العددي والبعد الوراثي المظهري اعتماداً على نتائج الصفات المظهرية المدروسة. وأظهرت النتائج تبايناً واضحاً بين الانواع ، تبين من نتائج التحليل الاحصائي لقيم البعد الوراثي المظهري والتي تراوحت بين (0.008-0.865) حيث كان أقل بعد وراثي بين العينة رقم 6 (*Locusta migratoria* بلد) ورقم 5 (تكريت *Locusta migratoria*) إذ بلغ 0.008 ويعد ذلك بمثابة اعلى نسبة تشابه بين العينتين ضمن الانواع المدروسة وهذا التقارب بين هذين النوعين جاء نتيجة التشابه في أكثر عدد من الصفات المظهرية المدروسة . أما أعلى بعد وراثي فقد بلغ 0.0865 بين العينة 2 (*Eypepochemis plorans* علم) والعينة 4 (*Phlaeoba infamata* شرقاط) ويوضح ذلك على أنه أقل تشابه بين النوعين ضمن الانواع المدروسة وهذا التباعد بين هذين النوعين جاء نتيجة عدم وجود تطابق في الصفات التي تم دراستها بين هذين العينتين في حين تراوحت قيم البعد الوراثي لباقي الأنواع بين تلك القيم.

الكلمات المفتاحية: الصفات المظهرية ، التصنيف العددي، العلاقة الوراثية ، الجراد

Introduction

Locusts belong to the family Acrididae (Usmani *et al.*, 2018), which in turn belongs to the order Orthoptera (Eades *et al.*, 2015). Locusts are swarming pests that in recent decades have begun to behave collectively, turning into swarms and epidemics that affect people, climate and the economy. Among the locust species that participate in the spread of the disease in regions of Asia and Africa, including (India, Pakistan and other continents (Hassan, A. & Aslam 2024), it is one of the most important and largest pests on the global level, which is a real threat to the economy (Shaha *et al.*, 2008).



In biodiversity, we cannot rely only on random genetic mutations, as there are apparent adaptive patterns that arise as a result of plastic interactions between the environment and genes. Locusts have a polymorphic stage, and it is known that environmental factors such as photoperiod, temperature, population density and resource availability affect phenotypic traits (Berthier *et al.*, 2010). There are recent studies indicating that There are 26.6 thousand described species of locusts (Eades *et al.*, 2015).

Locusts are found in temperate and tropical pastures all over the world, especially in arid areas (Latchininsky *et al.*, 2011). They are also found in developing countries in desert and semi-desert areas. There are many characteristics that help locusts spread and make them very dangerous and a transboundary pest, which is their ability to migrate long distances (Van Huis *et al.*, 2007).

There are a number of morphological studies on locusts that were initiated by scientists, where the morphological classification depends on the color of the body and the structure of the body, as the insects belonging to the order Orthopterygota appear to be externally winged, i.e. the wings develop from the outside in the embryonic stage. They are medium-sized insects with an elongated semi-cylindrical body, enlarged hind legs modified for jumping, the head is lower than the jaws, and the head is also characterized by the presence of two compound eyes, and simple eyes Ocelli are present or absent, the antennae are double-jointed, and the mouth parts Antennae are jawed (Daily, *et al.*, 1983).

Numerical classification (1957) Sneath is part of the multivariate scientific analyses and in parallel with the emergence of the computer, which helped and enabled quantitative approximation and the possibility of rapid processing of a huge number of data, and the term Adansonian Taxonomy is a term that refers to numerical classification also in Adansonian Taxonomy, or computer taxonomy, or numerical phenolic analysis. Quantitative methods have given important results in isolating and diagnosing taxonomic ranks based on a small number of selected traits within a population group based on this small number of traits. Researchers in entomology have used numerical classification in many taxonomic studies, and the first to use numerical classification for the first time was Al-Sagmiany (2010) on a number of species of the genus *Vitex*, and Al-Sagmiany (2017) also used it on a number of genetic structures of the fava bean plant *Faba vicia*, and it was used by (Al-Mashhadani, 2020) on insects and his study included the classification of a number of fly species, as he is considered one of the first to apply numerical classification programs to insects. The purpose of his study was to gain extensive experience in numerical classifications as well as to determine the degree of conformity between classifications based on phenotypic characteristics and their relationship to molecular indicators. The current study aimed to describe the phenotypic and numerical characteristics and the genetic relationship of a number



of phenotypic characteristics of 12 samples of locusts collected from different regions of central Iraq.

Materials and methods:

1 - Collection and preservation of samples: Samples were collected from different areas of central Iraq (Sharqat, Baiji, Al-Alam, Tikrit, Al-Dhuluiya, Balad, Al-Dujayl) in the period between 2023/8/11 to 2023/12/20 using two methods, the first method: direct hand collection.

The second method: using an aerial net collection The samples that were collected were frozen at minus 20 to preserve them (for the purpose of photography) and were preserved in another way using 70% ethanol alcohol and placed in special plastic tubes with the date of collection and the region from which they were collected written on them until the study was conducted.

2-Diagnosis of samples:

The types of locusts mentioned in Table 1 were diagnosed at the Natural History Museum Research Center / University of Baghdad, on 11/1/2023

Table (1) shows the sequence of samples and their collection areas

T	Common name	Scientific name	Area of sample collection
1	Egyptian locus	<i>Anacridiumaegyptium</i>	Al-Dhuluiyah District
2	Locust	<i>Eyprepocnemis plorans</i>	Al-Alam District
3	Locust	<i>Acridia</i> SP.	Tikrit City
4	L ocust	<i>Phlaeoba infumata</i>	Al-Sharqat District
5	Migratory locust	<i>Locusta migratoria</i>	Tikrit City
6	Locust	<i>Phlaeoba infumata</i>	Balad District
7	Locust	<i>Phlaeoba infumata</i>	Balad District
8	Locust	<i>Phlaeoba infumata</i>	Al-Dhuluiyah District
9	Locust	<i>Eyprepocnemis plorans</i>	Al-Dhuluiyah District
10	Locust	<i>Acridia</i> SP.	Al-Dujayl District
11	Locust	<i>Phlaeoba infumata</i>	Al-Sharqat District
12	Locust Migratory	<i>Locusta migratoria</i>	Al-Dujayl District

3- Numerical classification: (50) traits were selected for the phenotypic study and compared numerically. These traits were entered into the computer by



encoding the traits with the numbers 0,1)) when the trait is present or absent in the studied species, respectively. As mentioned previously, in this study, an approved method was used to analyze the molecular data and then calculate the similarity percentage as well as the similarity coefficient between the studied species using Nei's coefficient 72. All statistical analyses were conducted by computer using the program: NTSYS-PC. Version 2. 20i) and the samples were given symbols for ease of dealing with them and arranged sequentially from (1) to (12).

Results and discussion-:

1- Appearance characterization Morphological characteristics are the basis for the classification of organisms, including insects. The methods used to diagnose these characteristics are characterized by being easy, fast, and free of complications. These morphological characteristics can be studied by making temporary or permanent slides and determining the degree of similarity and difference between characteristics through the results of collecting locust samples that included different areas of central Iraq (Sharqat District, Tikrit City, Al-Alam District, Balad District, Al-Dhuluiya District, Al-Dujayl District) for 12 samples from those areas and recorded in Chapter Three, Table (1) sample code, collection site, and scientific name for each sample. There are six types of locusts according to the diagnosis of the Natural History Museum at the University of Baghdad, shown in Table (2) and Figure (1).



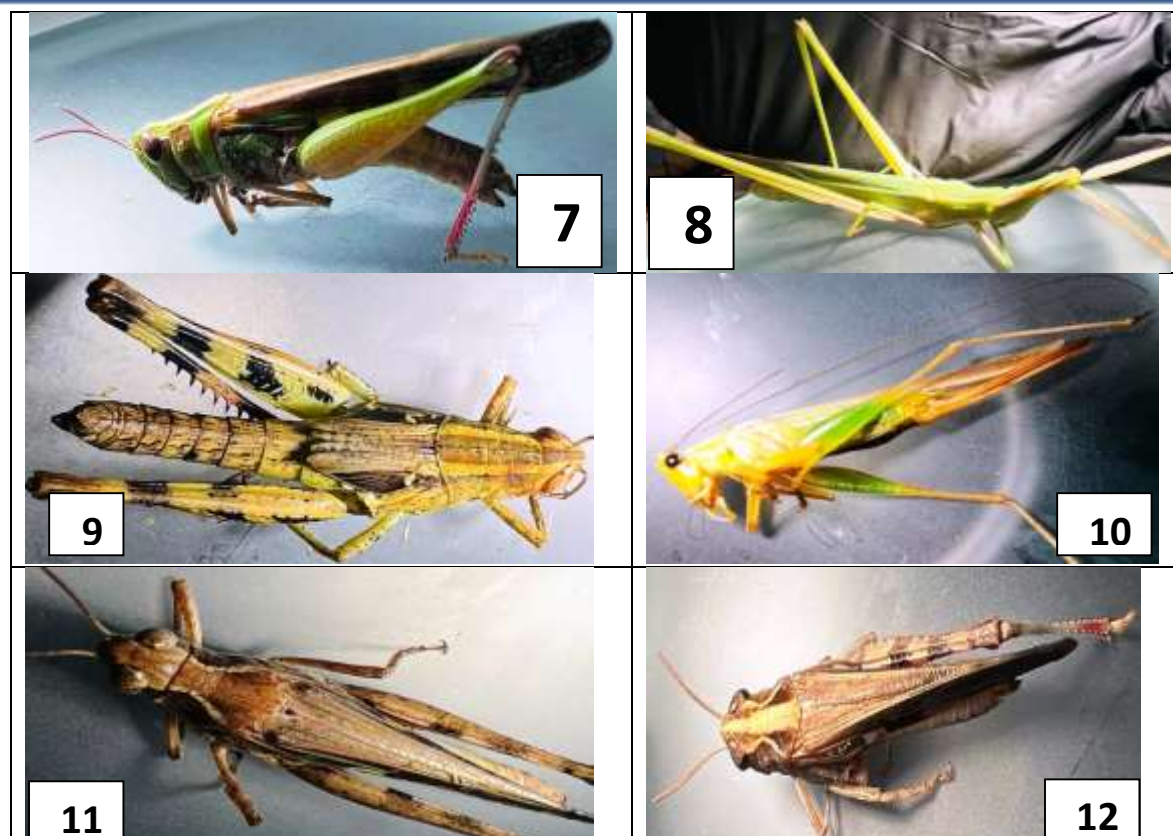


Figure (1) shows pictures of the general description of the studied *Locusta* and represents .

Through numerical classification, the first sample (*Phlaeoba infumata*) Ribular) was similar to the second sample (*Eyprepocnemis plorans*) in the color of the head, the shape of the antennae, and the tip of the horn. It was also similar to the second sample in the shape of the chest, chest color, chest dimensions, abdomen shape, abdomen color, abdomen width, abdomen size, number of abdominal segments, and shape of the middle abdominal segments. The genetic distance between the two samples was 0.491. The second sample (*Eyprepocnemis plorans*) was similar to the third sample (*Acrida* SP. Tikrit) in the color of the head, head width, as well as chest color, abdomen color, number of segments, and shape of the anterior and posterior abdominal segments. The genetic distance between the two samples was 0.062. The third sample (*Acrida* SP. Tikrit) was similar to the fourth sample (*Phlaeoba infumata*) Sharqat) in the shape of the head, head color, head dimensions, horn shape, horn length, horn color, number of horn segments, horn tip, chest shape, chest color, and chest dimensions. The genetic distance between the two samples was 0.796

The fourth sample (*Phlaeoba infumata*) Sharqat) was similar to the fifth sample (*Locusta migratoria* Tikrit) in the shape of the head, the color of the horn, as well as the shape of the middle and posterior rings of the abdomen, and the genetic distance between them was 0.606



The fifth sample (*Locusta migratoria* Tikrit) was similar to the sixth sample (*Phlaeoba infumata* Balad) in the shape of the head, the shape of the horn, the color of the horn, the tip of the horn, the shape of the chest, the shape of the abdomen, the number of abdominal rings, and the shape of the anterior and posterior rings of the abdomen, and the genetic distance between them was 0.008

The sixth sample (*Phlaeoba infumata* Balad) was similar to the seventh sample (*Phlaeoba infumata* Balad) in the shape of the head, the color of the head, the dimensions of the horn, the length of the horn, the color of the horn, the number of horn segments, the tip of the horn, the shape of the chest, the color of the chest, the dimensions of the abdomen, the shape of the abdomen, the number of abdominal rings, and the shape of the anterior and posterior rings of the abdomen, and the genetic distance between them was 0.746

The seventh sample (*Phlaeoba infumata* Balad) was similar to the eighth sample (*Phlaeoba infumata* Ribular) in head color, horn color, abdomen shape, number of abdominal rings, and shape of posterior abdominal rings, and the genetic distance between them was 0.594.

The eighth sample (*Phlaeoba infumata* Ribular) was similar to the ninth sample (*Phlaeoba infumata* Ribular) in head color, head dimensions, abdomen color, and number of abdominal rings, and the genetic distance between them was 0.452.

The ninth sample (*Phlaeoba infumata* Ribular) was similar to the tenth sample (*Phlaeoba infumata* Djil) in head color, horn shape, horn tip, chest shape, and chest color, and the genetic distance between them was 0.369.

The tenth sample (*Phlaeoba infumata* Djil) was similar to the eleventh sample (*Locusta migratoria* Sharqat) in head dimensions, horn shape, horn tip, chest shape, abdomen color, number of abdominal rings, and shape of anterior and posterior rings, and the genetic distance between them was 0.094.

The eleventh sample (*Locusta migratoria* Sharqat) was similar to The twelfth sample (*Locusta migratoria* Djell) had head shape, head color, head dimensions, horn shape, horn color, horn length, number of horn segments, and horn tip, and the genetic distance between them was 0.0586.

Table (2) Morphological characteristics of locust samples trampled and entered in the numerical classification

Characteristics		1	2	3	4	5	6	7	8	9	10	11	12
General shape	Straight	1	0	0	0	1	1	1	0	1	0	1	1



	Thick	0	1	0	0	0	0	0	0	0	0	0	0
	Elongated	0	0	1	1	0	0	0	1	0	0	0	0
	Conical	0	0	0	0	0	0	0	0	0	1	0	0
	Wide	0	0	0	0	0	0	0	0	0	0	0	0
Insect color	Brown	1	0	0	1	0	0	0	0	0	0	0	0
	Brown colored	0	1	1	0	0	0	0	0	0	0	1	1
	Green	0	0	0	0	1	1	1	1	1	1	0	0
Insect length	A	0	0	1	1	0	1	1	0	1	1	1	1
	B	1	1	0	0	1	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	1	0	0	0	0
Insect width	A	0	0	1	1	0	1	1	0	1	1	1	1
	B	0	1	0	0	0	0	0	1	0	0	0	0
	C	1	0	0	0	1	0	0	0	0	0	0	0
Insect size	Small	0	0	0	0	0	0	0	0	0	0	0	0
	Medium	0	0	1	1	0	1	1	0	1	1	1	1
	Large	1	1	0	0	1	0	0	1	0	0	0	0
Presence of hairs	Present	1	0	0	0	1	0	0	0	0	0	0	1
	None	0	1	1	1	0	1	1	1	1	1	1	0
Head shape	Circular	0	1	0	0	1	1	1	0	1	0	0	0
	Conical	0	0	1	1	0	0	0	1	0	1	0	0
	Straigh	1	0	0	0	0	0	0	0	0	0	1	1
Head color	Head color Brown	1	0	0	0	0	0	0	0	0	0	0	0
	Brown colored	0	1	1	1	0	0	0	0	0	0	1	1
	Green	0	0	0	0	1	0	1	1	1	1	0	0
Head length	A	0	1	0	0	0	1	1	0	0	1	1	1
	B	0	0	1	1	0	0	0	1	1	0	0	0
	C	1	0	0	0	1	0	0	0	0	0	0	0
Head width	A	0	1	1	1	0	1	1	0	0	1	1	1
	B	1	0	0	0	1	0	0	1	0	0	0	0
	C	0	0	0	0	0	0	0	0	1	0	0	0
Mouth length	A	0	1	1	1	0	1	1	0	0	1	1	1
	B	1	0	0	0	1	0	0	1	1	0	0	0
Mouth width	A	0	1	1	1	0	1	1	1	1	1	1	1
	B	1	0	0	0	1	0	0	0	0	0	0	0
Presence of hairs	Yes	1	0	0	0	1	0	0	0	0	0	0	1
	None	0	1	1	1	0	1	1	1	1	1	1	0
Eyes	Oval	1	1	0	0	0	1	1	0	1	0	1	1
	Circular	0	0	0	0	1	0	0	0	0	1	0	0
	Elongated	0	0	1	1	0	0	0	1	0	0	0	0
Eyes color	Brown	0	0	1	1	1	1	1	1	0	1	1	1



	Brown colored	1	1	0	0	0	0	0	0	1	0	0	0
	Green	0	0	0	0	0	0	0	0	0	0	0	0
Tentacle shape	Threadlike	1	1	0	0	1	1	1	0	1	1	1	1
	Daggerlike	0	0	1	1	0	0	0	1	0	0	0	0
Tentacle length	A	0	1	1	1	1	1	1	0	1	0	1	1
	B	1	0	0	0	0	0	0	1	0	0	0	0
	C	0	0	0	0	0	0	0	0	0	1	0	0
Tentacle color	Brown	0	0	1	1	1	0	0	0	0	0	1	1
	Brown colored	1	1	0	0	0	1	1	1	0	1	0	0
	Green	0	0	0	0	0	0	0	0	0	0	0	0
	Black	0	0	0	0	0	0	0	0	1	0	0	0
Number of segments	A	1	1	1	1	1	1	1	1	1	1	1	1
	B	0	0	0	0	0	0	0	0	0	1	0	0
Tentacle tip	Circular	1	1	0	0	1	1	1	0	1	1	1	1
	Acute	0	0	1	1	0	0	0	1	0	0	0	0
Thorax shape	Oval	1	1	0	0	1	1	1	0	0	0	0	0
	Rhombic	0	0	1	1	0	0	0	1	1	1	1	1
	Circular	0	0	0	0	0	0	0	0	0	0	0	0
Chest color	Brown	1	0	0	0	0	0	0	0	0	0	0	0
	Brown colored	0	1	1	1	0	1	1	0	0	0	1	1
	Green	0	0	0	0	1	0	0	1	1	1	0	0
Chest length	A	1	1	1	1	1	1	1	0	1	1	1	1
	B	0	0	0	0	0	0	0	1	0	0	0	0
Chest width	A	0	0	1	1	0	1	1	0	1	1	1	1
	B	1	1	0	0	0	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	1	0	0	0	0
Foreleg shape	Short	0	0	1	1	0	1	1	0	0	1	1	1
	Medium	1	1	0	0	1	0	0	0	1	0	0	0
	Long	0	0	0	0	0	0	0	1	0	0	0	0
Middle leg shape	Short	0	0	1	1	0	0	0	0	0	0	0	0
	Medium	1	1	0	0	1	1	1	0	0	1	1	1
	Long	0	0	0	0	0	0	0	1	1	0	0	0
Hind leg shape	Long	0	1	1	1	0	1	1	0	0	0	1	1
	Very long	1	0	0	0	1	0	0	1	1	1	0	0
Foreleg length	A	0	1	1	1	0	1	1	0	0	1	1	1
	B	1	0	0	0	1	0	0	0	1	0	0	0
	C	0	0	0	0	0	1	0	1	0	0	0	0
Middle leg length	A	0	1	1	1	0	1	1	0	0	1	1	1
	B	1	0	0	0	1	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	1	1	0	0	0
Hind leg length	A	0	0	1	1	0	1	1	0	0	1	1	1



	B	1	1	0	0	1	0	0	0	1	0	0	0
	C	0	0	0	0	0	0	0	1	0	0	0	0
Body hairs	Yes	1	1	1	1	1	0	0	0	0	1	0	1
	None	0	0	0	0	0	1	1	1	1	0	1	0
Wing shape	Straight	0	0	0	0	0	0	1	0	0	0	0	1
	Nose	1	1	1	1	1	1	1	0	1	1	1	1
Forewing length	A	1	1	1	1	1	1	1	0	1	1	1	1
	B	0	0	0	0	0	0	0	1	0	0	0	0
Hindwing length	A	0	0	1	1	0	1	1	0	1	1	1	1
	B	1	1	0	0	1	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	1	0	0	0	0
Forewing colour	Brown	0	0	1	1	0	0	0	0	0	0	0	0
	Brown coloured	1	1	0	0	1	0	0	0	0	0	1	1
	Green	0	0	0	0	0	1	1	1	1	1	0	0
Hindwing colour	Brown	1	1	0	0	1	0	0	0	1	0	1	1
	Brown coloured	0	0	1	1	0	1	1	0	0	0	0	0
	Green	0	0	0	0	0	0	0	1	0	1	0	0
Wing venation	Anterior	1	1	1	1	1	1	1	1	1	1	1	1
	Posterior	1	1	1	1	1	1	1	1	1	1	1	1
Forewing type	Semi-elympha	0	1	1	1	1	1	1	0	1	0	1	1
	Hindwing type	1	0	0	0	0	0	0	1	0	1	0	0
	Scaly												
Number of veins	A	1	1	1	1	1	1	1	1	1	1	1	1
Number of veins of sphenoid wing	B	1	1	0	0	0	0	0	0	0	0	0	0
	C	0	0	0	0	1	0	0	1	1	1	0	0
	A	0	0	1	1	0	1	1	0	0	0	1	1
Abdominal shape Conical	A	0	0	1	1	0	1	1	0	0	1	0	0
	B	0	0	0	0	1	0	0	1	1	0	1	1
	C	1	1	0	0	0	0	0	0	0	0	0	0
Abdominal colour	Straight	1	1	0	0	1	1	1	1	0	0	1	1
	Brown	0	0	1	1	0	0	0	0	1	1	0	0
Abdominal length coloured	Brown	0	0	0	1	0	0	0	0	0	0	0	0
	Green	1	1	1	0	0	1	1	0	0	1	1	1
	Abdominal length A	0	0	0	0	1	0	0	1	1	0	0	0
Abdominal width	A	0	0	1	1	0	1	1	0	1	1	1	1
	B	1	1	0	0	1	0	0	0	0	0	0	0
	C	0	0	0	0	0	0	0	1	0	0	0	0
Hindwing length	2mm	0	0	1	1	0	1	1	0	1	0	1	1
	4mm	1	1	0	0	1	0	0	0	0	0	0	0
	6mm	0	0	0	0	0	0	0	1	0	0	0	0
Abdominal size	Large	1	1	0	0	1	0	0	1	0	0	0	0



	Medium	0	0	1	1	0	1	1	0	1	0	1	1
	Small	0	0	0	0	0	0	0	0	0	1	0	0
Presence of hairs	Yes	1	0	0	0	1	0	0	0	0	0	0	1
	None	0	1	1	1	0	1	1	1	1	1	1	0
Number of abdominal segments	8	0	1	1	0	0	0	0	0	1	1	0	1
	7	1	0	0	1	1	1	1	1	0	0	1	0
Shape of anterior abdominal	segments Square	1	0	0	0	1	1	1	0	0	1	1	1
	Rectangular	0	0	0	0	0	0	0	1	0	0	0	0
	Cylindrical	0	1	1	1	0	0	0	1	0	0	0	0
Shape of median abdominal	segments Square	1	1	0	1	1	0	0	0	0	1	0	0
	Rectangular	0	0	1	0	0	1	1	0	1	0	1	1
	Cylindrical	0	0	0	0	0	0	0	1	0	0	0	0
Shape of posterior	Square	0	0	0	0	0	0	0	0	0	1	1	0
	Rectangular	0	0	0	0	0	0	0	0	1	0	0	0
	Cylindrical	1	1	1	1	1	1	1	1	0	0	0	1

Estimation of genetic distance based on phenotypic traits: The phenotypic genetic distance was estimated based on the results of the studied phenotypic traits for 12 locust samples, using the genetic program (NTSYS-PC. Version 2. 20i) and based on the Nei equation (1979) in its analysis. It was found that the values of the genetic distance referred to in Table (2) ranged between 0.008-0.865, where the lowest genetic distance was between sample No. 5 and No. 6, reaching 0.008, which is considered the highest similarity rate between the two samples among the studied samples.

This convergence between these two samples came as a result of the similarity in the largest number of studied phenotypic traits, so the two types matched in several phenotypic traits. The highest genetic dimension reached 0.865 between sample 2 and sample 4, which indicates that there is less similarity between the two samples among the studied samples. This divergence between these two samples was due to the lack of matching in the traits studied between these two samples, while the values of the genetic dimension for the rest of the samples ranged between these values.

The cluster analysis group dendrogram was divided in Table (3) based on the values of the phenotypic genetic dimension of the locust samples using the results of the cluster analysis. The genetic relationship showed through the diagram that it was divided into: The first main group: This group included one sample No. 7. The second main group: This group included all the samples except sample No. 7, then this was divided into two secondary groups (A, B), where group A included



samples 1 and 4, while group B was divided into two subgroups (B1, B2), group B1 was divided into two subgroups (B1a, B1b). Group B1a was divided into B1a1, B1a2. Group B1a1 included samples 2 and 3, while group B1b was divided into two groups B1b1, B1b2. Group B1b1 included samples 5 and 6, and this group has the highest similarity rate among the studied groups. Group B1b2 included samples 10 and 11.

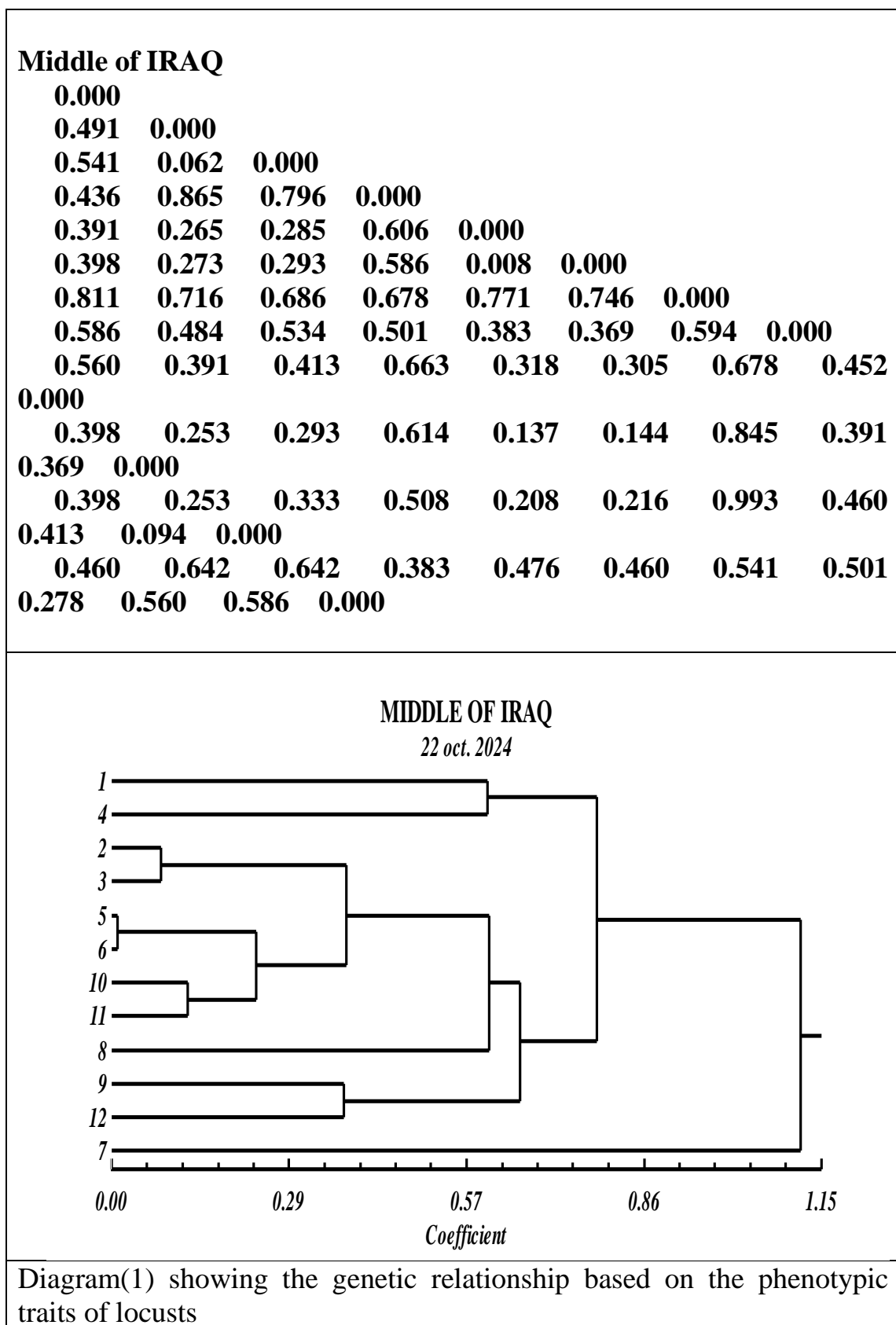
This is consistent with the results reached by Al-Rubaie (2023) in his study of the phenotypic and molecular characterization of a number of true ant species in some central and northern governorates of Iraq, as well as revealing genetic similarity and difference based on phenotypic and molecular traits and determining the genetic fingerprint using RAPD-PCR indicators and finding a correlation between the two indicators for 16 samples of true ants. In the study of Al-Shamani (2021), the study aimed to know the prevalence of lice and areas of infection in herds of buffaloes, sheep and goats in three governorates: Baghdad, Salah al-Din (Samarra), Kirkuk, and to know the genetic relationship and genetic distance between the same species for each of them and other species using RAPD-PCR indicators.

It was consistent with the study of Badejo *et al.*, (2020) in his study on insect colors and revealed the extent of the impact of the environment on the change in locust colors. It was consistent with the study of Soomro (2023) in a study he conducted on taxonomic and morphological studies on different genera of locusts. It was also consistent with the study of Tanaka (2024) in his study of geographical variation in the body size of (Orthoptera) migratory locusts. It was consistent with the study of Nishide (2016) in his study of the genetics of the migratory locust with black eyes.

It was also consistent with the study of Ochieng (1998) in his study of the fine structure and distribution of antennae sensitivities of locusts. Desert. It also agreed with the study of researchers Faisal and Matheson (2001) in their study of coordinated correction behavior in locusts. It also agreed. It agreed with the study of Muhammad (2016) A morphological study of some species of the short-horned locust family (Orthoptera: Acridida) in some governorates of Iraq. It also agreed with the study of Al-Jubouri (2021) A morphological and taxonomic description of species of the order Orthoptera in Salah al-Din Governorate.



Table 3: Phenotypic genetic distance values of the studied locust samples





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