PHYSIOLOGICAL AND MOLECULAR CHARACTERIZATION OF Ascochyta rabiei ISOLATES FROM VARIOUS CHICKPEA AREAS ACROSS IKR, IRAQ

Emad M. Al-Maaroof Prof. Rezan M. Salih Lecturer

College of Agricultural Engineering Sciences, University of Sulaimani, IKR, Iraq Email: emad.ghalib@univsul.edu.iq

ABSTRACT

From 2017 to 2019, 51 A. rabiei isolates were isolated from 259 chickpea fields across IKR. On different media, 32 isolates showed significant differences in morphological characteristics. The isolates were divided into six groups based on colony color, five groups on mycelium color and three groups on pycnidia color. CSMDA was the best media for mycelial growth. AS-28 significantly surpassed all other isolates in colony diameter despite media type. A. rabiei growth varied between 15-35°C, the maximum growth occured at 25°C and ceased at 35°C. The mean conidia and pycnedia dimensions in isolates AS-19 and AS-9 ranged from 20.0*7.5µm and 70.8*47.9µm to 21.8*9.0µm and 140.7*93.6um in AS-11 and AS-18 respectively. The isolates were classified into four groups and 15 races based on pathogenicity and virulence. Race 1 exhibited high aggressiveness and virulence against all differentials, whereas the other races explored variable virulence spectrum. Sulaimani had the greatest A. rabiei diversity, with nine different races accounting for 60% of population, followed by Erbil with five races (33%). Halabja and Garmian each contribute three and two races, accounting for 20% and 12% of the total. Races 4 and 5 were the most populous and widely spread in IKR. The ITS region was amplified to a541bp band in all A. rabiei isolates. The length of the nucleotide sequences ranged from 481 to 541bp. The ITS sequences of all the isolates were registered at the NCBI Gen Bank under different accession numbers. The phylogenetic tree clearly shows that all the isolates are grouped in one cluster and have a high degree of similarity.

Key words: Aschochta blight disease, *Cicer arietinum*, Physiological races, molecular diagnosis, fungal disease.

المعروف وصالح	مجلة العلوم الزراعية العراقية -2022: 53: 2022-314
Ascoci من مناطق انتاج الحمص المختلفة في كردستان العراق	hyta rabiei التوصيف الفسيولوجي والجزيئي لعزلات الفطر
ريزان محمد صالح	عماد محمود المعروف
مدرس	أستاذ
ىلىمانىيە، سلىمانىيە، اقلىم كردستان،العراق.	كليه علوم الهندسية الزراعيه، حامعه الير

المستخلص

خلال الفترة 2017 إلى 2019، تم عزل 51 عزلة من الفطر A. rabie من و259 حقل حمص في إقليم كردستان. أظهرت 23 عزلة فروقات معنوية في الخصائص المظهرية على اوساط غذائية مختلفة. صنفت عزلات الفطر لست مجاميع اعتمادا على لون المستعمرة، خمس مجاميع اعتمادا على لون الخصائص المظهرية على اوساط غذائية مختلفة. صنفت عزلات الفطر لست مجاميع اعتمادا على لون المستعمرة، خمس مجاميع اعتمادا على لون الخيوط الفطرية، وثلاث مجاميع وفق لون البيكنيديا. كان الوسط الغذائي CSMDA أفضل بيئة لنمو الفطر. تفوقت العزلة 28-AS معنويا على جميع العزلات في متوسط قطر المستعمرة بغض النظر عن الوسط المستخدم. تباين نمو الفطر *interne مدى حراري 15-35* م، سجل اعلى معدل العزلات في متوسط قطر المستعمرة بغض النظر عن الوسط المستخدم. تباين نمو الفطر *interne A. عند مدى حراري 15-35* م، سجل اعلى معدل نمو عند 25°م وتوقف عند 35°م. تراوح متوسط أبعاد السبورات الكونيدية والبكنيديا في العزلات 10-8A و19-8A من 20.02*7.5 ميكرون أو عند 25°م وتوقف عند 35°م. تراوح متوسط أبعاد السبورات الكونيدية والبكنيديا في العزلات 10-8A و10-8A من 20.02*7.5 ميكرون أو عند 25°م وتوقف عند 35°م. تراوح متوسط أبعاد السبورات الكونيدية والبكنيديا في العزلات 10-8A و10-8A من 20.02*7.5 ميكرون أو عند 25°م ميكرون و 70.01*60 ميكرون في العزلات 11-3A و18-8A على التوالي. صنفت عزلات الفطر الى أربع مجاميع و15 سلالة اعتمادا على ضراوتها وفوعتها المرضية. اظهرت السلالة الأولى ضراوة وفوعة عالية على جميع الأصناف التفريقية، بينما المتكشفت السلالات الأخرى عن طيف متغاير من الفوعة. تميزت السليمانية بتنوع وراثي عالي وضمت تسع سلالات مختلفة تمثل 60٪ من السكان، أستكشفت السلالات الأخرى عن طيف متغاير من الفوعة. تميزت السليمانية بتنوع وراثي عالي وضمت تسع سلالات مختلفة تمثل 60٪ من السكان، أستكشفت السلالات الخرى عن طيف متغاير من الفوعة. تميزت السليمانية الملابي وسلالتين وينسبة 20.0 و21٪ على التصاليان السكان، المتكشفت السلالات الخرى عن طيف متغاير من الفوعة. تميزت السليمانيا وعقبه أربيل بخمس سلالات مختلفة تمثل 60٪ من السكان، ألبوري بغرم في ملولة 211 عن حزمة 5414 في جميع عزلات الفطر أ60٪ من السلال 4.0 وقبرما لميوا والغليمين ماليا وقل تسلسل 60 في بلالات وسلالين وينية الفل أفلوا منمام مكن ملول في المالى 4.0 في مليل من المل المال معال عرومة أو

كلمات مفتاحية: لفحة الأسكوكايتا، Cicer arietinum، سلالات فسلجية، تشخيص جزيئي، امراض فطرية.

Received:22/3/2021, Accepted:15/6/2021

INTRODUCTION

Chickpea (Cicer arietinum L.) is a native Asian pules plant that is grown as the most important cash and food security crop in the drylands of West Asia and Indian subcontinent (30). It is an important protein source in many parts of central Asia and Africa, and it is thought to be one of the first grain legumes domesticated in the old world, having originated in southeastern Turkey and northern Syria (1). It can be used as a common carbohydrate and protein source, making it more cost-effective and affordable for while developing countries maintaining nutritional quality (29). From 2008 to 2017, the average annual production shares of chickpeas by region revealed that Asia acounted for 83% of the global chickpea production (16). The crop is affected by various pathogens including fungi, viruses, nematodes and other pests such as insects. Several diseases, including Ascochyta blight (AB) caused by Ascochyta rabiei, Fusarium wilt (FW) incited by Fusarium oxypsorum f sp. ciceris, and Botrytis gray mold (BGM) caused by Botrytis cinerea, limit chickpea production (35). AB, also known as chickpea blight, gram blight, ascochytosis, anthracnose, rabia or chickpea scorch, affects all above ground parts of the host plant. The disease is one of the most damaging to chickpeas, resulting in significant yield and quality losses (17). Cool, cloudy, humid, and rainy weather (15-25C° and >150 mm of annual rainfall) during the growing season promotes disease development, resulting in yield losses of up to 100%. The infection is spread by airborne spores. Fungicide can be used to control the disease in the majority of developing countries (26). The disease remains one of the most serious chickpea diseases in many parts of the world, particularly in Western Asia, North Africa and the Northwestern region of India and Pakistan (39). The recent widespread damage to chickpea cultivars released as resistant to AB suggests the presence of different races of the pathogen. Pathogenic variation has been reported in A. rabiei isolates from India, Syria, Lebanon, Pakistan, Tunisia and Israel (21, 43). The first evidence of races in A. rabiei was discovered in 1963, when the resistant Indian chickpea cultivar C12/34,

became susceptible (32). several races were held in the Indian state of Punjab according to Bedi and Aujla (9). Vir and Grewal, (44) used five differential cultivars to identify races I and 2 and one biotype of race-2 in India, and was later confirmed using this three differential cultivars (19). Qureshi and Alam (37) discovered five races of A. rabiei in Pakistan, whereas Reddy et al. (40) reported that some resistant chickpea genotypes developed in Syria were susceptible in Pakistan, suggesting differences between the existence races of A. rabiei in Pakistan and Syria. Despite significant variation in the aggressiveness of the isolates, as well as variation in the size of pycnidia, colony growth rate and sporulation in vitro, Gowen, et al. (18), found no evidence for the existence of races. By inoculating a set of six differential cultivars, six pathogenic groups or races were identified. All of the differentials in Syria, Lebanon and Italy were susceptible to race 6, suggesting that the three countries share a common race (36). Chongo et al. (13) used eight differentials to identify fourteen races of A. rabiei from forty isolates in Canada, whereas 13 differentials were used to identify only five races of the pathogen in Iraq (4). Fungal identification using traditional methods requires long time, effort, and knowledge of classical taxonomy knowledge and may result in unreliable results due to identification issues since it requires experts and specialists with experience (11). A wide range of molecular methods, based on genotypic characteristics, are increasingly becoming valuable tools in all aspects of fungal diagnostics, providing fast, highly specific, effective, and potentially more accurate results. Nucleic acid-based methods enable the identification of closely related species as well as fungal races [40]. The current study was conducted to identify the physiological specialization in A. rabiei isolates from IKR, Iraq, as well as to detect any genetic variation among pathogen isolates. **MATERIALS AND METHODS**

Isolation and purification of *A. rabiei* **isolates:** Infected ABD samples collected from chickpea stem, branches, pod, and seeds were used for isolation *A. rabiei*. Samples were collected during 2017-2019 from 259 fields in 29 districts of Sulaymaniyah, Garmian, Halabja, and Hawler provinces IKR, Iraq. Chickpea seed meal dextrose agar (CSMDA) was used for isolation and purification of the isolates (41). The infected samples were cut into 1 cm pieces, surface sterilized with 0.5% NaOCl for 2-3 min., rinsed three times in sterilized distilled water(SDW), dried with sterile filter paper for one minute and plated on CSMDA. Plates were incubated upside down at 20°C. After four days, a cork borer used to cut a 5 mm dia. agar plug from the margin of an actively growing culture and transfer it to CSMDA plates (10). Inoculated plates were incubated at 20±2°C for 2 weeks (46). Each isolate was purified as single spore culture and incubated for two weeks at 22±2°C. Pycnidial fungi were tentatively identified using Sutton key. A. rabiei single spore isolate colonies were preserved on CSMDA slants at 4°C as short term storage for further studies(22). While long term preservation was conducted by placing the pycnidiospores in a solution of $5mgL^{-1}$ skim milk powder dissolved in 25% glycerol and water and stored in cryofreezer at -80°C until used for DNA extraction.

Cultural and Morphological Characteristics All the isolates. were morphologically examined visually or with microscope including colony morphology, conidia and pycnidia shape and size, and mycelial growth. Effect of eight culture media, CSMDA, Oat meal agar (OMA), Potato dextrose agar (PDA), Corn meal agar (CMA), Czapex-Dox+lignocellulose agar (COMPLETE), Nutrient Agar (NA), Sabouraud Dextrose Agar (SDA), and MacConkey agar (MA) were studied on growth rate, colony color and zonation patterns of different A. rabiei isolates, While CSMDA, OMA and PDA were only used to study the conidiospore and pycnidium shape and size after 20 days of incubation at 25°C. A 5mm diameter disc of 7 days old culture inoculum of each isolate was transferred to 90mm petri plates center. The inoculated plates were arranged in complete randomized design (CRD)with three replicates and incubated at 20±2°C. Growth rate of each isolate was studied at 15, 20, 25, 30 and 35°C on CSMDA. Three petri plates were used for each treatment with three replicates. Mean radial mycelium growth in centimeters was measured from the center of the inoculum disc

to the tip of the hypha in four directions after 20 days of inoculation.

Phenotyping of A. *rabiei* isolates

Pathogenicity of A. rabiei isolates was conducted in a greenhouse covered with 200µm thick polyethylene plastic film in Bazian to pathotype the isolates. Ten chickpea differentials provided by ICARDA used to characterize physiological races of the isolates according to their virulence (41). Ten seeds of each genotype were sown in plastic pots filled with 12 kg/pot of sterilized sandy loam. The seedlings were kept in a greenhouse for 14days before inoculation. Twenty-three A. rabiei isolates were assessed for virulence variation in a greenhouse at 20/25°C. 14 daysold culture of each isolate grown on CSMDA at 20±2°C was flooded with 10ml of sterile water and disrupted with a sterile glass rod to release the conidia. The conidial suspension was filtered through three layers of cloth cheese to remove mycelia fragments, and the spore concentration was adjusted to 1×10^{6} /ml (22). The seedlings were artificially inoculated with the spore suspension until runoff then covered with transparent polyethylene bags for 48h to maintain high humidity and promote infection. Control treatment was sprayed with sterile distilled water. Plants were kept under glass house conditions at 21-25°C and mist irrigated each 1h for 30sec to keep the humidity at 70-80%. Pots were arranged in randomized complete block design (RCBD) with three replicates. Blight severity was assessed after 21 days of inoculation using 0-9 scale described by Udupa et al. (43). The different classified into isolates were pathotypes as follows. Av=Avirulent (1-40%), (41-50%), MV=Moderately virulent V=Virulent (51-60%), HV=High virulent (61-100%). While cultivars rated based on their mean severity: R=Resistant (1-15%),(16-40%), MS=Moderately T=Tolerant Susceptible (41-50%), S=Susceptible (51-75%).

Genotyping of A. rabiei isolates DNA extraction

Mycelial inoculum from pure slant of *A. rabiei* isolates was used to inoculate CSMDA plates supplemented with streptomycin sulfide (250ppm). A loop of mycelium was transferred to Eppendorf PCR tubes after 10day incubation period at 25°C (1.5 ml) or by flooding the plates with sterilized normal saline (0.9% NaCl) before pipetting the suspension into a clean sterile PCR tube, spinning and discarding the supernatant before using the pellet. The genomic DNA of 35 samples was extracted according to the Addbio DNA extraction protocol from fungal mass growing in 2-YEG broth using the prime prep genomic DNA extraction kit according to NORGEN kit fungi genomic DNA isolation kit.

DNA Quantification and purification

DNA concentration and purity was determined using spectrophotometer. The extracted DNA was placed on the device lens and measured in a double beam UV-visible spectrophotometer. DNA samples with an OD 260/280 ratio of 1.8 2.0. The extracted nucleic to acid concentrations ranged from 66 to 533 ng/l, with (1.5-2.0 ng) purity. The extracted DNA was run on 1% agarose gel to confirm its amount. 81 of extracted DNA was mixed with 2 1 of 6x loading buffer before being electrophoresed in 1% agarose gel and stained with Ethidium bromide. The bands were visualized with UV light, and photos were taken with a gel documentation system (Sygene, UK) The DNA concentration was measured in Nanograms per liter (ng/l), as described by (14).

Agarose Gel Electrophoresis

By combining 100mL of 10X TBE with 900mL of ddH2O in a suitable container, the 10X TBE buffer was diluted tenfold to the prepare 1X TBE buffer. Followed the instructions, a one percent agarose gel was prepared for electrophoresis, and DNA was loaded onto the gel (45).

Amplification of internal transcribed spacer (ITS) region (rDNA Analysis)

A. rabiei isolates were used for rDNA analysis, nuclear ribosomal, internal transcribed spacer ITS Sequencing–primer ITS1(TCCGTAGGTGAACCTGCGG) and ITS4 (TCCTCCGCTTATTGATATGC), were used to amplify approximately 540bp of ITS1, 5.8S ribosomal gene, and ITS2 region from all the isolates using 2xEasyTaq master mix.=

Phylogenic analysis

About 12µl (35-55ng/µl) of *A. rabiei* PCR products were amplified by both ITS1 and

ITS4 primers, and 5µl of each primer was placed in a 0.5ml Eppendorf tube separately, sealed tightly with parafilm and sent to Macrogen Co. South-Korea for sequencing. Capillary DNA analyzer was used to purify and sequence the product (ABI3730XL; Applied Biosystems, Japan). The obtained nucleotide sequences were then deposited in the GenBank databases (https://www.ncbi.nlm.nih.gov). Clustal W2 was used to generate phylogenic trees (27). (https://.www.ebi.ac.uk/Tools/phylogeny/.sim

ple-phylogeny).

RESULTS AND DISCUSSION Cultural and morphological characteristics of *A. rabiei* isolates

Fifty-one A. rabiei isolates were isolated from chickpea samples collected from 141 infected fields from 29 districts in Sulaimania, Garmian, Halabja, and Hawler across IKR. Comparison of A. rabiei isolates based on macroscopic and microscopic criteria reveal significant variation among 32 tested isolates. Cultural characteristics single spore culture isolates of A. rabiei differed on various media types, including CSMDA, OMA, PDA, CMA, and Czapx. In general, the isolates' colonies were flat and submerged, with sparse mycelium. As the pathogen grows, colony color changes in different isolates. Mycelial colonies were dense, grow slowly and initially appear creamy, then take a variety of colors depending on media type. Ability of the isolates to produce chlamydospores has been attributed to colony color variation, with numerous chlamydospores the culture turns to black. Mycelium of majority isolates were pale cream, beige, buff beige, and white buff at first, then darkened and varied in intensity at colonies' margins.

Macroscopic characteristics of *A. rabiei* **isolates:** Table 1 shows significant differences among *A. rabiei* isolates in morphological characteristics such as colony color, mycelial color, presence of grooves, carrot-red spore mass, zonation, conidia and pycnidia size, and mycelial growth grown on CSMDA. The isolates were divided into six groups based on colony colors, which ranged from light brown (1 isolate) to black (1 isolate), with 5 brown, 1 greenish white, 21 dark brown, and three blackish brown. The majority of colony center colors were fluffy, flossy, or downy olive green, with only one isolate being velvet brown and two being semi-velvets. Mycelium colors varied greatly among the isolates, with some being gravish white (10 isolates), others being grayish beige (6 isolates), beige (11 isolates), buff beige (3 isolates), and creamy aspect (2 isolates). Pycnidia color ranged from brown (7 isolates) to black (1 isolate), with 21 isolates exploring dark brown color and 3 isolates exploring blackish brown (Table 1). On OMA, A. rabiei isolates explored differences in morphological characters. The majority of isolates were greenish brown (21 isolates), greenish white (1 isolate), and greenish olive (3 isolates), with only two isolates being gravish white and five being brown. All the colonies had fluffy greenish white centers. Mycelia of all isolates were intensely colored, ranging from creamy to white buff. (Fig.1). Pycnidia color ranged from brown (3 isolates) to dark brown (29 isolates). The majority of the colonies have concentric zonation with scattered pycnedia and grooves.Significant differences in morphological characteristics were detected between A. rabiei isolates on PDA. The isolates were divided into three groups based on colony colors, ranged from gravish white (3 isolates) to black (26 isolates), with only three isolates showed dark brown. The majority of colony center colors ranged from downy gravish white (28 isolates) to downy gravish (2 isolates) or velvet brown (1 isolate) to velvet dark brown (lisolate) (Fig.1). Mycelia color ranged from creamy (2 isolates) to beige (12 isolates) or creamy beige (12 isolates) and creamy aspect (2 isolates). Except two isolates that show dark brown color, all pycnedia shoed black color. Zonation has been observed in all the isolates and groves as well present in most of the isolates (Fig1). On CMA isolates colonies are distinguished by dark olive green and beige color, presence of downy or fluffy in the colony center in beige to gray, absence of grooves in most isolates, appearance of colonies surface almost smooth or velvet or semi-velvet shape, and scattering of pycnidia on colony surface.

Table 1. Morphology and culture characteristics of various Ascochyta rabiei isolates on
CSMDA at 25°C after 20 days

Iso.	Colony color	Center color	Pycnidi a color	Mycelial color	Myc. Inte.	Presence of grooves	Carrot-red spore mass	Zonation
AS-1	Dark brown	Fluffy or flossy or downy olive green	Dark brown	Creamy aspect	+++	Presence from the center towards the edge Radially furrowed	Presence or appears	Concentric zones
AS-2	Light brown	Velvet brown	brown	Beige	++	Presence on the edge	Absent	Concentric zones
AS-3	Dark brown	Semi- velvet	Dark brown	Creamy aspect	+	Presence from the middle towards the edge	Absent	Concentric zones with scattered pycnidia
AS-4	Greenis h brown	Fluffy or flossy or downy grayish white	brown	Beige	+++	Presence from the center towards the edge Radially furrowed	Absent	Concentric zones
AS-5	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Presence from the center towards the edge less dense	Absent	Concentric zones with scattered pycnidia
AS-6	Brown	Fluffy or flossy or downy grayish white	brown	Beige	+++	Presence from the middle towards the edge	Absent	Concentric zones with scattered pycnidia
AS-7	Brown	Fluffy or flossy or downy grayish white	brown	Grayish beige	+++	Presence on the edge	Absent	Concentric zones
AS-8	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones with scattered pycnidia
AS-9	Blackish brown	Fluffy or flossy or downy grayish white	Blackish brown	Grayish white	+++	Presence from the center towards the edge Radially furrowed	Absent	Concentric zones
AS-10	Blackish brown	Fluffy or flossy or downy grayish white	Blackish brown	Grayish beige	+++	Presence from the center towards the edge Radially furrowed	Presence or appears	Concentric zones with scattered pycnidia
AS-11	Blackish brown	Fluffy or flossy or downy grayish white	Blackish brown	Beige	+++	Presence from the middle towards the edge	Presence or appears	Concentric zones with scattered pycnidia
AS-12	Brown	Fluffy or flossy or downy grayish white	brown	Buff beige	+++	Without grooves the surface of the colony is smooth	Presence or appears	Concentric zones with scattered pycnidia
AS-13	Dark	Semi- velvet	Dark	Grayish	+++	Presence from the middle	Absent	Concentric zones

Iraqi Journal of Agricultural Sciences -2022:53(2):297-314

Al-Maaroof & Salih

	brown		brown	white		towards the edge less dense		with scattered
AS-14	Brown	Fluffy or flossy or downy grayish white	Brown	Grayish white	+++	Presence from the middle towards the edge less dense	Absent	Concentric zones with scattered pycnidia
AS-15	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Buff beige	++++	Presence from the center towards the edge Radially furrowed	Presence or appears	Concentric zones
AS-16	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish white	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones with scattered pycnidia
AS-17	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish white	+++	Presence from the middle towards the edge	Absent	Concentric zones with scattered pycnidia
AS-18	Black	Fluffy or flossy or downy grayish white	Black	Grayish white	+++	Presence from the center towards the edge Radially furrowed	Absent	Concentric zones with scattered pycnidia
AS-19	Brown	Fluffy or flossy or downy grayish white	Brown	Grayish white	+++	Presence from the center towards the edge Radially furrowed	Presence or appears	Concentric zones with scattered pycnidia
AS-20	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Buff beige	+++	Presence from the center towards the edge Radially furrowed	Presence or appears	Concentric zones with scattered pycnidia
AS-21	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones
AS-22	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones
AS-23	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish white	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones
AS-24	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones
AS-25	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones
AS-26	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish white	+++	Presence from the center towards the edge Radially furrowed	Absent	Concentric zones with scattered pycnidia
AS-27	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones with scattered pycnidia
AS-28	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	+++	Without grooves the surface of the colony is smooth	Absent	Concentric zones with scattered pycnidia
AS-29	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Beige	++++	Without grooves the surface of the colony is smooth	Absent	Concentric zones with scattered pycnidia
AS-30	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish white	+++	Presence from the middle towards the edge	Absent	Concentric zones
AS-31	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish beige	+++	Presence from the middle towards the edge less dense	Absent	Concentric zones with scattered pycnidia
AS-32	Dark brown	Fluffy or flossy or downy grayish white	Dark brown	Grayish beige	+++	Presence from the middle towards the edge less dense	Absent	Concentric zones with scattered pycnidia

Colonies grown on Czapx were distinguished by dark color in general, while some isolates emerged in complete beige. Presence of grooves strongly was the most distinctive feature of the developing isolates which makes the colony surface wrinkled. The presence of pycnidia scattered on the colony surface especially at the edge, as well as the absence of carrot-red spore mass and the solid or compact colonies consistency, indicates zonation in most of the colonies (Fig 1). Cultural characteristics could not be linked to pathogenic variability. In this regard, molecular techniques may be useful in further confirming the association and correlation.



Fig.1. Colony morphology of different *A. rabiei* isolates grown on a. OMA, b. PDA, c. CMA and d. Czapx DA at 25°C after 20d

Effect of culture media on mycelial growth of *A. rabiei* isolates

Table 2 results shows that all the tested culture media significantly supports the mycelial growth of A. rabiei isolates to varying degrees at P \leq 0.05 after 20 days of incubation at 25°C. the mean colony diameter on the media ranged from 2.00cm on MAC to 8.04cm on OMA. Mycelial growth mean rate of the isolates on CSMDA (7.35 cm) significantly outperformed all other media's, followed by OMA (7.24cm) and Czapx (6.49cm), while the lowest growth rate was observed on MAC (2.67 cm) and NA(3.33cm). Variation in colony diameter was also observed among A. rabiei isolates on the used media. Isolate AS-28 significantly surpassed all other isolates in mean colony diameter (5.93cm) at P \leq 0.05 despite the used media followed by isolate AS-11. While the lowest colony diameter mean was detected in isolate AS-27 (5.16cm) followed by isolate (5.22 cm)without any significant AS-5 differences (Table 2). High significant differences in growth rate among A. rabiei isolates were detected on CSMDA. Isolate AS-6 (7.99cm) significantly surpassed all other isolates at $P \le 0.05$, except AS-11. While the lowest growth was detected in AS-19 (6.73cm). Colony diameter ranged from 6.20-8.04cm on OMA. Isolate AS-12 significantly surpassed all other isolates except AS-28.

CSMDA is clearly better suited media for vegetative growth of A. rabiei than others, that is why widely used for multiplication and maintenance of the isolates during the study. Czapx and CMA also produced moderate mycelial growth, whereas OMA produced comparable maximum growth. The presence of chickpea seed as one of main ingredients in CSMDA which provides additional nutrients requirement for pathogen growth and development, may explain the high mycelial growth rate of A. rabiei. Selecting is the suitable culture media for pathogen growth, sporulation, and cultural characteristics is crucial. culture media showed significant impact on A. rabiei growth, pycnidia and conidia formation, and sporulation during this study. Several studies reported similar results in various fungi (31). CSMDA and OMA were found to be the best media for A. rabiei mycelial growth. while, PDA, moderately supported mycelial growth of the fungal isolates. This could be explained by differences in the concentrations of C, N, and other nutrients in each medium. Fresh media preparations from chickpea, oat meal, corn meal, and potato contained high concentrations of C and N sources, which promote the mycelial pathogen's maximum growth. Previous studies with various fungi have also refer to the effect of high C and N

concentrations in inducing vegetative and abundant mycelia growth (31).

Microscopic characteristics of *A. rabiei* isolates

Effect of culture media on conidia and pycnedia of the isolates

Conidia of A. rabiei isolates in general was hyaline, oval to oblong, and straight to slightly bent at one or both ends. Under compound microscope, they were single-celled, occasionally two-celled, and rounded at both ends. They grew on short conidiophores embedded in mucilage in a cream-pink to light-tan mass. The conidia are released from a wet mount of mature pycnidium. At moist conditions, pycnidia materials absorbs water and swollen, causing conidia to ooze out the ostiole in a slimy mass. The pycnedia is pearshaped with a single opening called ostiole, it contains numerous hyaline unicellular and occasionally bicellular spores, Conidia and pycnedia morphology match the original described A. rabiei stock culture. High significant variations in conidia and pycnedia dimensions were observed among A. rabiei isolates on different media. CSMDA, OMA, and PDA affected conidia and pycnedia dimension differently. The highest effect was recorded in PDA, the mean conidia and pycnedia dimension $(43.9*18.9\mu m)$ and (284.3*196.6µm) significantly outperformed followed other media. by OMA all $(12.7*5.0\mu m)$ and $(82.0*54.4\mu m)$ respectively (Table 3). Conidia and pycnedia size were high on PDA, the mean sizes of isolates (670.91 µm and 20130.9 µm) being 1394% and 680% larger than those on OMA (48.4 μm and 2959.8 µm) respectively and 1600% and 711% larger than those on CSMDA (41.93um and 2831.2µm) respectively.

Table 2. Growth rate of different A. rabiei isolates collected from various chickpea fields inIKR on various media type at 25°C after 20 days.

Isolata	Colony Diameter (cm)								
Isolate	CSMDA	OMA	PDA	CMA	Czapx	N.A	S.A	Mac.	Mean
AS-1	7.7 ^{a.g}	7.02 ^{1.af}	6.35 ^{ah.ax}	6.23 ^{ak.bc}	6.59 ^{z.as}	3.22 ^{co.cu}	4.42 ^{cb.ck}	3.43 ^{cm.cr}	5.62 ^{b.d}
AS-2	7.35 ^{d.q}	6.37 ^{ah.ax}	4.97 ^{bt.cc}	6.49 ^{ae.au}	7.03 ^{k.ae}	3.37 ^{cm.cs}	5.67 ^{bc.bp}	3.34 ^{cm.ct}	5.57 ^{b.f}
AS-3	7.43 ^{b.n}	6.97 ^{m.ag}	5.3 ^{bk.bw}	6.34 ^{ah.ax}	7.02 ^{1.af}	3.83 ^{ck.cn}	4.92 ^{bt.ce}	2.11 ^{dd.de}	5.49 ^{c.1}
AS-4	7.35 ^{d.q}	7.63 ^{a.j}	5.25 ^{bl.by}	6.09 ^{aq.bh}	6.70 ^{u.an}	3.38 ^{cm.cs}	4.28 ^{cg.ck}	2.33 ^{cz.de}	5.38 ^{e.1}
AS-5	7.12 ^{g.ab}	7.12 ^{g.ab}	5.28 ^{bl.bx}	5.97 ^{at.bi}	6.71 ^{s.an}	2.92 ^{cq.cy}	4.68 ^{by.ch}	2.00 ^{de}	5.22 ^{1.m}
AS-6	7.99 ^{a.b}	7.64 ^{a.i}	5.07 ^{bq.ca}	6.17 ^{am.be}	6.44 ^{af.av}	2.90 ^{cq.cz}	5.59 ^{bf.br}	2.02 ^{de}	5.48 ^{c.j}
AS-7	7.27 ^{f.v}	6.68 ^{v.ap}	5.70 ^{ba.bo}	6.26 ^{ai-bb}	5.42 ^{bi.bt}	3.03 ^{cq.cy}	5.37 ^{bk.bu}	3.03 ^{cq.cy}	5.34 ^{g.m}
AS-8	7.62 ^{a.k}	7.61 ^{a.k}	4.53 ^{ca.ci}	6.69 ^{u.ao}	6.52 ^{ac.au}	3.18 ^{co.cw}	5.01 ^{br.ca}	2.92 ^{cq.cy}	5.51 ^{c.h}
AS-9	7.05 ^{j.ae}	7.19 ^{f-x}	5.29 ^{bl.bw}	6.66 ^{w.aq}	6.13 ^{an.bh}	3.2 ^{co.cv}	4.83 ^{bu.cg}	2.28 ^{db.de}	5.31 ^{h.m}
AS-10	7.08 ^{h.ad}	7.23 ^{f.x}	5.58 ^{bh.bs}	6.52 ^{ac.au}	6.18 ^{am.be}	3.02 ^{cq.cy}	4.56 ^{ca.ci}	2.77 ^{ct.dc}	5.37 ^{f.m}
AS-11	7.87 ^{a.e}	7.30 ^{e.r}	5.27 ^{bl.bx}	6.34 ^{ah.ax}	6.64 ^{y.as}	3.65 ^{cl.cp}	6.17 ^{am.bg}	2.88 ^{cq.da}	5.76 ^{Ab}
AS-12	7.38 ^{c.p}	8.04 ^a	5.36 ^{bk.bu}	6.66 ^{w.aq}	6.50 ^{ad.au}	3.43 ^{cm.cq}	4.66 ^{bz.ch}	2.46 ^{cy.cd}	5.56 ^{b.f}
AS-13	7.42 ^{b.o}	7.23 ^{f.x}	5.33 ^{bk.bv}	6.56 ^{aa.as}	6.11 ^{ap.bh}	3.92 ^{cj.cm}	5.58 ^{bg.bs}	2.61 ^{cw.dd}	5.60 ^{b.d}
AS-14	7.20 ^{f.y}	7.16 ^{g.z}	5.15 ^{bo.bz}	5.32 ^{bk.bv}	6.27 ^{ai.bb}	3.37 ^{cm.cs}	4.77 ^{bv.ch}	2.87 ^{cq.da}	5.26 ^{k.m}
AS-15	7.33 ^{d.q}	7.10 ^{h.ac}	5.35 ^{bk.bv}	5.88 ^{av.bk}	6.37 ^{ah.ax}	2.82 ^{cs.db}	4.51 ^{ca.ci}	2.84 ^{cr.db}	5.27 ^{j.m}
AS-16	7.47 ^{a.n}	7.27 ^{f.u}	4.82 ^{bu.cg}	6.56 ^{aa.as}	6.37 ^{ah.ax}	3.02 ^{cq.cy}	4.92 ^{bt.ce}	3.40 ^{cm.cs}	5.48 ^{c.j}
AS-17	7.07 ^{i.ae}	6.5 ^{ad.au}	5.62 ^{be.bq}	6.59 ^{z.as}	6.71 ^{s.an}	3.17 ^{co.cw}	6.70 ^{t.an}	2.30 ^{da.de}	5.58 ^{b.e}
AS-18	7.62 ^{a.j}	7.48 ^{a.n}	6.06 ^{as.bh}	6.24 ^{ak.bc}	6.41 ^{ag.av}	4.22 ^{ch.cl}	4.78 ^{bv.ch}	2.48 ^{cy.cd}	5.66 ^{b.c}
AS-19	6.73 ^{r.am}	7.26 ^{f.v}	4.95 ^{bt.cc}	6.80 ^{p.ak}	6.79 ^{q.al}	3.68 ^{cl.co}	4.7 ^{bx.ch}	3.37 ^{cm.cs}	5.45 ^{c.g}
AS-20	7.43 ^{b.n}	7.24 ^{f.w}	5.47 ^{bi.bt}	6.32 ^{ai.ay}	6.68 ^{v.ap}	4.35 ^{cd.ck}	4.8 ^{bu.ch}	2.97 ^{cq.cy}	5.66 ^{b.c}
AS-21	7.52 ^{a.m}	6.98 ^{1.ag}	4.92 ^{bt.ce}	6.07 ^{ar.bh}	6.84 ^{o.al}	2.82 ^{cs.db}	5.22 ^{bm.bz}	2.00 ^{de}	5.29 ^{i.m}
AS-22	7.67 ^{a.h}	7.67 ^{a.h}	5.38 ^{bj.bu}	5.96 ^{au.bj}	6.38 ^{ah.aw}	3.37 ^{cm.cs}	4.53 ^{ca.ci}	2.62 ^{cv.dd}	5.45 ^{d.k}
AS-23	7.02 ^{1.af}	6.20 ^{am.be}	5.79 ^{ax.bm}	6.17 ^{am.bf}	6.51 ^{ad.au}	3.15 ^{co.cw}	5.20 ^{bn.bz}	2.50 ^{cx.de}	5.32 ^{h.m}
AS-24	6.83 ^{0.aj}	7.94 ^{a.c}	4.33 ^{ce.ck}	6.7 ^{t.an}	6.66 ^{w.aq}	3.32 ^{cn.ct}	5.72 ^{az.bo}	3.23 ^{co.ct}	5.59 ^{b.d}
AS-25	7.50 ^{a.n}	7.18 ^{f.y}	5.25 ^{bl.by}	7.17 ^{f.z}	6.30 ^{ai.az}	3.00 ^{cq.cy}	4.66 ^{bz.ch}	2.77 ^{ct.dc}	5.48 ^{c.j}
AS-26	7.29 ^{e.s}	7.75 ^{a.f}	4.72 ^{bw.ch}	6.50 ^{ad.au}	6.23 ^{ak.bc}	3.30 ^{cn.ct}	4.40 ^{cc.ck}	2.51 ^{cx.de}	5.34 ^{g.m}
AS-27	7.43 ^{b.n}	7.20 ^{f.y}	4.50 ^{ca.cj}	6.25 ^{aj.bc}	6.21 ^{al.bd}	3.28 ^{cn.ct}	4.32 ^{cf.ck}	2.11 ^{dd.de}	5.16 ^m
AS-28	7.36 ^{c.q}	7.89 ^{a.d}	5.82 ^{aw.bl}	6.72 ^{r.am}	7.15 ^{g.aa}	3.25 ^{cn.ct}	6.10 ^{aq.bh}	3.13 ^{co.cw}	5.93 ^a
AS-29	6.92 ^{n.ah}	7.30 ^{e.r}	4.90 ^{bt.cf}	6.55 ^{ab.at}	6.26 ^{ai.bb}	3.10 ^{co.cw}	5.44 ^{bi.bt}	2.50 ^{cx.de}	5.37 ^{f.1}
AS-30	7.35 ^{d.q}	6.58 ^{z.as}	4.93 ^{bt.cd}	6.70 ^{t.an}	6.65 ^{x.ar}	3.27 ^{cn.ct}	5.75 ^{ay.bn}	2.63 ^{cu.dd}	5.48 ^{c.1}
AS-31	7.25 ^{f.w}	7.57 ^{a.1}	5.00 ^{bs.cb}	6.27 ^{ai.ba}	6.59 ^{z.as}	4.05 ^{ci.cl}	5.68 ^{bb.b}	2.87 ^{cq.d}	5.66 ^{b.c}
AS-32	7.63 ^{a.j}	7.28 ^{e.}	5.08 ^{bp.ca}	6.11 ^{ao.bh}	6.37 ^{ah.ax}	3.08 ^{cp.cx}	5.63 ^{bd.b}	2.2 ^{dc.de}	5.42 ^{d.1}
Mean	7.35 ^a	7.24 ^b	5.23 ^e	6.37 ^d	6.49 ^c	3.33 ^g	5.11 ^f	2.67 ^h	5.47

* Each no. is a mean of three replicates. ** Numbers followed by the same symbols significantly are not different at 0.05 level. Despite the media, isolate AS-11 had the largest conidial dimension $(21.8*9.0\mu m)$ and significantly and $296.61 \mu m$, and isolate AS-9, with $20.1*9.5 \mu m$ and $290.59 \mu m$ respectively. Outperformed all other isolates except isolate While isolate AS-19 ($202.29\mu m$) and isolate

AS-5 $(19.0*7.6\mu m)$ had the smallest conidial size. On the other hand, the largest means of pycnedia dimension (140.7*93.6µm) and size (20565.1µm) was recorded on isolate AS-18 and significantly outperformed all other isolates, followed by isolate AS-2 with dimension $(123.9*86.9\mu m)$ and size $(14581.5\mu m)$, and isolate AS-9 with the lowest dimension and size $(70.81*47.9\mu m)$ and 4143.5 µm respectively. Conidial dimensions on CSMDA ranged from $9.5-12.1*3.5-4.4\mu m$. The maximum conidia size recorded in AS-20 (53.6µm) which significantly outperformed all other isolates, and the smallest size was found in AS-5 (33.92µm). Pycnidia dimensions ranged from 43.9-86.5* 27.4-58.5µm on CSMDA. The highest pycnidia size was recoded in isolate AS-4 (5061.9 μ m), which significantly surpassed all other isolates, while the lowest size was found in isolate AS-9 (1206.0µm). Conidia dimensions ranged from 8.6-12.7*3.7-5.2µm on OMA. AS-20 recorded Τ

the highest conidia size (63.48µm) while AS-26 showed the lowest size $(39.17\mu m)$. while pycnidia dimension ranged from 47.9-82.0*33.2-55.7µm. the maximum pycnidia size was detected in isolate AS-12 (4464 μ m) and the minimum size in isolate AS-4 (1607.7µm). Conidia and pycnedia dimensions varied greatly on PDA compared to other media's. Conidia size ranged from 36.3-43.9*13.8-19.7µm. The largest size (828.31µm) recorded in isolate AS-11, while the smallest size was found in AS-19 (506.73 *µm*). Pycnidia dimensions ranged from 114.1- $284.3*81.9-196.6\mu m$, the largest size observed in AS-18 (55905.1 μ m) and the lowest size in AS-9 (9356.1 μ m). It is not possible to distinguish A. rabiei races based on colony color and morphological traits. However, morphological variation can provide preliminary variation among the isolates. because these variations did not

Fable 3. Conidia and Pycnedia dimensions of different A. rabiei isolates collected from var	ious
chickpea fields in IKR on various media at 25°C.	

Isolate	CSMDA		O	MA	PDA		
	Conidia (µm)	Pycnedia (µm)	Conidia (µm)	Pycnedia (µm)	Conidia (µm)	Pycnedia (µm)	
AS-1	10.2 ^{w-ae} *3.7 ^{z-ac}	78.3°-t*52.1 ^{n-r}	10.9 ^{o-ad} *3.7 ^{z-ac}	70.3°-z*50.6 ^{n-t}	37.5 ^{k-m} *16.0 ^{l-n}	182.4 ^{d-f} *135.5 ^{c-e}	
AS-2	9.7 ^{ad-af} *3.8 ^{z-ac}	82.3°p*43.9°-z	11.4 ⁿ⁻ x*4.0 ^{u-ac}	71.7°-z*48.8°-v	38.5 ^{g-k} *15.8 ^{mn}	217.9 ^{bc} *168.0 ^b	
AS-3	10.3v- ^{ae} *3.9 ^{v-ac}	69.0°-z*37.6 ^{t-ab}	10.80-ad*3.9 ^{v-ac}	76.2°-v*45.8 ^{n-z}	39.8 ^{c-g} *16.9 ^{i-k}	198.9 ^{c-e} *144.9 ^c	
AS-4	10.9 ^{o-ad} *4.1 ^{t-ac}	86.5°*58.5 ⁿ	11.30-y*4.0 ^{u-ac}	48.5 ^{aa-ad} *33.2 ^{y-ab}	39.0 ^{e-j} *16.9 ^{h-k}	130.1 ^{mn} *99.1 ^{kl}	
AS-5	9.7 ^{ad-af} *3.5 ^{ac}	67.5°-aa*44.9 ^{n-z}	10.7 ^{p-ae} *3.9 ^{u-ac}	61.6 ^{r-ab*} 35.8 ^{u-ab}	36.5 ^{lm} *15.3 ^{no}	154.3 ^{h-j} *127.8 ^{d-g}	
AS-6	10.5 ^{r-ae} *4.3 ^{r-ab}	56.9 ^{w-ad} *37.7 ^{t-ab}	10.6 ^{q-ae} *4.0 ^{u-ac}	60.4 ^{t-ad} *38.8 ^{r-ab}	39.3 ^{e-i} *17.7 ^{c-i}	201.0 ^{cd} *140.2 ^{cd}	
AS-7	11.2°-aa*4.3 ^{r-ab}	65.4 ^{p-ab} *42.0 ^{o-aa}	11.1 ^{o-ac} *4.4 ^{r-aa}	64.6 ^{p-ab} *40.4 ^{q-ab}	39.6 ^{d-g} *17.9 ^{c-f}	227.1 ^b *165.2 ^b	
AS-8	10.0 ^{z-ae} *3.95 ^{u-ac}	73.6° ^{c-x*} 53.1 ^{n-q}	10.9 ^{°-ad} *4.4 ^{r-z}	66.5 ^{p-ab} *38.3 ^{r-ab}	38.2 ^{h-k} *15.6 ^{m-o}	173.1 ^{f-h} *124.9 ^{e-h}	
AS-9	9.5 ^{ae-af} *4.1 ^{t-ac}	43.9 ^{ac-ad} *27.4 ^{ab}	11.2 ^{o-ab} *4.6 ^{q-y}	54.3 ^{y-ad} *34.4 ^{w-ab}	39.6 ^{d-g*} 19.7 ^a	114.1 ⁿ *81.9 ^m	
AS-10	9.8 ^{ac-af} *3.5 ^{ab-ac}	71.8°-z*47.2 ^{n-y}	11.3°-z*4.1t-ac	76.2°-**43.0°-aa	36.3 ^m *17.4 ^{e-j}	140.5 ^{j-m} *93.0 ^{lm}	
AS-11	10.8°-ae*3.78 ^{z-ac}	69.4 ^{o-z} *40.5 ^{p-ab}	10.7 ^{p-ae} *4.4 ^{r-aa}	47.9 ^{ab-ad} *34.0 ^{x-ab}	43.9 ^a *18.9 ^b	162.5 ^{g-i} *124.7 ^{e-h}	
AS-12	10.4 ^{t-ae} *3.8 ^{y-ac}	63.8 ^{p-ab} *33.6 ^{x-ab}	11.2°-aa*4.6°-w	82.0 ^{op} *54.4 ^{n-p}	43.6 ^a *18.3 ^{b-d}	147.8 ^{i-m} *114.9 ^{g-j}	
AS-13	10.7 ^{p-ae} *4.4 ^{q-z}	72.1 ^{°-y} *40.1 ^{q-ab}	11.2 ^{o-ab} *3.9 ^{v-ac}	60.6 ^{s-ad} *44.8 ^{n-x}	39.5 ^{e-h} *17.0 ^{h-k}	144.4 ^{i-m} *95.1 ^{lm}	
AS-14	$10.2_{v-ae} * 4.2^{t-ac}$	41.8 ^{ad} *29.4a ^{a-ab}	11.7 ^{n-t} *4.3 ^{r-ab}	72.9°-y*43.8°-z	40.3 ^{c-e} *17.1 ^{g-k}	149.9 ^{i-l} *110.2 ^{i-k}	
AS-15	10.4 ^{u-ae} *4.1 ^{t-ac}	80.8 ^{0-q} *44.9 ^{n-z}	8.6 ^{af} *5.2 ^q	73.6°-×*41.9°-aa	39.6 ^{d-h} *17.7 ^{c-h}	145.4 ^{i-m} *112.8 ^{h-k}	
AS-16	10.5 ^{s-ae -ac} *3.8 ^{w-ac}	74.9 _{0-w} *44.1 ^{0-z}	11.6 ^{n-u} *4.4 ^{r-aa}	75.5°-***51.9 ^{n-s}	41.1 ^{b-c} *18.4 ^{bc}	150.9 ^{i-k} *94.9 ^{lm}	
AS-17	10.2 ^{v-ae} *4.1 ^{t-ac}	79.7 ^{o-s} *39.4 ^{q-ab}	11.8 ^{n-s} *5.0 ^{q-s}	80.0°-r*55.7 ^{no}	41.9 ^ь *17.9с-е	131.2 ^{l-n} *95.7 ^{lm}	
AS-18	10.4 ^{t-ae} *4.0 ^{u-ac}	75.6°-**41.3 ^{p-ab}	9.8 ^{ab-af} *4.4 ^{r-aa}	62.2 ^{q-ad} *42.9 ^{o-aa}	38.2 ^{i-k} *15.7 ^{mn}	284.3 ^a *196.6 ^a	
AS-19	11.8 ^{n-r} *4.2 ^{s-ac}	65.4 ^{p-ab} *41.9 ^{o-aa}	11.5 ^{n-v} *4.4 ^{r-aa}	73.6 ^{°-x} *49.7 ^{n-u}	36.7 ^{lm} *13.8 ^p	161.5 ^{g-i} *114.6 ^{g-j}	
AS-20	12.1 ^{no} *4.4 ^{r-z}	72.2°-y*43.1°-aa	12.7 ⁿ *5.0 ^{qr}	73.8°-x*49.4 ^{n-u}	39.5 ^{e-i} *17.1 ^{h-k}	154.5 ^{h-j} *113.9 ^{g-j}	
AS-21	9.8 ^{ac-af} *3.8 ^{w-ac}	73.6°-x*36.5 ^{u-ab}	9.9 ^{ab-af} *4.5 ^{q-z}	55.0 ^{z-ad} *35.2 ^{v-ab}	40.9 ^{b-d} *16.7 ^{j-l}	147.7 ^{i-m} *105.2 ^{j-1}	
AS-22	10.1 ^{w-ae} *4.1 ^{t-ac}	67.8°-z*33.9 ^{z-ab}	11.9 ^{n-q} *4.8 ^{q-t}	68.1°-z*42.2°-aa	37.5 ^{k-m} *15.8 ^{mn}	132.7 ^{k-n} *104.1 ^{j-1}	
AS-23	10.0 ^{y-ae} *3.8 ^{x-ac}	57.2 ^{v-ad} *38.1 ^{s-ab}	11.3 ^{°-y} *4.7 ^{q-u}	67.1 ^{p-aa} *42.3 ^{o-aa}	39.7 ^{d-g} *18.8 ^b	146.9 ^{i-m} *93.5 ^{lm}	
AS-24	10.1 ^{w-ae} *3.6 ^{aa-ac}	52.7 ^{z-ad} *32.6 ^{z-ab}	11.9 ^{n-p} *4.5 ^{q-z}	68.2 ^{o-z} *36.9 ^{t-ab}	37.5 ^{k-m} *14.8°	150.2 ^{i-l} *106.5j ^{-l}	
AS-25	10.1 ^{x-ae} *3.9 ^{v-ac}	56.7 ^{w-ad} *34.5 ^{w-b}	11.6 ^{n-u} *4.6 ^{q-x}	74.4 ^{o-w} *49.3 ^{n-u}	39.4 ^{e-i} *17.2 ^{e-j}	137.2 ^{j-m} *103.8 ^{j-l}	
AS-26	11.6 ^{n-u} *4.0 ^{u-ac}	59.9 ^{t-ad} *37.3 ^{t-ab}	9.9 ^{aa-af} *4.0 ^{u-ac}	58.5 ^{u-ac} *40.4 ^{p-ab}	37.8 ^{j-l} *17.0 ^{h-k}	180.4 ^{e-g} *120.8 ^{f-i}	
AS-27	10.6 ^{r-ae} *4.4 ^{r-aa}	65.1 ^{p-ab} *39.1 ^{r-ab}	10.7 ^{p-ae} *4.3 ^{r-ab}	62.1 ^{q-ac} *37.4 ^{t-ab}	39.7 ^{d-g} *18.2 ^{b-d}	151.4 ^{i-k} *106.1 ^{j-l}	
AS-28	11.7 ^{n-u} *4.4 ^{r-aa}	66.8 ^{p-ab} *38.9 ^{r-ab}	11.1 ^{o-ab} *4.2 ^{t-ac}	76.3°-v*49.6 ^{n-u}	40.1 ^{c-f} *16.3 ^{k-m}	186.0 ^{d-f} *132.4 ^{c-f}	
AS-29	10.7 ^{p-ae} *3.9 ^{w-ac}	73.6°-×*41.9°-aa	11.1°-ac*4.2 ^{s-ac}	75.2°-**49.4 ^{n-u}	39.1 ^{e-j} *17.6 ^{d-i}	151.6 ^{i-k} *102.0 ^{j-l}	
AS-30	10.6 ^{q-ae} *4.0 ^{u-ac}	67.7°-z*40.3°-ab	11.4 ^{n-w} *4.4 ^{r-aa}	65.9 ^{p-ab} *37.1 ^{t-ab}	39.4 ^{e-i} *17.3 ^{e-j}	173.9 ^{fg} *114.5 ^{g-j}	
AS-31	10.9 ^{0-ad} *4.0 ^{t-ac}	73.9°-×*44.5 ^{n-z}	11.9 ^{n-p} *4.7 ^{q-v}	72.3 ^{o-y} *48.4 ^{n-w}	40.2 ^{c-f} *17.9 ^{c-g}	175.1 ^{fg} *110.1 ^{i-k}	
AS-32	10.2 ^{v-ae} *3.9 ^{w-ac}	77.3°-u*43.7°-z	10.2 ^{v-ae} *4.6 ^{q-x}	81.1 ^{o-q} *47.2 ^{n-x}	39.0 ^{f-j} *17.1 ^{f-k}	180.5 ^{e-g} *121.5 ^{f-i}	
Mean	10.5 ^C *4.0 ^C	68.2 ^B *40.8 ^C	$11.1^{B*}4.4^{B}$	68.0 ^B *43.5 ^B	39.3 ^A *17.1 ^A	164.2 ^A *117.9 ^A	

* Each no. is a mean of three replicates

** Numbers followed by the same symbols significantly are not different at 0.05 level according to Duncan's multiple test analysis

correlate with geographical origin, pathogenic variations, and disease development, as indicated in several previous studies (34). So, in the current study, the isolates were identified using a combination of different parameters and criteria (morphology, pathogenicity, and molecular) that resolved the identification, and as a result, 32 isolates were designated as A. rabiei. The differences between isolates may be important in the epidemiology of AB and may also affect the ability of isolates to create epiphytotic of the disease.

Effects of temperature on mycelial growth and colony characteristics of *A. rabiei* isolates: Mycelial growth average of *A. rabiei* isolates at various temperatures exhibited varying linear growth rates at temperatures ranges15-35°C (Table 4). The isolates showed radial mycelial growth at 15-30°C, and the growth ceased at 35°C after 20 days of incubation, even after 10 days of incubation at 25°C, all the tested isolates failed to resume growth. Mycelial growth rate increases as temperature increased up to 20°C (4.64cm), reached to maximum growth (7.35cm) at 25°C, then decreased as temperature increased and ceased at 35°C. Bedi and Aujla (9) found that at temperature higher than 31°C, growth continued but sporulation stopped on Richards agar medium. In general, isolates AS-11, AS-6, AS-32, AS-25, and AS-3 grew faster than other isolates, with no significant differences between them. While isolates AS-22, AS-19, AS-20, and AS-29 growth were slow. The current study clearly indicates the effect of temperature on mycelial growth of A. rabiei and demonstrate that different temperatures have significant effect on fungal mycelial growth. In general, the isolates grow well at temperature rang 20-25°C, and the best rapid mycelium growth occurred at 25°C. The isolates' mycelial growth rate slow below 15°C and above 30°C. When the temperature rises above 30°C, mycelial growth is terminated and completely stopped at 35°C. The discovered optimum temperature requirement for A. rabiei isolates growth was broadly consistent with previous research findings (40).

Icoloto			Growth r	ate (cm)		
Isolate	15 °C	20 °C	25 °C	30 °C	35 °C	Mean
AS-1	2.40 ^{aq-az}	4.86 ^{m-s}	7.70 ^{a-c}	3.17 ^{ac-ag}	0 ^{be}	3.63 ^{b-f}
AS-2	2.43 ap-ay	4.70 ^{n-x}	7.35 ^{c-j}	3.16 ac-ah	0 ^{be}	3.53 ^{d-h}
AS-3	2.52 an-ax	5.12 ^{m-o}	7.43 ^{b-i}	3.19 ac-af	0 ^{be}	3.65 ^{a-e}
AS-4	2.18 ^{aw-bc}	4.98 ^{m-q}	7.35 ^{c-j}	2.77 ^{af-ar}	0 ^{be}	3.46 ^{e-j}
AS-5	2.22 ^{av-bc}	4.29 ^{x-z}	7.12 ^{f-1}	2.72 ^{ai-at}	0 ^{be}	3.27 ^{j-m}
AS-6	2.72 ^{ai-at}	5.03 ^{m-p}	7.99 ^a	3.30 ac-ae	0 ^{be}	3.81 ^{ab}
AS-7	2.33 ^{as-az}	4.38 ^{u-z}	7.27 ^{c-k}	3.11 ^{ad-al}	0 ^{be}	3.42 ^{g-k}
AS-8	2.67 ^{aj-au}	4.53 ^{r-z}	7.62 ^{a-e}	3.32 ^{ab-ae}	0 ^{be}	3.63 ^{b-f}
AS-9	2.12 ax-bd	4.11 ^{z-aa}	7.05 ^{h-1}	2.74 ^{ag-at}	0 ^{be}	3.20 ^{Im}
AS-10	2.12 ax-bd	4.45 ^{s-z}	7.08 ^{f-1}	2.75 ^{ag-as}	0 ^{be}	3.28 ^{j-m}
AS-11	2.72 ^{ai-at}	5.28 ^m	7.87 ^{ab}	3.30 ab-ae	0 ^{be}	3.83 ^a
AS-12	2.32 at-ba	4.33 ^{w-z}	7.38 ^{c-i}	2.70 ai-at	0 ^{be}	3.35 ^{h-1}
AS-13	2.43 ap-ay	4.36 ^{v-z}	7.42 ^{c-i}	3.05 ^{ad-aj}	0 ^{be}	3.45 ^{f-j}
AS-14	2.35 ^{ar-az}	4.49 ^{r-z}	7.20 ^{d-k}	2.55 am-ax	0 ^{be}	3.32 ⁱ⁻¹
AS-15	2.23 ^{ay-bb}	4.68 °-x	7.33 ^{c-j}	2.82 af-aq	0 ^{be}	3.41 ^{g-k}
AS-16	2.50 an-ay	5.12 ^{mn}	7.47 ^{b-h}	2.85 ^{af-ap}	0 ^{be}	3.59 ^{d-g}
AS-17	1.98 az-bd	4.58 ^{q-y}	7.07 ^{g-1}	2.52 an-ax	0 ^{be}	3.23 ^{k-m}
AS-18	2.58 al-aw	4.68 °-x	7.62 ^{a-e}	3.03 ^{ad-ak}	0 ^{be}	3.58 ^{d-g}
AS-19	1.85 ^{bb-bd}	4.22 ^{yz}	6.73 ¹	2.77 ^{af-ar}	0 ^{be}	3.11 ^{mn}
AS-20	2.45 ao-ay	4.64 ^{p-y}	7.43 ^{b-i}	2.91 ad-an	0 ^{be}	3.49 ^{d-i}
AS-21	2.52 an-ax	4.97 ^{m-q}	7.52 ^{b-f}	2.95 ^{ad-am}	0 ^{be}	3.59 ^{d-g}
AS-22	1.73 ^{bd}	3.56 ab-ac	7.67 ^{a-d}	2.07 ^{ay-bd}	0 ^{be}	3.00 ⁿ
AS-23	2.13 ax-bd	4.48 ^{s-z}	7.02 ⁱ⁻¹	2.71 ^{ai-at}	0 ^{be}	3.27 ^{j-m}
AS-24	1.78 bc-bd	4.83 ^{n-t}	6.83 ^{kl}	2.79 af-aq	0 ^{be}	3.25 ^{k-m}
AS-25	2.60 ak-aw	5.12 ^{mn}	7.50 ^{b-g}	3.17 ^{ac-ah}	0 ^{be}	3.68 ^{a-d}
AS-26	2.58 al-aw	4.74 ^{n-w}	7.29 ^{c-j}	3.00 ^{ad-al}	0 ^{be}	3.52 ^{d-h}
AS-27	2.18 ^{aw-bc}	4.74 ^{n-w}	7.43 ^{b-i}	2.88 ae-ao	0 ^{be}	3.45 ^{f-j}
AS-28	2.60 ^{ak-aw}	4.79 ^{n-v}	7.36 ^{c-i}	3.11 ^{ad-al}	0 ^{be}	3.57 ^{d-g}
AS-29	1.88 ba-bd	4.40 ^{t-z}	6.92 ^{j-1}	2.73 ^{ah-at}	0 ^{be}	3.19 ¹⁻ⁿ
AS-30	2.63 ^{aj-av}	4.92 ^{m-r}	7.35 ^{c-j}	3.13 ^{ac-al}	0 ^{be}	3.61 ^{c-g}
AS-31	2.73 ^{ah-at}	4.40 ^{t-z}	7.25 ^{d-k}	3.33 ^{ab-ad}	0 ^{be}	3.54 ^{d-g}
AS-32	2.83 ^{at-aq}	4.80 ^{n-u}	7.63 ^{a-e}	3.73 ^{aa-ab}	0 ^{be}	3.80 ^{a-c}
Mean	2.35 ^a	4.64 ^b	7.35 ^a	2.95 ^c	0.00 ^e	3.46

 Table 4. Growth rate of different Aschochyta rabiei isolates collected from various chickpea fields in IKR on CSMDA at different temperatures after 20 days.

Similar to our findings, Bahr et al. (7) reported that A. rabiei isolates grew at very slow rate after 25°C and the mycelial growth was completely terminated after 28°C. On the other hand, Ozkilinc et al. (33), reported that origin A. rabiei isolates grew at the same rates at 15°C and 25°C with faster grow at 25°C than 15°C on PDA. This is consistent with our findings, which show that the optimal mycelial growth temperature of A. rabiei is around 25°C. Ascochyta isolates may have different growth rates at different temperatures, such as A. zeicola isolated from maize exhibited optimal growth at 24.2°C, but the optimal growth of A. stipae and A. ducisaprutii from Antarctica was at 15°C (25). The current study confirms that temperature has a significant effect on A. rabiei mycelial growth rates. The optimum growth rate occurred at 25°C. This finding could help the future research on ABD and the natural behavior of A. rabiei. Such research could lead to abetter understanding of the conditions required for disease development, as well as improvement in disease control strategies. Furthermore. estimating the effects of environment factors on pathogens and their interactions in the field.

Phenotyping of A. rabiei isolates

Pathogenic variability results classified A. rabiei isolates into four groups (GA, GB, GC and GD) and 15 physiological races based on the isolates pathogenicity and virulence on a set of 10 chickpea differentials (Table 5). Race 1 characterized by its high aggressiveness and virulence against all the tested differentials. It was represented by 5 isolates (AS-1, AS-7, AS-9, AS-11 and AS-20) collected from Sulaimaniyha, Erbil and Garmian. Races 2, 3, and 4 were only avirulent on one genotype, FLIP07-197C, FLIP07-228C and Ghab-3 respectively. Race 2 and 3 are represented by a single Sulaimani isolate for each AS-23 and AS-3, respectively, whereas Race 4 represented by five isolates from Sulaimaniyha, Garmian and Erbil. Four races (5, 6, 7, 8 and 9) were found to be a virulent on two differentials (FLIP07-361C, FLIP09-388C; Ghab-3, FLIP09-388C; Ghab-3, FLIP09-222C; FLIP07-228C, FLIP09-248C; Ghab-3, FLIP09-229C) represented by isolates AS-4, AS-5, AS-12, AS-14 and AS-21 in Sulaimaniyha, Garmian and Erbil. Race 10

represented isolate AS-2 from Sulaimani was a virulent on three differentials, while Races 11 and 12 represented by AS-6 and AS-17 isolates from Sulaimani and Erbil were avirulent on 4 differentials each. Two races (13 and 14) represented by Halabja isolates AS-10 and AS-8 were weak and showed virulence on 3 differentials, whereas Race 15 represented by Erbil isolate AS-15 was a virulent and showed virulence only on FLIP09-197C (Table 5). Distribution of the supposed 15 A. rabiei races across different IKR provinces was quite variable. Pathogen diversity was high in Sulaimani, with nine different races (1, 2, 3, 4, 5, 6, 9, 10, and 11) discovered in various chickpea fields. This account for 60% of all races, followed by Erbil, which has five races (1, 4, 8, 12 and 15)and accounts for 33%. Halabja and Garmian each contributed three races (1, 13, 14) and two races (4, 7), accounting for 20% and 12% of the total. Races 4 and 5, each with 5 isolates, account for 43.47% of all the isolates and may be the largest and wide distributed races in Kurdistan region. The mean virulence of the tested isolates on ten differentials revealed four distinct virulence groups, GAhighly virulent, characterized by high level of virulence including five isolates (AS-7, AS-9, AS-19, AS-20, and AS-21) representing 21.73% of all isolates, GB- Virulent isolates included AS-1, AS-3, AS-5, AS-11, AS-12, AS-13, AS-16, AS-18, AS-22, and AS-23, representing the largest and most widely distributed group with 43.47%. GC-Moderately virulent, with moderate levels of virulence in AS-2, AS-4, AS-6, AS-14, and AS-17 (five isolates) representing 21.73%, and GD- A virulent, with low levels of virulence (13.04%) including three isolates AS-8, AS-10, and AS-15. Kaur, (24) found that A. rabiei isolates that grew quickly and produced little spores were less virulent than those produce a lot of spores. In other studies, no correlations were found between isolate virulence, geographical origin. morphological and characteristics such as spore size, colony color, and radial growth in vitro (2). Pathogenicity of various A. rabiei isolates in India was found to be highly correlated with the amount of phytotoxins produced (24). It would be interesting to investigate toxin production by various Kurdistan isolates and see if there is a link to aggressiveness. The existence of different races of *A. rabiei* is suspected due to differences in host-pathogen interaction and breakdown of host resistance in some cultivars (23). Mutation is thought to have evolved aggressive isolates in response to a change in host resistance. Pathogenic variability in *A. rabiei* has been reported from many countries, including India (5), Syria and Lebanon (43), and United States (20). These studies were based on 3 to 15 chickpea differentials tested with 11-130 *A. rabiei* isolates and classified into 3 to 14 races.

Table 5. Pathogenicity and virulence spectrum of twenty-three Aschochyta rabiei isolates collected from major chickpea growing area across Iraq under artificial inoculation conditions under control conditions

					Gei	otypes						
Isolate	FLIP0 7 - 197C	ILC 263	Ghab3	FLIP07 -228C	FLIP09 -222C	FLIP09 -229C	FLIP09 -248C	FLIP09 -384C	FLIP07 -361C	FLIP09 - 388C	Mean	Supposed Race
AS-1	V ^{a-z}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V^{a-h}	V^{a-y}	V^{a-aa}	V ^{a-ac}	V ^{a-v}	V^{a-t}	V ^{a-z}	V^{a-p}	V ^{a-c}	1
AS-2	V ^{a-x}	V ^{a-v}	Av ^{m-al}	$\mathbf{V}^{\mathbf{c} \cdot \mathbf{al}}$	V ^{a-z}	$\mathbf{V}^{\mathbf{a} \cdot \mathbf{ac}}$	V ^{a-ae}	Av ^{f-al}	Av ^{a-s}	V ^{c-al}	MV ^{c-f}	10
AS-3	V ^{a-w}	V ^{a-v}	V ^{a-x}	Av^{k-al}	V ^{c-al}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{p}}$	$\mathbf{V}^{\mathbf{b} \cdot \mathbf{af}}$	V ^{a-s}	V ^{a-x}	V ^{b-af}	V ^{b-e}	3
AS-4	V ^{a-aa}	V ^{a-z}	V ^{a-x}	$\mathbf{V}^{\mathbf{b}\text{-}\mathbf{ae}}$	V ^{a-ac}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{t}}$	V ^{a-z}	$\mathbf{V}^{\mathrm{a-ac}}$	$\operatorname{Av}^{\operatorname{g-al}}$	Av ^{l-al}	MV ^{c-f}	5
AS-5	V ^{a-x}	V ^{a-w}	$\mathbf{Av}^{\mathbf{j}\cdot\mathbf{al}}$	V ^{a-aa}	V ^{a-x}	\mathbf{V}^{b-ae}	V ^{a-t}	V ^{a-w}	V ^{a-z}	$\operatorname{Av}^{\operatorname{g-al}}$	V ^{b-e}	6
AS-6	Av ^{m-al}	Av ^{e-al}	Av ^{k-al}	Av ^{g-al}	V ^{a-z}	V ^{a-z}	V ^{a-w}	V ^{a-ab}	V ^{a-x}	$\mathbf{V}^{\mathbf{c}\text{-}\mathbf{ag}}$	\mathbf{MV}^{d-f}	11
AS-7	V ^{a-x}	V ^{a-r}	V ^{a-x}	V ^{a-ab}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V ^{a-u}	V ^{a-n}	V ^{a-n}	V ^{a-v}	V ^{a-r}	\mathbf{HV}^{ab}	1
AS-8	Av ^{m-al}	V ^{c-ah}	Av ^{ae-al}	Av ^{v-al}	V ^{c-al}	V ^{c-al}	Av ^{s-al}	Av ^{q-al}	Av ^{q-al}	Av ^{x-al}	Av ^g	14
AS-9	V ^{a-n}	V ^{a-k}	V ^{c-al}	V^{a-1}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{k}}$	V ^{a-c}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V^{a-f}	V ^{a-x}	HV ^a	1
AS-10	Av ^{k-al}	Av ^{r-al}	V ^{a-aa}	Av ^{w-al}	Av ^{f-al}	V ^{a-x}	Av ^{h-al}	Av ^{k-al}	V ^{a-x}	Av ^{g-al}	Av ^{fg}	13
AS-11	V^{a-l}	V ^{a-ad}	V ^{a-ad}	V ^{a-z}	V ^{a-aa}	V ^{a-ad}	V ^{c-al}	V ^{a-x}	V ^{d-al}	V ^{a-r}	V ^{b-e}	1
AS-12	V ^{c-al}	V ^{a-y}	Av ^{f-al}	V ^{a-y}	Av ^{j-al}	V ^{a-x}	V ^{a-y}	V ^{a-x}	V ^{a-x}	V ^{a-q}	V ^{b-f}	7
AS-13	V ^{a-ac}	V ^{b-ar}	Av ^{r-al}	V ^{b-ar}	V ^{a-z}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V ^{a-aa}	V ^{a-ad}	V ^{a-x}	V ^{a-o}	V ^{D-e}	4
AS-14	V ^{c-ai}	\mathbf{V}^{a-ac}	V ^{c-ai}	Av ^{r-ar}	V ^{r-ai}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{t}}$	Av ^{K-al}	V ^{a-x}	V^{a-y}	V ^{a-j}	MV ^{c-r}	8
AS-15	V ^{b-ae}	Av ^{o-al}	Av ^{z-al}	Av ^{k-al}	Av ^{l-al}	$\mathbf{A}\mathbf{v}^{\mathbf{p}\text{-}\mathbf{al}}$	$\mathbf{A}\mathbf{v}^{\mathbf{p}\cdot\mathbf{al}}$	Av ^{f-al}	Av ^{n-al}	$\mathbf{A}\mathbf{v}^{\mathbf{j}\cdot\mathbf{al}}$	Av ^g	15
AS-16	V ^{a-x}	V ^{a-aa}	Av ^{r-al}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{t}}$	V ^{a-z}	$\mathbf{V}^{\mathrm{a-w}}$	$\mathbf{V}^{\mathbf{c-al}}$	$\mathbf{V}^{\mathrm{a-ac}}$	V ^{a-v}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{ad}}$	$\mathbf{V}^{\mathbf{b} \cdot \mathbf{f}}$	4
AS-17	V ^{a-ae}	V^{a-aa}	Av ^{e-al}	Av ^{k-al}	Av ^{f-al}	V ^{c-al}	Av ^{i-al}	$\mathbf{V}^{\mathbf{c}\text{-}\mathbf{ag}}$	V ^{a-v}	V ^{a-ad}	MV ^{ef}	12
AS-18	$\mathbf{V}^{\mathbf{a}}$	V ^{a-x}	Av ^{a-ae}	V ^{a-n}	V ^{a-u}	V ^{a-x}	V ^{a-ad}	V ^{b-ae}	V ^{a-v}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V ^{a-c}	4
AS-19	V ^{a-v}	V ^{a-i}	Av ^{k-al}	V ^{a-1}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{q}}$	V ^{a-t}	V ^{a-j}	V^{a-t}	V ^{a-f}	V ^{a-i}	HV ^a	4
AS-20	V ^{a-1}	V ^{a-d}	V ^{c-af}	V ^{a-k}	V ^{a-v}	V ^{a-t}	V ^{a-I}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{g}}$	V ^{a-v}	V^{a-i}	HV ^a	1
AS-21	V ^{a-e}	$\mathbf{V}^{\mathbf{ab}}$	Av ^{h-al}	V ^{a-I}	$\mathbf{V}^{\mathbf{a}\cdot\mathbf{p}}$	Av ^{i-al}	V^{a-1}	V ^{a-i}	$\mathbf{V}^{\mathbf{a}}$	V ^{a-v}	HV ^a	9
AS-22	V ^{b-af}	V^{a-w}	Av ^{t-al}	V ^{a-r}	V^{a-v}	V ^{a-o}	V ^{a-m}	V^{a-t}	V ^{a-v}	V ^{a-x}	V ^{a-d}	4
AS-23	Av ^{u-al}	V ^{a-w}	V ^{a-t}	V ^{a-t}	V ^{a-u}	V ^{a-v}	V ^{a-v}	V ^{a-z}	V ^{a-u}	V ^{a-h}	V ^{a-c}	2
Control	Av ^{ag-al}	Av ^{ah-al}	Av ^{y-al}	Av ^{aa-al}	Av ^{ad-al}	Av ^{af-al}	Av ^{ab-al}	Av ^{ah-al}	Av ^{ac-al}	Av ^{al}	Av ^h	-
Mean	MS"	5.	1~	M8"	MS"	2.	2.	5.	5.	5.	8	

* Av= Avirulent (1-40 % severity), MV= Virulent (41-50% severity), V= Virulent (51-60% Severity), HV= Highly virulent (61-100%

** T= Tolerant (16-40% Severity), MS= Moderately Susceptible (41-50% Severity), S= Susceptible (51-75% Severity).

Al-Maaroof & Salih

Udupa and Weigand (43) suggested that standard set of 3 chickpea differentials is sufficient in pathotyping A. rabiei isolates into 3 pathotypes based on increasing level of aggressiveness. Reddy and Kabbabeh (41) proposed a set of 6 differential genotypes to determine 6 physiological races. A. rabiei pathotypes were obtained using 130 and 64 isolates from Pakistan and Turkey. respectively (59). Udupa et al. (43) found 5 isolates from pathotype II in Syria. All the 6 physiological races of A. rabiei were found by Reddy and Kabbabeh (41) using 64 isolates from Syria and Lebanon. Using the same set Dolar and Gürcan (15) reported races 1, 4 and 6 in Turkey. all the 6 races reported in Turkey in 2009 (42). Chen et al. (12) reported that all the 5 races except race 6 are pathotype I. Chickpea cultivar ILC 3279 which is source of resistance to ABD and shows high level of resistance in several countries have been identified to be susceptible to race 6 (28), Thus, pathotype III was designated to both race 5 and race 6. A new highly aggressive pathotype known as IV was discovered in Syria (20). Currently, almost all studies around the world use pathotype rather than race to determine the virulence of isolates. It is difficult to study the pathogen's pathogenic variability and compare it to other researcher's findings because they used different methods and chickpea genotypes (12). There had been previous studies physiological no on characterization of A. rabiei isolates in Iraq particularly in Kurdistan region, with the exception of Al-Taee study (4), which identified five A. rabiei races namely A, B, C, D and H in Nineveh province. The current study is the first in Iraq to classify twentythree A. rabiei isolates collected from various chickpea fields in Iraqi Kurdistan region into four groups and 15 physiological races.

Analysis of ITS sequences

The ITS 1 and ITS 4 primers amplified a 541bp band in all *A. rabiei* isolates (Figure 3). The sequencing results of 35 representative isolates confirmed identification of the fungal pathogen as *A. rabiei* with 100% nucleotide sequence similarity to the ITS region sequences available on the National Center for Biotechnology Information (NCBI). The number of nucleotide sequences, on the other

hand ranged from 481 to 541bp. The shortest sequence (361bp) was found in AS-29, followed by (421bp) in AS-20 and AS-35, and the longest (541bp) was found in Isolates AS-2, AS-5, AS-6, AS-8, AS-10, AS-11, AS-13, AS-15, AS-16, AS-19, AS-24, AS-28, AS-30, AS-31, AS-32, AS-33, and AS-34, while other isolates such as AS-1, AS-3, AS-4, AS-7, AS-9, AS-12, AS-14, AS-17, AS-18, AS-21, AS-AS-23, AS-25, AS-26, and AS27 22. characterized with 481bp. The ITS sequences of all the isolates were registered at NCBI Gen Bank under different accession numbers (Table 6). Amplification of nuclear ITS sequences resulted in a single band in each accession (Figure 3). The bootstrap values of these sequences were low. This is because the polymorphism caused by sequence alignment is a single nucleotide polymorphism. The outgroup species Alternaria arborescens was well resolved from the target sequences A. rabiei.

Phylogenic analysis

The phylogenetic tree built using the ITS sequences generated in this study grouped of all the isolates into a single cluster (Figure 4). A. rabiei isolates were highly similar, with 100% similarity. The phylogenetic tree which was contricted using the sequences of the representative isolates sequences as well as six ITS sequences from other countries submitted to NCBI GenBank, showed that the six international isolates from Argentina, Germany and India were clustered in the same group as our isolates (Figure 4). All the isolates grouped together showed high level of similarity (100%) in term of the pathogen ITS region. The phylogenetic tree clearly indicates that isolates originated from the same district can be partially clustered together and share high degree of similarity. Despite their high similarity, the tested isolates had little variation in the number of ITS sequences (481-541bp), which could be attributed to variations in the specific genotypes cultivated area as well as variations in environmental conditions, causing pathogen populations to adopt variability. Previous findings support the current findings which refer to the close relationship and high level of similarity of ITS1-5.8S-ITS2 rDNA regions in A. rabiei isolate sequences (8).



Figure 3. Agarose gel electrophoresis of PCR amplified ITS region of Ascochyta rabiei isolates, locations and isolate number. Iso. 1 to 35 represents: Bngrd/l, Khrabeh/2, Greza/3, Saraw/4, Kani speka/5, Mowan/6, Bershka/7, Basharty khwaraw/8, Hana zhalla/9, Banishar/10, Gula khana/11, Ganma rash/12, Bawa Nur/13, Afryan/14, Batas/15, Bawyan/16, Sisawa/17, ShawrAwa/18, Shewa Rash/19, Belangry Khwaraw/20, Grdjan/21, Kani Maran/22, Sultanade/23, Sarwchawa/24, Dwawa/25, Shkarta/26, Badawan/27, Shamsawa/28, Wazha/29, Kani waysa/30, Bakrajo/31, Bakrajo/32, Bizeniyan/33, Qaymasa/34, Khewata/35, and M-100bp DNA ladder

 Table 6. Accession numbers of A. rabiei isolates from different chickpea fields identified using ITS1 and ITS4 sequences.

Isolate	Fungal Identified	Accession Numbers	Query Cover %	Identic Number %	Accession No. of Blast Identification	Country Identification
AS-1	Ascochyta rabiei	MZ323178				
AS-2	Ascochyta rabiei	MZ323179				
AS-3	Ascochyta rabiei	MZ323180	100	00.26	KU0/9512	Angonting
AS-4	Ascochyta rabiei	MZ323181	100	99.20	KU940313	Argentina
AS-5	Ascochyta rabiei	MZ323182				
AS-6	Ascochyta rabiei	MZ323183				
AS-7	Ascochyta rabiei	MZ329151				
AS-8	Ascochyta rabiei	MZ323184	100	98.37	MT252609	India
AS-9	Ascochyta rabiei	MZ323185				
AS-10	Ascochyta rabiei	MZ323186				
AS-11	Ascochyta rabiei	MZ314597				
AS-12	Ascochyta rabiei	MZ314598				
AS-13	Ascochyta rabiei	MZ314599	100	99.56	EU167600.1	Germany
AS-14	Ascochyta rabiei	MZ314600				
AS-15	Ascochyta rabiei	MZ314601				
AS-16	Ascochyta rabiei	MZ314602				
AS-17	Ascochyta rabiei	MZ314603				
AS-18	Ascochyta rabiei	MZ314604	100	99.36	MT252615	India
AS-19	Ascochyta rabiei	MZ314605				
AS-20	Ascochyta rabiei	MZ314606				
AS-21	Ascochyta rabiei	MZ323092				
AS-22	Ascochyta rabiei	MZ323093	100	98.71	KT962083.1	India
AS-23	Ascochyta rabiei	MZ323094				
AS-24	Ascochyta rabiei	MZ323095				
AS-25	Ascochyta rabiei	MZ323096				
AS-26	Ascochyta rabiei	MZ323097				
AS-27	Ascochyta rabiei	MZ323098				
AS-28	Ascochyta rabiei	MZ323099				
AS-29	Ascochyta rabiei	MZ323100				
AS-30	Ascochyta rabiei	MZ323101	100	98.37	MT252609	India
AS-31	Ascochyta rabiei	MZ323102				
AS-32	Ascochyta rabiei	MZ323103				
AS-33	Ascochyta rabiei	MZ323104				
AS-34	Ascochyta rabiei	MZ323105				
AS-35	Ascochyta rabiei	MZ323106				

The use of sequence information from rDNA repeat units is well established in fungal taxonomy for characterizing isolates and resolving taxonomic ambiguities and isolate definition as this gene cluster occurs within chromosomes with multiple copies in a single nucleus (3). These rDNA arrays have been homogenized by evolution, and the functional nature of these gene blocks minimizes mutation within sequences, making them useful in taxonomy (38). As a result, a nucleotide sequence comparison of the ITS region of the tested Ascochyta isolatess with other sequences available online in NCBI gene bank confirmed the isolates identity as A. rabiei.

Conclusions. The current study indicates that AB is a significant disease in various chickpea

production areas in Iraqi Kurdistan region. macroscopic and Cultural, microscopic differences between A. rabiei isolates were found to be significant. Fifteen races were identified by phenotyping all A. rabiei isolates on 10 differentials. Pathogen diversity was high in Sulaimani, where 9 different races were found in various chickpea fields. followed by Erbil, which had five races. The ITS sequences classified all the races into three groups within one cluster, which were all registered at NCBI Gen Bank under different accession numbers. This is, to the best of our knowledge, the first report in Iraq on the full identification of A. rabiei isolates using morphological and molecular methods.

MT252609-Ascochyta rabie MH858706 - Ascochyta rabiei MT252615-Ascochyta rabiei - MZ323178-Ascochyta rabiei (Rezan-1) MZ314597-Ascochyta rabiei(Rezan-11) MZ314598-Ascochyta rabiei(Rezan-12) MZ314599-Ascochyta rabiei(Rezan-13) MZ314600-Ascochyta rabiei(Rezan-14) MZ314601-Ascochyta rabiei(Rezan-15) MZ314602-Ascochyta rabiei(Rezan-16) MZ314603-Ascochyta rabiei(Rezan-17) MZ314604-Ascochyta rabiei(Rezan-18) MZ314606-Ascochyta rabiei(Rezan-20) MZ323092-Ascochyta rabiei(Rezan-21) MZ323093-Ascochyta rabiei(Rezan-22) MZ314605-Ascochyta rabiei(Rezan-19) MH191218- Ascochyta rabiei KU948513-Ascochyta rabiei EU167600- Ascochyta rabiei MZ323094-Ascochyta rabiei(Rezan-23) MZ323095-Ascochyta rabiei(Rezan-24) MZ323096-Ascochyta rabiei(Rezan-25) MZ323097-Ascochyta rabiei(Rezan-26) MZ323098-Ascochyta rabiei(Rezan-27) MZ323099-Ascochyta rabiei(Rezan-28) MZ323100-Ascochyta rabiei(Rezan-29) MZ323101-Ascochyta rabiei(Rezan-30) MZ323102-Ascochyta rabiei(Rezan-31) MZ323103-Ascochyta rabiei(Rezan-32) MZ323179-Ascochyta rabiei (Rezan-2) MZ323180-Ascochyta rabiei(Rezan-3) MZ323181-Ascochyta rabiei(Rezan-4) MZ323182-Ascochyta rabiei(Rezan-5) MZ323183-Ascochyta rabiei(Rezan-6) MZ323184-Ascochyta rabiei(Rezan-8) MZ323185-Ascochyta rabiei(Rezan-9) MZ329151-Ascochyta rabiei (Rezan-7) MZ323186.1-Ascochyta rabiei(Rezan-10) MZ323106-Ascochyta rabiei(Rezan-35) MZ323105-Ascochyta rabiei(Rezan-34) MZ323104-Ascochyta rabiei(Rezan-33) AB244779- Alternaria arborescens

0.020

Figure 4. Phylogenetic tree generated from the ITS sequences of *Ascochyta rabiei* isolates and other International isolates using MEGA X software and neighbor-joining methods with bootstrap values (1000 replicates).

REFERENCES

1. Abbo, S., Y. Saranga, Z. Peleg, Z. Kerem, S. Lev-Yadun, and A. Gopher. 2009. Reconsidering domestication of legumes versus cereals in the ancient near east. Quart. Rev. Biolog. 84: 29-50.

2. Ali, S.R., S.M. Iqbal, U. Iqbal, A. Ghafoor, and A. Akram. 2009. Pathogenic diversity in *Ascochyta rabiei* (PASS.) Lab., of chickpea. Pakistan J. of Botany. 41(1): 413-419

3. Alnuaimi, A.D., D. Wiesenfeld, N. O'Brien-Simpson, E.C. Reynolds, B. Peng, and M. McCullough. 2014. The development and validation of a rapid genetic method for species identification and genotyping of medically important fungal pathogens using high-resolution melting curve analysis. Mol. Oral. Microbiol. 29(3):117-130

4. Al-Taae A.K. 2006. Record of new race of *Ascochyta rabiei* on chickpea in Nineveh province. J. of Al-Rafedian Sci. 17: 27-38

5. Ambardar, V.K and S.K. Singh. 1996. Identification and elucidation of *Ascochyta rabiei* isolates of chickpea in Jammu. Indian J. Plant Pathol. 26: 4-8

6. Atik, O., S. Ahmed, M. Abang, A. Imtiaze, A. Baum, M.Yaprak, and S. Murad. 2013. Pathogenic and genetic diversity of *Didymella rabiei* affecting chickpea in Syria. Crop Prot. 46:70-79

7. Bahr, L., M. María, N. Barolo, M. Tosello and S. López. 2016. Ascochyta blight: isolation, characterization, and development of a rapid method to detect inhibitors of the chickpea fungal pathogen *A. rabiei*. Fungal Biol., 120(3): 424-432.

8. Bayraktar, H., F.S. Dolar, and M. Tör. 2007. Determination of genetic diversity within *Ascochyta rabiei* (Pass.) Labr., the cause of Ascochyta blight of chickpea in Turkey, J Plant Pathol. 89(3): 341–347

9. Bedi P.S, and S.S. Aujla. 1969. Variability in *Phyllosticta rabiei* (Pass.) Trot., the incidents of blight disease of gram. Punjab J. of Res. 6: 103-106

10. Benzohra, I.E., B.S. Bendahmane, M. Labdi, and M.Y. Benkada. 2013. Sources of resistance in chickpea germplasm to three pathotypes of *Ascochyta rabiei* in Algeria. World App. Sci. J. 21(6): 873-878

11. Chalupova, J., Raus, M., Sedlářová, M. and Šebela, M. 2014. Identification of fungal

microorganisms by MALDI-TOF mass spectrometry. Bio. Ad. 32(1): 230–241.

12. Chen, W., C.J. Coyne, T.L. Peever and F.J. Muhlbauer. 2004. Characterization of chickpea differentials for pathogenicity assay of Ascochyta blight and identification of chickpea accessions resistant to *Didymella rabiei*. Plant Pathol. 53(6): 759-769

13. Chongo, G., B. Gossen, D. Adhikari and S. Rimmer. 2004. Genetic Diversity of *Ascochyta rabiei* in Canada. Plant Dis. 8(1): 4-10

14. Desjardins, P. and D. Conklin. 2010. Nano Drop micro volume quantitation of nucleic acids. J. of Vis. Exp. 22 (45): 2565.

15. Dolar, F.S., and A. Gürcan. 1992. Pathogenic variability and race appearance of *Ascochyta rabiei* (Pass.) Labr. in Turkey. J. Turk. Phytopathol., 21: 61-65

16. FAO. 2019. FAOSTAT Statistical Database of the United Nation Food and Agricultural Organization (FAO) statistical division, Rome, Italy

17. Gharbi S, N. Karkachi, M. Kihal and j. Henni. 2013. Carbon sources and pH effect on pectinolytic activity production by *Ascochyta rabiei* isolated from chickpea (*Cicer arietinum* L.) in West Algeria. African J. of Microbiol Res. 7(27): 3483-3488

18. Gowen S.R, M. Orton, B. Thurley and A. White. 1989. Variation in pathogenicity of *Ascochyta rabiei* on chickpeas. Tropical Pest Manag. 35(2): 180–6

19. Grewal, J.S. 1981. Evidence of physiological races in *Ascochyta rabiei* in chickpea. In: Ascochyta blight and winter sowing of chickpea. Saxena, MC and Singh, KB (eds), CAB, ICARDA, Syria

20. Imtiyaz, M., M. Abang, S. Ahmed, B. Bayaa and M. Baum. 2011. Pathotype IV, a new and highly virulent pathotype of *Didymella rabiei*, causing ascochyta blight in chickpea in Syria. Plant Dis. 95(9): 1192-1193 21. Iqbal, S., A. Ghafoor, N. Ayub and Z.Ahmad. 2004. Pathogenic diversity in *Ascochyta rabiei* isolates collected from Pakistan. Pakistan J. of Bot. 36: 429–37

22. Jamil, F.F., I. Haq, N. Sarwar, S. Alam, J. Khan, M. Hanif, I. Khan, M. Sarwar and M. Haq. 2002. Screening of ten advanced chickpea lines for blight and wilt resistance. The Nucleus. 39(1-2): 95-100

23. Jamil, F.F, M. Sarwar, J. Khan, M. Zahid, S. Yousaf, H. Arshad and I. Haq. 2010. Genotyping with RAPD markers resolves pathotype diversity in the Ascochyta blight and Fusarium wilt pathogens of chickpea in Pakistan. Pakistan J. Bot. 42(2): 1369-1378

24. Kaur, S. 1995. Phytotoxicity of solanapyrones produced by the fungus *Ascochyta rabiei* and their possible role in blight of chickpea (*Cicer arietinum*). Plant Sci. 109(1): 23-29

25. Kosiada, T. 2012. In vitro growth of some species of *Ascochyta* Lib. Cent. Eur. J. Biol., 76: 1076-1083

26. Kottapalli P., P.M. Gaur, S. Katiyar, S. Pande and K. Gali. 2009. Mapping and validation of QTLs for resistance to an Indian isolate of Ascochyta blight pathogen in chickpea. Euphytica. 165(1): 79-88

27. Madeira F., Y.M. Park and J. Lee. 2019. The EMBL-EBI search and sequence analysis tools APIs in 2019. Nucleic Acids Res. 47(1): W636-W641. DOI:10.1093/nar/gkz 268

28. Mahiout, D., B.S. Bendahmane, M.Y. Benkada, and M. Rickauer. 2015. Characterization of *Ascochyta rabiei* (Pss.) Labr. Isolated from diseased chickpea field in six region of Northwestern Algeria. Am.-Euras.J. Agric. Env. Sci. 15(6):1136-1146

29. Malunga, L.N., S.D. Bar-El, E. Zinal, Z. Berkovich, S. Abbo and R. Reifen. 2014. The potential use of chickpeas in development of infant follow-on formula. Nut. J. 13(8): 1-6

30. Merga, B. and J. Haji. 2019. Economic importance of chickpea: Production, value, and world trade. Cogent Food and Agr. 5: 1615718.

31. Mishra, N.K., and B.P. Tripathi. 2015. Effect of culture media on growth, colony character and sporulation of three foliar pathogens of guava. The Bioscan.10(4):1701-1705

32. Nene, Y.L., and M.V. Reddy. 1987. Chickpea diseases and their control. In 'The chickpea'. (Eds MK Saxena, KB Singh, C Johansen) pp, 233-270. (CAB International: Oxon, UK).

33. Ozkilinc, H., O. Frenkel, S. Abbob, R. Eshed, A. Sherman, R. Ophirc and C. Can. 2010. A comparative study of Turkish and Israeli populations of *Didymella rabiei*, the

Ascochyta blight pathogen of chickpea. Plant Pathol. 59(3): 492–503.

34. Pande, S., K.H Siddique, G.K Kishore, B.M. Bayaa, P.M. Guar, C.L. Gowda and J.H. Crouch. 2005. Ascochyta blight of chickpea: a review of biology, pathogenicity, and disease management. Aus. J. Ag. Res., 56(4): 317-332 35. Pande, S., P.Guar, M. Sharma, J. Rao, B. Rao and G. Kishore. 2007. Identification of single and multiple disease resistance in desi chickpea genotypes to Ascochyta blight, Botrytis gray mold and Fusarium wilt. Sat e Journal. 3(1):1-4.

36. Porta-Puglia A, A. Infantino, P. Crino, R. Angelini and G. Venora. 1997. Ascochyta blight of chickpea: present status and prospects. Pakistani J. of Phytopathol. 9: 8-15

37. Qureshi, S.H. and S.S. Alam. 1984. Pathogenic behavior of *Ascochyta rabiei* isolates on different cultivars of chickpea in Pakistan. Int. chickpea News.,10: 29-31

38. Schoch, C.L, K.A. Seifert, S. Huhndorf, V. Robert, J. Spouge and W. Chen. 2012. Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. Proc Natl Acad Sci USA 109(16): 6241-6246

39. Ram,S. and P. Mahinder. 1993. Comparative growth and sporulation of *Ascochyta rabiei* races on different media and temperature. J. Mycol. Pl. Pathol. 23(2):200-203

40. Reddy, M.V. and S. Kabbabeh. 1985. Pathogenic variability in *Ascochyta rabiei* (Pass.) Labr. in Syria and Lebanon. Phytopathol. Medit., 24: 265-266

41. Rhaiem, A., M. Chérif, P. Dyer and T.L. Peever, (2007). Distribution of mating types and genetic diversity of *Ascochyta rabiei* populations in Tunisia revealed by matingtype specific PCR and random amplified polymorphic DNA (RAPD) markers. J. Phytopathol. 155(10): 596–605

42. Türkkan, M. and F.S. Dolar. 2009. Determination of pathogenic variability of *Didymella rabiei*, the agent of ascochyta blight of chickpea in Turkey. Turkish J. Agric. For., 33(6): 585-591

43. Udupa, S., F. Weigand, M. Saxena, and G. Kahl. 1998. Genotyping with RAPD and microsatellite markers resolves pathotype

diversity in the ascochyta blight pathogen of chickpea. Theo. and App. Gen. 97(1): 299-307 44. Vir S, and J. Grewal. 1974. Physiologic specialization in *Ascochyta rabiei* the causal organism of gram blight. Indian Phytopathol. 27(3): 355–360

45. Wang, T., L. Wang, J. Zhang and W. Dong. 2011. A simplified universal genomic

DNA extraction protocol suitable for PCR. Genet Mol. Res. 10(1): 519-525

46. Wiese, K.A., C.A. Bradely, J.S. Pasche, and N.C. Gudmestand. 2009. Resistance to QoI fungicides in *Ascochyta rabiei* from chickpea in the Northern Great Plains. Plant Dis., 93(5): 528-536.