

# Cultural, molecular and genetic variability of *Ustilaginoidea virens* causing rice false smut disease

## Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript

## ABSTRACT

Rice false smut disease is caused by *Ustilaginoidea virens*, an ascomycetous fungi. Thirty isolates of *U. virens* showed well defined colonies on potato sucrose medium (PSA). The maximum colony diameter was found to be 85.68 mm with a growth rate of 2.85 mm in the UV23 isolate and the minimum colony diameter was found to be 10.14 mm with a growth rate of 0.33 mm, which was observed in the UV15 isolate. However, thirty isolates exhibit various cultural and morphological characteristics like colony color, growth pattern, elevation, and chlamydospore formation. In cluster analysis, two major groups (I) and (II) were formed. The first major group (I) contains UV15 isolates and the second major group (II) contains 29UV isolates. Furthermore, the division of group II includes subgroup IIa, which contains 22 isolates, and subgroup IIb, with 7 isolates. The PCR amplification was done with a species-specific primer which yielded products of 380 bp and 230 bp, respectively. The results of the phylogenetic tree analysis revealed that cluster I contained 5 isolates and cluster II contained 28 isoates from China and Japan. The MAT1-1-1 primer yielded a product of 250 bp that contains 18 isolates. whereas the MAT1-2-1 primer yielded a product of 220 bp with 12 isolates. The nucleotide divergence analysis results revealed 7 polymorphic sites (s), 10 mutations (*Eta*), 0.76515 nucleotide diversity (*k*) and -2.13885 for the tajimas test value. Likewise, haplotype analysis revealed 10 haplotype(h)groups, with a haplotype diversity (*hd*) of 0.4773. With 24 isolates, hap-1 was the most common. Similarly, clear nucleotide variation was observed between Indian and Chinese isolates as well as Japanese ones. The genetic similarity coefficient matrix revealed that thirty Indian isolates showed maximum similarity (0.9). whereas the UV32 isolate showed 0.6, the UV31 isolate exhibited 0.5, and the UVA33 isolate had 0.4. These results indicate a genetic variability between the Indian UV isolates and the isolates from China.

**Keywords:** Rice, false smut, Cultural variability, Molecular , Nucleotide, diversity, Haplotype

## 1. INTRODUCTION

Rice is an main staple food crop in the world. Various biotech and abotech factors influence rice production; among these false smut of rice caused by *Ustilaginoidea virens* (Cooke.) Takahashi, which causes significant quantitative and qualitative losses in grain yield [1]. In India, disease incidence of up to 85% and grain yield losses of up to 49% have been reported [3; 4; 5; 6; 7]. *U. virens* is an ascomycetous fungus that produces multinuclear, intracellular and intercellular, homothallic or heterothallic mycelia, which infects the booting stage of the rice crop. The symptoms produced by *U. virens* are visible after flowering only, when the fungus transforms individual grains of the panicle into a yellowish smut ball, which changes to yellowish orange, green, olive green, and finally to greenish black [5]. In the *U. virens* life cycle, both ascospores (sexual) and chlamydospores (asexual) are produced [4].

Knowing the cultural, molecular, genetic variability and population divergence of *U. virens* will be useful information to develop more accurate disease management tools. The *U. virens* isolates were collected from different geographical locations on various rice varieties and have been reported to produce diverse mycelial (colour, growth pattern, and size of conidia) characters on culture media [5; 8; 9]. Previously, the genetic diversity of *U. virens* has been studied using different genetic markers such as internal transcribed spacer (ITS) [5; 8; 10], randomly amplified polymorphic DNA [8; 9; 11; 12], amplified fragment length polymorphism [10], and single nucleotide polymorphism [13], and also

based on whole-genome sequences [14; 15]. Even though these studies were focused on documenting the disease status and management, whereas the studies on cultural, molecular, genetic, and population diversity among the *U. virens* isolates are limited [5; 8; 9]. In ascomycetous fungi, sexual reproduction and development are governed by a single locus called mating-type locus 1 (MAT1), which has two idiomorphs, MAT1-1-1 and MAT1-2-1 [16; 17]. Heterothallic strains contain either MAT1-1 or MAT1-2 idiomorphs at the MAT1 locus, whereas homothallic strains harbour both idiomorphs with different arrangements [17; 18]. Mating-type analysis plays an important role in determining the molecular and genetic basis of sexual reproduction and pathogen genetic variation. In this study, the cultural, morphological, molecular, genetic variability, population divergence, and mating type analysis of thirty Indian isolates were described as well as two Chinese and one Japanese isolates of the *U. virens* pathogen.

## 2. MATERIALS AND METHODS

### 2.1 Collection and isolation of *U. virens* isolates

False smut Infected spikelets were collected from different cultivars of rice growing areas in India (Fig. 1). The smutted balls were thoroughly washed with distilled water and surface sterilised for 1 minute with a 0.1% mercuric chloride solution and washed three times with sterile distilled water. Using a sterilised needle, a mass of chlamydospores was streaked onto Petri dishes containing potato sucrose agar (PSA) medium under sterile and aseptic conditions. To check bacterial contamination, streptomycin (100 ppm) was incorporated into the medium. For fungal growth, the Petri dishes were incubated at  $26 \pm 2^\circ\text{C}$  for 2 weeks. A single, isolated colony of the fungus was picked up using a sterilised needle, transferred to the fresh PSA slants, and maintained as a pure culture for further studies [5]. A total of thirty isolates were collected and purified. Details of all thirty isolates with respect to varieties and geographical areas are given in Table 1.

**Table 1. Isolates of *U. virens* collected from different states of India**

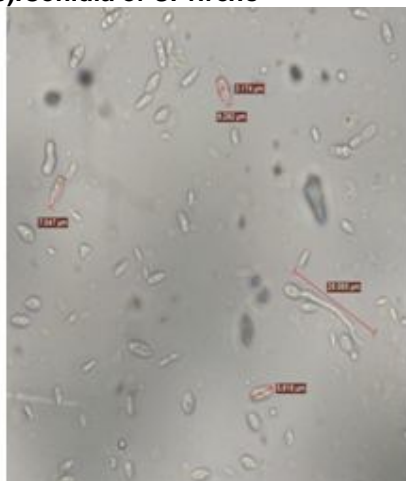
Isolate no	Isolate code	Variety	State	Geographical coordination
UV-1	TNADT	ADT51	Tamil Nadu	11.0140°N, 79.4751° E
UV-2	TNKNP	BPT5204	Tamil Nadu	12.8185° N, 79.6947° E
UV-3	TNBS	CO43	Tamil Nadu	11.4792°N, 77.1341°E
UV-4	TNTNJ	CR1009	Tamil Nadu	10.7870° N, 79.1378° E
UV-5	TNGDLR	CO43	Tamil Nadu	11.5030° N, 76.4917° E
UV-6	TNKB	CR1009	Tamil Nadu	10.9602° N, 79.3845° E
UV-7	TNTY	IWPONNI	Tamil Nadu	10.7905° N, 78.7047° E
UV-8	TNTVLR	BPT5204	Tamil Nadu	13.1231° N, 79.9120° E
UV-9	TNTIR	CR1009	Tamil Nadu	10.7661° N, 79.6344° E
UV-10	TNPBS	IWPONNI	Tamil Nadu	10.9953° N, 76.9165° E
UV-11	TNWTL	CO43	Tamil Nadu	10.9945° N, 76.9117° E
UV-12	TNKP	BPT5204	Tamil Nadu	11.3185° N, 77.7106° E
UV-13	TNARG	CR1009	Tamil Nadu	10.1692° N, 79.0023° E
UV-14	APNDL	NDLR7	Andhra Pradesh	15.4777° N, 78.4873° E
UV-15	APVZ	BPT5204	Andhra Pradesh	17.8629° N, 82.1965° E
UV-16	APPV	BPT5204	Andhra Pradesh	17.2479° N, 81.6432° E
UV-17	APMND	NDRL7	Andhra Pradesh	15.4709° N, 78.6255° E
UV-18	APMTR	MTU1010	Andhra Pradesh	16.6269° N, 81.7389° E
UV-19	APWG	BPT5204	Andhra Pradesh	16.8073° N, 81.5316° E
UV-20	APELR	BPT5204	Andhra Pradesh	16.7107° N, 81.0952° E
UV-21	APEG	BPT5204	Andhra Pradesh	16.9666° N, 82.0434° E
UV-22	APRJY	BPT5204	Andhra Pradesh	17.0005° N, 81.8040° E
UV-23	APKNL	NLR35559	Andhra Pradesh	15.8281° N, 78.0373° E

UV-24	APNLR	BPT5204	Andhra Pradesh	14.4426° N, 79.9865° E
UV-25	TSWGL	Warangal sannalu	Telangana	17.9689° N, 79.5941° E
UV-26	TSJGL	JGL3838	Telangana	18.7895° N, 78.9120° E
UV-27	MPJP	JRH124	Madhya Pradesh	23.1858° N, 79.9743° E
UV-28	MPJNKV	Kranthi	Madhya Pradesh	23.2072° N, 79.9540° E
UV-29	KAGVT	BPT5204	Karnataka	15.4319° N, 76.5281° E
UV-30	DRRPN	BPT5204	Telangana	17.3201° N, 78.3939° E

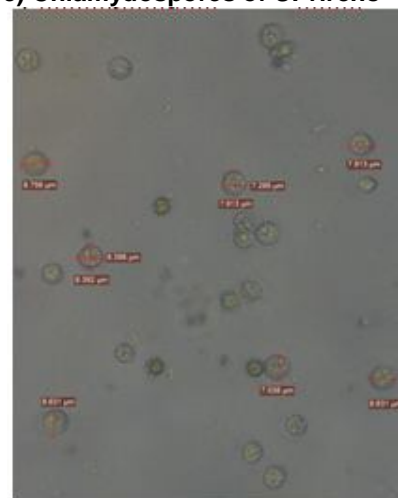
a). White & yellow-orange smut ball



b). Conidia of *U. virens*



c) Chlamydo spores of *U. virens*



**Fig. 1. Typical symptoms showing a) White & yellow-orange smut ball, b) Conidia of *U. virens* & c) Chlamydo spore of *U. virens* causing rice false smut disease**

## 2.2 Cultural variability among the different isolates of *U. virens*

A total of thirty isolates of *U. virens* obtained from diseased samples were studied for morphological variations. Observations on colony diameter, colony colour, growth pattern (elevation and mycelia form), chlamydo spore formation, and furrow formation were recorded after 15 and 30 days after inoculation. All thirty isolates of *U. virens* were grouped on the basis of their morphological characteristics using the R software clustering technique [19]. Cultures of *U. virens* obtained on potato sucrose agar (PSA) slants were examined under a phase contrast microscope in bright field (Leica DM 3000) using image analyzer software at 40X magnification.

## 2.3 Extraction of fungal DNA, primer synthesis, and PCR profiling

Thirty isolates were grown on PSB for 7 days at 26°C with 125 rpm for continued shaking in a shaker cum incubator. After 7 days, the mycelial mat was harvested and used for DNA isolation following the protocol described by [20]. The concentration of genomic DNA was measured and quantified using a NanoDrop spectro-photometer (Thermo Scientific, Wilmington, DC, USA). The specific primers were used to confirm *U. virens* [5]. The polymerase chain reaction (PCR) mixture (20 µl) consisted of 0.5 µl of 2.5 mM of dNTPs and 10 pmol of each primer (US1-5/US3-3 or US2-5/US4-3). Oligonucleotide primers designed and synthesised by [21] were used to characterise mating type analysis of the MAT1-1-1 and MAT1-2-1 ideomorphs. All oligonucleotides were synthesised using a commercial facility (Eurofins Ltd., Bengaluru, India). The nucleotide sequences of all the primers used are given in Table 2. The PCR profiling for mating type analysis consisted of one unit of Taq polymerase, DNA template (20 ng), initial denaturation at 96°C for 2 min, 30 cycles of amplification (20 s for denaturation at 96°C, 30s for primer annealing at 53°C (for mating type of primers, annealing temperature is 56°C) and 30s for extension at 70°C) and one cycle of final extension at 72°C for 7 min. The amplification was carried out on a Thermocycler (Applied Biosystems). PCR-amplified products were analysed by 1% agarose gel electrophoresis.

## 2.4. Sequencing and phylogenetic tree construction

The amplified PCR products of thirty isolates of *U. virens* were sequenced at Barcode Bioscience (Bangalore, India) by the sanger's sideoxy method and the sequences were compared with other ribosomal RNA genes of *U. virens* available at the NCBI database using the BLAST programme. The sequences were submitted to the NCBI gene bank and the accession numbers were obtained (Table 2). A phylogenetic tree was constructed with ribosomal RNA sequences using MEGA 7.0 software to assess the variability among the thirty isolates. For the phylogenetic study, two isolates from China and one isolate from Japan were also used.

**Table 2. List of primers used in this study**

Genes	Primer name	Sequence (5' → 3')	Amplification size	Tm (°c)	Reference
Ribosomal rRNA gene	Us1-5 F	CCGGAGGATACAACCAAAAAA ACTCT	380bp	53	Zhou et al. (2003)
	Us3-3 R	GCTCCAAGTGCGAGGATAACTGAAT			
	Us2-5 F	CAATGCATGTCTGAGTGGATTTTTG	232bp		
	Us4-3 R	CCAACACCAAGCGCAAGACAGA			
MAT1 locus	MAT1F2	GAAACTCCA ACTCAAACGAAGTCG	250bp	56	Fu et al. (2014)
	MAT1R2	GTAAACTTTGGCTATCAACGCCC			
	MAT2F2	GGAGCGACATAATACCGTCAAAGA	220bp		
	MAT2R2	GGGGTGT TTTTCTAAGAGGGCCT			

## 2.5 Nucleotide variability, haplotypes and genetic similarity of *U. virens* isolates

The nucleotide diversity analysis, a total of 33 isolates were studied, and of those, two isolates were from China and one isolate from Japan. In that, an isolate of *U. albicans*, which causes white false smut disease in China, was also used. 33 sequences were aligned using the ClustalW multiple alignment method in the BioEdit Software 7.2.5 version [22]. The nucleotide sequences of 33 isolates were used for the analysis of DNA polymorphism, the number of polymorphic/segregating sites (S), nucleotide diversity (Pi), Theta (per site) from S (Theta-W), the average number of nucleotide differences (k), Tajima's D (D), the number of haplotypes and haplotype diversity using DnaSP v5.10 software [23]. Further, the haplotype data exported from DnaSP v5.10 software was utilised to construct the haplotype tree based on the median-joining algorithm calculation method using software of NETWORK 10.1.1.0 (<https://fluxus-engineering.com/>). [24]

## 3. RESULTS

### 3.1 Cultural variability of thirty *U. virens* isolates

The cultural variability of all the thirty isolates of *U. virens* showed well-defined colonies on potato sucrose agar (PSA) medium. The maximum colony diameter (85.68 mm) was observed in isolate UV23, whereas the minimum colony diameter (10.14 mm) was observed in UV15 after 30 days of incubation. However, when the growth rate was calculated, the UV23 isolate exhibited a maximum growth rate of 2.85 mm/day and the UV15 isolate exhibited a minimum growth rate of 0.33 mm/day. Initially, most of the isolates of *U. virens* in culture medium showed white colonies, which later exhibited different colour colonies. However, eighteen isolates showed white colonies, including UV3, UV5, UV6, UV8, UV9, UV10, UV11, UV12, UV13, UV16, UV17, UV19, UV21, UV22, UV23, UV28, UV29, and UV30. Whereas UV2, UV7, UV14, UV20, UV24, UV26, and UV27 isolates produce white yellow colonies, Uv25 isolates produce white yellow green colonies, UV1 and UV18 isolates produce yellow colonies, Uv4 isolates produce yellow green color, and UV15 isolate produced green colonies after 30 days of incubation. The isolates also exhibit different growth patterns. Like, UV1, UV4, UV15, UV24, UV26 isolates exhibit raised elevation and the remaining isolates show flat elevation, where as UV1, UV3, UV4, UV5, UV6, UV9, Uv11, Uv12, Uv13, Uv20, Uv22, Uv23, Uv25, and Uv30 isolates exhibit circular growth patterns. Similarly, UV2, UV7, UV8, UV10, UV14, UV15, UV16, UV17, UV18, UV19, Uv21, Uv24, Uv26, Uv27, Uv28, and Uv29 isolates produced irregular growth patterns on culture media. Likewise, some of the isolates produced chlamydospores on culture media viz., UV1,

UV2, UV4, UV14 UV18, UV20 UV25, UV26, UV27, UV29, and the rest of the isolates did not produce chlamydospores. (Table 3, Fig. 2)

**Table 3. Cultural and morphological variability of thirty isolates of *U. virens***

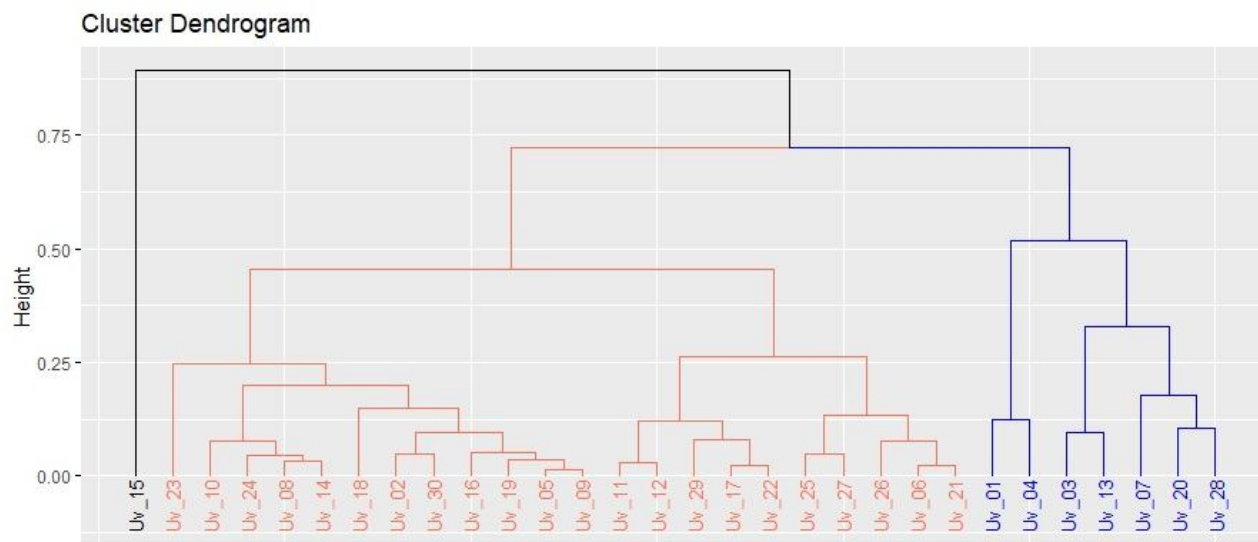
Isolate	Colony color	Growth pattern		Chlamydo spore format ion	Furrow format ion	Radial growth (mm) after 15 days	Radial growth (mm) after 30 days	Average growth rate/ day (mm)
		Elevatio n	Mycelia form					
UV-1	Yellow	Raised	Circular	Yes	+++	12.75	25.17	0.83
UV-2	White yellow	Flat	Irregular	Yes	No	35.25	79.26	2.64
UV-3	White	Flat	Circular	No	No	14.28	31.42	1.04
UV-4	Yellow green	Raised	Circular	Yes	+	12.35	26.65	0.88
UV-5	White	Flat	Circular	No	No	35.47	76.58	2.55
UV-6	White	Flat	Circular	No	No	25.36	48.75	1.62
UV-7	White yellow	Flat	Irregular	No	No	18.89	38.47	1.28
UV-8	White	Flat	Irregular	No	No	32.47	68.65	2.28
UV-9	White	Flat	Circular	No	No	35.38	75.58	2.51
UV-10	White	Flat	Irregular	No	No	31.56	65.17	2.17
UV-11	White	Flat	Circular	No	No	29.48	60.35	2.01
UV-12	White	Flat	Circular	No	No	31.65	62.14	2.07
UV-13	White	Flat	Circular	No	No	15.68	34.78	1.15
UV-14	White yellow	Flat	Irregular	Yes	No	32.66	68.47	2.28
UV-15	Green	Raised	Irregular	No	++	5.04	10.14	0.33
UV-16	White	Flat	Irregular	No	No	36.40	73.56	2.45
UV-17	White	Flat	Irregular	No	No	25.38	55.49	1.84
UV-18	Yellow	Flat	Irregular	Yes	++	36.37	74.17	2.47
UV-19	White	Flat	Irregular	No	No	37.56	77.46	2.58
UV-20	White yellow	Flat	Circular	Yes	No	22.78	45.37	1.51
UV-21	White	Flat	Irregular	No	No	23.71	48.87	1.62
UV-22	White	Flat	Circular	No	No	26.08	55.74	1.85
UV-23	White	Flat	Circular	No	No	43.72	85.68	2.85
UV-24	White yellow	Raised	Irregular	No	No	33.56	67.45	2.24
UV-25	White yellow green	Flat	Circular	Yes	No	22.34	52.47	1.74
UV-26	White yellow	Raised	Irregular	Yes	No	24.15	48.78	1.62
UV-27	White yellow	Flat	Irregular	Yes	No	23.47	51.77	1.72
UV-28	White	Flat	Irregular	No	No	22.70	43.28	1.44
UV-29	White	Flat	Irregular	Yes	No	24.17	58.47	1.94
UV-30	White	Flat	Circular	No	No	41.87	80.14	2.67
CD(0.05)						1.17	1.12	



Fig. 2. Cultural and morphological variability among the thirty isolates of *U. virens*

### 3.2 clusters of analysis for *U. virens* isolates

To study the cultural variability among the *U. virens* isolates, colony color, elevation, mycelial form, chlamyospore formation, furrow formation, and radial growth rate were evaluated in all the thirty isolates by cluster analysis and a dendrogram was generated using R software (Version 4.2.0) (Fig. 3). The results revealed that significant variation was observed with respect to colony color, elevation, mycelia form, chlamyospore formation, and furrow formation. These characters were coded as numbers and then scored. Two major groups (I, II) were formed, in which the first major group (I) included one isolate (UV15), and the second major group (II) included a total of 29 isolates. Subgroup (IIa) included 22 isolates (UV23, UV10, UV24, UV18, UV2, UV30, UV16, UV19, UV5, UV9, UV11, UV12, UV29, UV17, UV26, UV6, UV21) and the second subgroup (IIb) included 7 isolates (UV1, UV4, UV13, UV7, UV20, UV28), (Table 4)



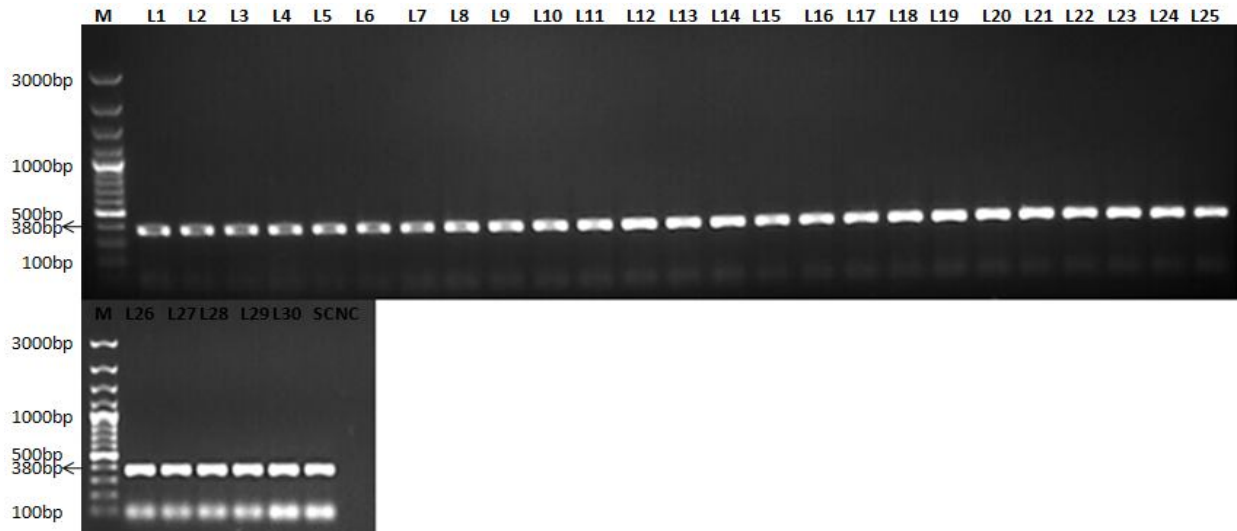
**Fig. 3. Dendrogram generated based on cultural variability of thirty isolates *U. vires* using R software (V 4.2.0)**

**Table 4. Grouping of thirty isolates of *U. vires* based on the cultural variability characters**

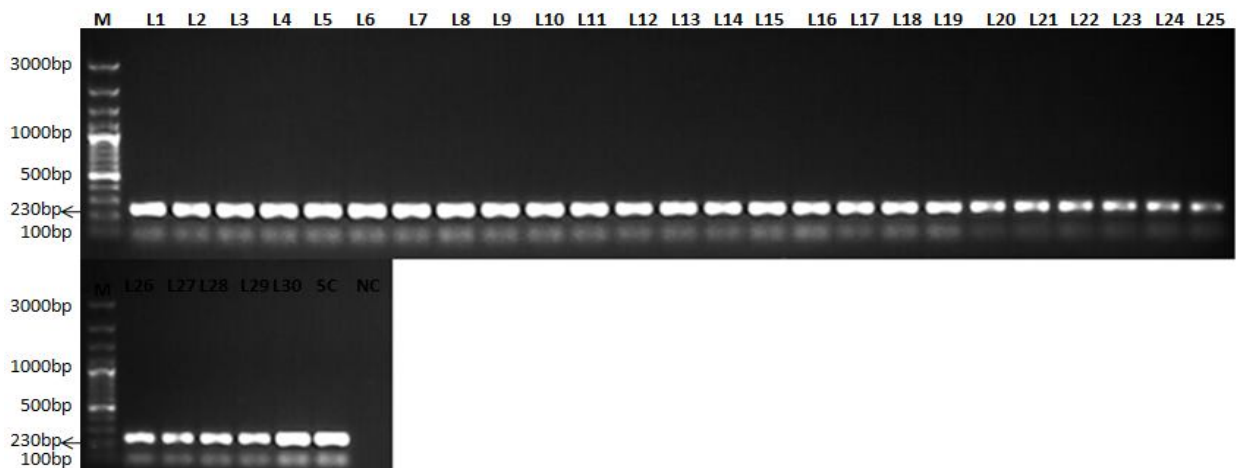
Group	Sub-group	Name of the isolates
1	1	Uv15
2	2a	Uv23, Uv10, Uv24, Uv8, Uv14, Uv18, Uv2, Uv30, Uv16, Uv19, Uv5, Uv9, Uv11, Uv12, Uv29, Uv17, Uv22, Uv25, Uv27, Uv26, Uv6, Uv21
	2b	Uv1, Uv4, Uv3, Uv13, Uv7, Uv20, Uv28

### 3.3 Molecular differences among *U. vires* isolates

The thirty isolates of *U. vires* were subjected to PCR analysis for molecular conformation. The genomic DNA was isolated from all the isolates and PCR amplification was done with false smut specific primers viz., US1-5/US3-3 and US2-5/US4-3 and amplified from Lane 1 to Lane 30 a product of 380 bp (Fig. 4a) and 230 bp (Fig. 4b), respectively.



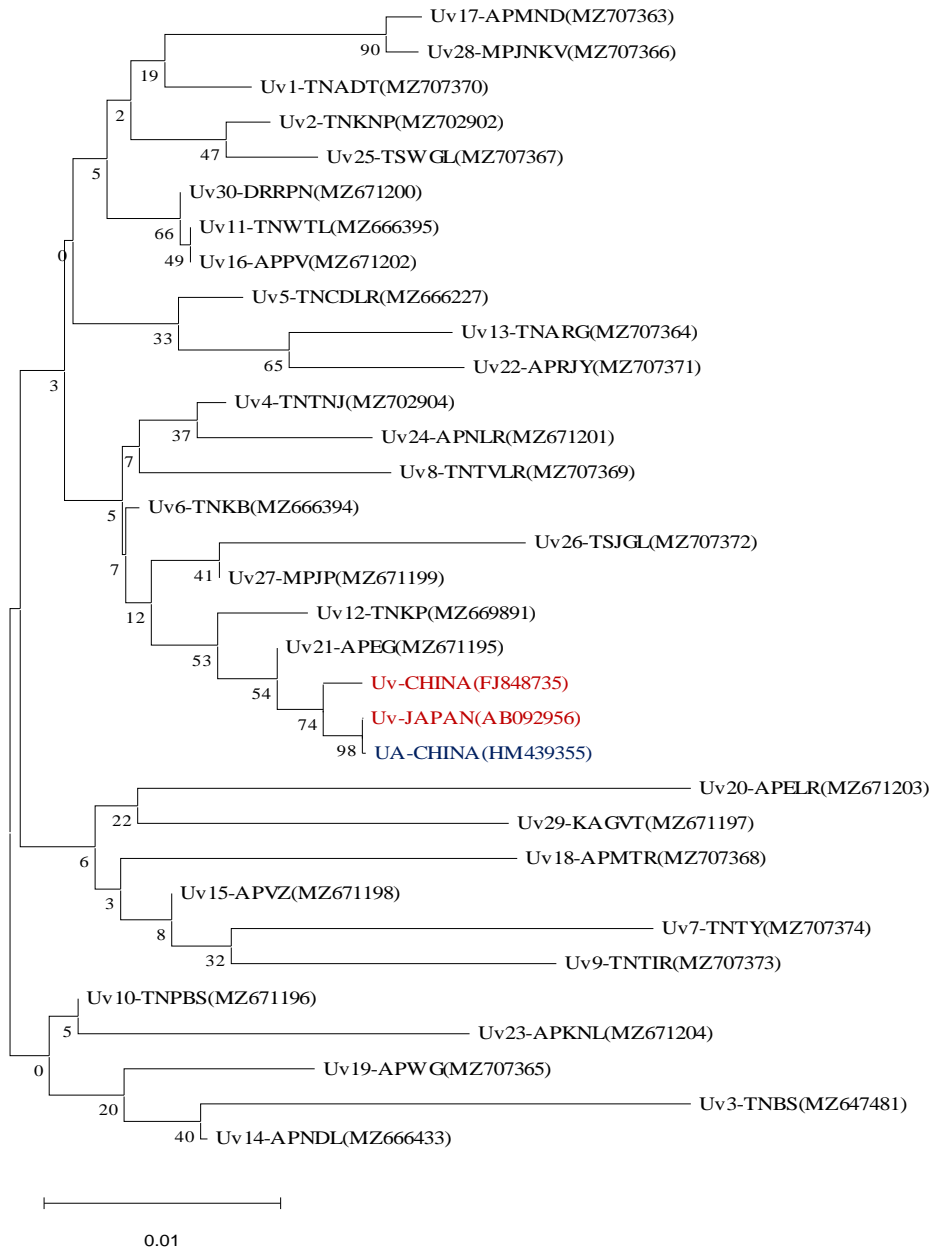
**Fig.4a. Molecular conformation of *U. virens* using species specific primer (US1-5/US3-3) amplified at 380 bp. M-3000bp marker; Lane 1-30 different isolates of *U. virens*; NC- negative control.**



**Fig.4b. Molecular conformation of *U. virens* using species specific primer (US2-5/US4-3) amplified at 230 bp. M-3000bp marker; Lane 1-30 different isolates of *U. virens*; NC- negative control.**

### 3.4 Phylogenetic analysis of *U. virens* isolates

The sequenced products of 30 isolates were analysed using the BLAST programme in NCBI. Then, all sequences were submitted to NCBI GenBank and obtained the accession numbers (Table 5). The phylogenetic tree was constructed with 33 isolates, among them two isolates from China and one isolate from Japan retrieved from NCBI. The results revealed that two clusters were formed, cluster I and cluster II. Cluster I contained five isolates (UV3, UV10, UV14, UV19, UV23), whereas cluster II contained 28 isolates including China and Japan isolates (UV1, UV2, UV4, UV5, UV6, UV7, UV9, UV12, UV13, UV15, UV16, UV18, UV20, UV21, UV22, UV24, UV26, UV28, UV29, UV30, UV-china, UV-japan and UVA-china (causing white false smut in rice), (Fig. 5).



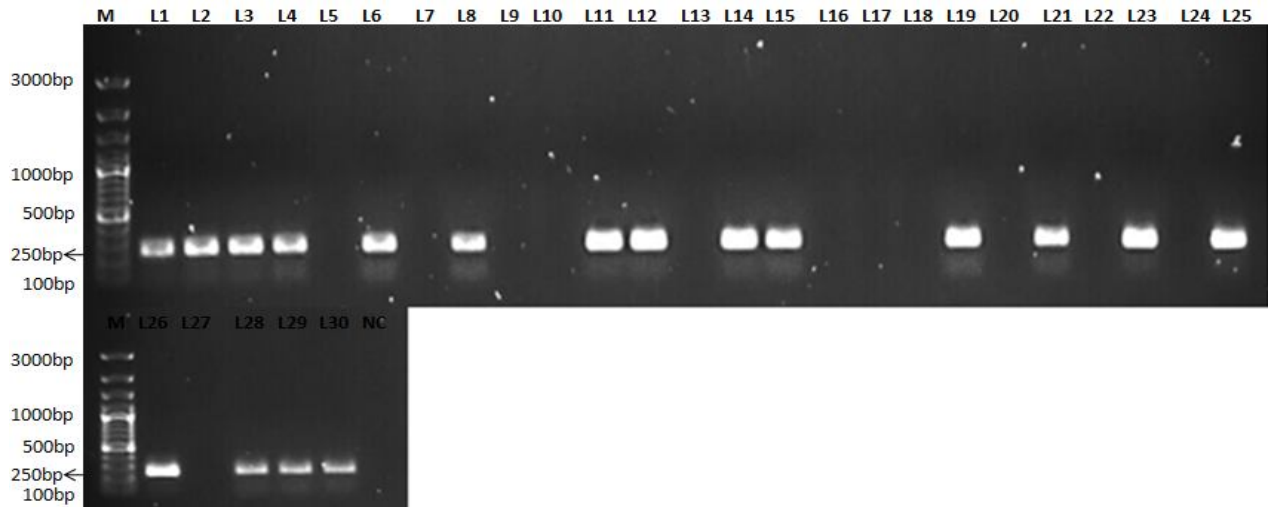
**Fig. 5.** Phylogenetic tree were constricted based on nucleotide sequences of ribosomal RNA gene of thirty three isolates using mega 7 software with 1000 bootstrip replications. Red color represents Uv-FJ848735, Uv-AB092956, whereas blue color is *U. albicans* (UA-HM439355) sequence retrieved from NCBI database and remaining all were study isolates.

### 3.5 Mating type analysis of *U. virens* isolates

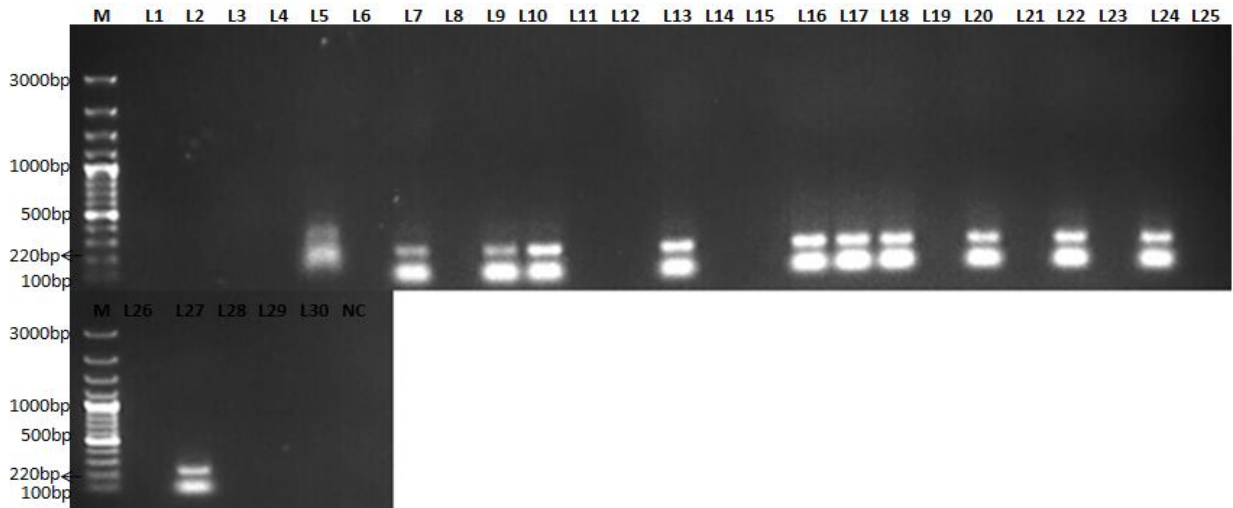
To determine the sexuality of pathogens, conducted the mating type of analysis among the *U. virens* isolates. Thirty isolates of genomic DNA were isolated and PCR was performed with mating type specific primers, viz., MAT1-1-1 and MAT1-2-1. The MAT1-1-1 primer was amplified to a product of 250 bp and contained 18 isolates (UV1, UV2, UV3, UV4, UV6, UV11, UV12, UV14, UV15, UV19, UV21, UV23, UV26, UV28, UV29, UV30), whereas the MAT1-2-1 primer yielded a product of 220 bp and contained 12 isolates (UV5, UV7, UV9, UV10, UV13, UV16, UV17, UV18, UV20, UV22, UV24, UV27), (Table 5, Fig. 6a & 6b)

**Table 5. GeneBank accession numbers for ribosomal RNA gene present in *U. virens* and Mating type studies of thirty isolates of *U. virens***

Isolate no.	Gen bank Accession numbers	Mating type	
		MAT1-1-1	MAT1-2-1
UV-1	MZ707370	Yes	No
UV-2	MZ702902	Yes	No
UV-3	MZ647481	Yes	No
UV-4	MZ702904	Yes	No
UV-5	MZ666227	No	Yes
UV-6	MZ666394	Yes	No
UV-7	MZ707374	No	Yes
UV-8	MZ707369	Yes	No
UV-9	MZ707373	No	Yes
UV-10	MZ671196	No	Yes
UV-11	MZ666395	Yes	No
UV-12	MZ 669891	Yes	No
UV-13	MZ707364	No	Yes
UV-14	MZ666433	Yes	No
UV-15	MZ671198	Yes	No
UV-16	MZ671202	No	Yes
UV-17	MZ707363	No	Yes
UV-18	MZ707368	No	Yes
UV-19	MZ707365	Yes	No
UV-20	MZ671203	No	Yes
UV-21	MZ671195	Yes	No
UV-22	MZ707371	No	Yes
UV-23	MZ671204	Yes	No
UV-24	MZ671201	No	Yes
UV-25	MZ707367	Yes	No
UV-26	MZ707372	Yes	No
UV-27	MZ671199	No	Yes
UV-28	MZ707366	Yes	No
UV-29	MZ671197	Yes	No
UV-30	MZ671200	Yes	No



**Fig.6a.** Determining the mating type of *U. virens* using primer MAT 1-1-1 amplified at 250bp. M-3000bp marker; Lane 1,2,3,4,6,8,11,12,14,15,19,21,23,25,26,28,29,30 isolates were presence of *U. virens* DNA; NC- negative control.



**Fig.6b.** Determining the mating type of *U. virens* using primer MAT 1-2-1 amplified at 220bp. M-3000bp marker; Lane 5,7,9,10,13,16,17,18,20,22,24,27 isolates were presence of *U. virens* DNA; NC- negative control.

### 3.6 Nucleotide diversity among the *U. virens* isolates

The nucleotide diversity among the 33 sequences of *U. virens* was analysed using DnaSP software version 5.10.01 (Julio Rozas et al., 2010), (developed by Universitat de Barcelona). The number of sites analysed was 686. Among them, excluding sites with gaps or missing data, there were 267. The number of pairwise comparisons was found to be 528. In this average number of sites were analysed, 343.01 with differences of 8.106 and nucleotide diversity ( $P_i$ ) was found to be 0.02356. The tajimas test analysis revealed that the number of polymorphic sites (s) was found at 7, mutations ( $E_{ta}$ ) was 10, nucleotide diversity ( $k$ ) was 0.76515, the tajimas test value was -2.13885, and stastiscal significance was found at  $P$  0.05.

### 3.7 Haplotypes of *U. virens* isolates

The haplotypes analysis among the 33 sequences included two sequences from China and one sequence from Japan, which were analysed using DnaSP software version 5.10.01. The total number of sites was analysed at 686. Among them, the total number of sites (excluding sites with gaps/missing data) was found at 267. A total of 10 haplotype groups were found (*h*) 10, whereas haplotype diversity was (*hd*) 0.4773. among them hap\_1 were major group and contain 24 isolates (UV1-MZ707370, UV2-MZ702902, UV4-MZ702904, UV5-MZ666227, UV6-MZ666394, UV7-MZ707374, UV8-MZ707369, UV9-MZ707373, UV11-MZ666395, UV12-MZ6669891, UV13-MZ707364, UV14-MZ666433, UV16-MZ671202, UV17-MZ707363, UV19-MZ707365, UV21-MZ671195, UV22-MZ707371, UV24-MZ671201, UV27-MZ671199, UV28-MZ707366, UV30-MZ671200, UV31-FJ848735, UV32-AB092956, UA33-HM439355), followed by hap\_2 (UV3-MZ647481), hap\_3 (UV10-MZ671196), hap\_4 (UV15-MZ671198), hap\_5 (UV18-MZ707368), hap\_6 (UV20-MZ671203), hap\_7 (UV23-MZ671204), hap\_8 (UV25-MZ707367), hap\_9 (UV26-MZ707372) and hap\_10 (UV29-MZ671197), (Table 6). Using PopART software version 1.70 developed by the Allan Wilson Centre imaging evolution initiative, the distribution of ten haplotype groups was represented in a pictorial tree (Fig.7).

**Table 6. Haplotype Distribution among the thirty three isolates of *U. virens***

Haplotype group	Number of isolates	Isolates distribution
Hap_1	24	UV1-MZ707370, UV2-MZ702902, UV4-MZ702904, UV5-MZ666227, UV6-MZ666394, UV7-MZ707374, UV8-MZ707369, UV9-MZ707373, UV11-MZ666395, UV12-MZ6669891, UV13-MZ707364, UV14-MZ666433, UV16-MZ671202, UV17-MZ707363, UV19-MZ707365, UV21-MZ671195, UV22-MZ707371, UV24-MZ671201, UV27-MZ671199, UV28-MZ707366, UV30-MZ671200, UV31-FJ848735, UV32-AB092956, UA33-HM439355.
Hap_2	1	UV3-MZ647481
Hap_3	1	UV10-MZ671196
Hap_4	1	UV15-MZ671198
Hap_5	1	UV18-MZ707368
Hap_6	1	UV20-MZ671203
Hap_7	1	UV23-MZ671204
Hap_8	1	UV25-MZ707367
Hap_9	1	UV26-MZ707372
Hap_10	1	UV29-MZ671197

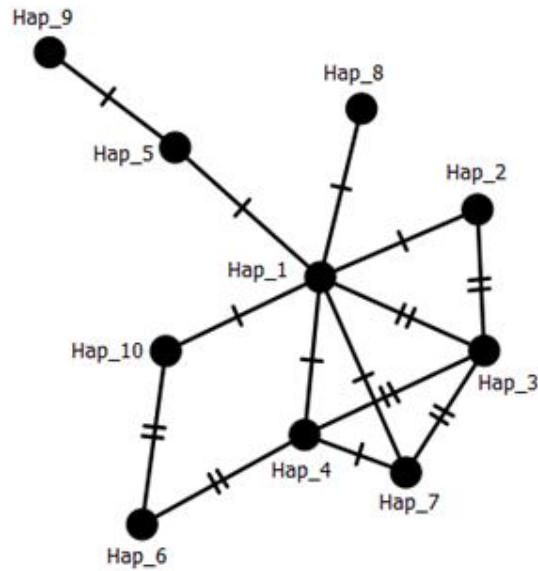


Fig.7. Haplotypes group's distribution among the thirty three *U. virens* isolates and the tree represents distance between among the each group.

### 3.8 Multiple sequence alignment and genetic similarity coefficient matrix among the *U. virens* isolate

A total of 33 sequences were analysed for nucleotide variability of *U. virens* isolates using the ClustalW multiple alignment method of BioEdit Software 7.2.5 version. The results revealed that clear nucleotide variations were observed between Indian isolates and Chinese (UV31-FJ848735, UA33-HM439355) as well as Japanese (UV32-AB092956) isolates. The genetic similarity coefficient matrix revealed that thirty Indian isolates showed maximum similarity (0.9). Whereas Uv32-AB092956 showed (0.6), Uv31-FJ848735 showed (0.5), and UA33-HM439355 showed (0.4), these findings indicate that genetic variability was observed between Indian *U. virens* isolates and *U. virens* isolates from other countries (Table7).

**Table 7. Genetic similarity coefficient matrix for thirty three *U. virens* sequences based on ribosomal RNA gene sequencing and red colorrepresents were Uv31, Uv32 & Uv33 isolates wereother countryobtained from NCBI Gen Bank**

Seq->	Uv1	Uv2	Uv3	Uv4	Uv5	Uv6	Uv7	Uv8	Uv9	Uv10	Uv11	Uv12	Uv13	Uv14	Uv15	Uv16	Uv17	Uv18	Uv19	Uv20	Uv21	Uv22	Uv23	Uv24	Uv25	Uv26	Uv27	Uv28	Uv29	Uv30	Uv31	Uv32	UA33
Uv1	ID	0.952	0.936	0.960	0.955	0.957	0.944	0.955	0.944	0.896	0.949	0.729	0.958	0.911	0.891	0.949	0.938	0.939	0.955	0.910	0.865	0.958	0.939	0.960	0.958	0.949	0.955	0.936	0.947	0.946	0.537	0.609	0.493
Uv2	0.952	ID	0.935	0.988	0.960	0.994	0.932	0.974	0.941	0.909	0.988	0.732	0.971	0.918	0.901	0.988	0.921	0.935	0.927	0.918	0.869	0.963	0.929	0.991	0.963	0.974	0.985	0.921	0.941	0.957	0.534	0.605	0.490
Uv3	0.936	0.935	ID	0.935	0.936	0.935	0.946	0.925	0.969	0.888	0.941	0.743	0.935	0.921	0.878	0.941	0.943	0.944	0.952	0.910	0.882	0.938	0.955	0.932	0.944	0.919	0.930	0.946	0.960	0.941	0.542	0.614	0.497
Uv4	0.960	0.988	0.935	ID	0.958	0.994	0.927	0.977	0.938	0.909	0.982	0.735	0.974	0.921	0.901	0.982	0.921	0.927	0.930	0.912	0.872	0.971	0.927	0.997	0.963	0.980	0.991	0.918	0.935	0.949	0.535	0.607	0.491
Uv5	0.955	0.960	0.936	0.958	ID	0.955	0.930	0.947	0.936	0.891	0.963	0.729	0.952	0.903	0.883	0.963	0.927	0.928	0.930	0.905	0.865	0.952	0.928	0.955	0.944	0.944	0.949	0.925	0.930	0.941	0.535	0.606	0.491
Uv6	0.957	0.994	0.935	0.994	0.955	ID	0.929	0.977	0.943	0.912	0.982	0.735	0.974	0.921	0.903	0.982	0.924	0.930	0.930	0.912	0.872	0.966	0.929	0.997	0.966	0.980	0.991	0.924	0.941	0.951	0.535	0.607	0.491
Uv7	0.944	0.932	0.946	0.927	0.930	0.929	ID	0.922	0.966	0.901	0.930	0.743	0.933	0.918	0.891	0.930	0.954	0.963	0.969	0.913	0.880	0.933	0.957	0.929	0.947	0.922	0.929	0.952	0.957	0.941	0.540	0.612	0.496
Uv8	0.955	0.974	0.925	0.977	0.947	0.977	0.922	ID	0.930	0.896	0.969	0.724	0.969	0.908	0.891	0.969	0.908	0.919	0.925	0.899	0.860	0.963	0.914	0.974	0.958	0.969	0.971	0.908	0.928	0.935	0.533	0.604	0.489
Uv9	0.944	0.941	0.969	0.938	0.936	0.943	0.966	0.930	ID	0.896	0.935	0.745	0.941	0.921	0.886	0.935	0.952	0.963	0.963	0.916	0.885	0.944	0.974	0.941	0.952	0.927	0.935	0.955	0.977	0.946	0.544	0.616	0.499
Uv10	0.896	0.909	0.888	0.909	0.891	0.912	0.901	0.896	0.896	ID	0.904	0.707	0.899	0.898	0.964	0.904	0.890	0.904	0.899	0.917	0.843	0.904	0.891	0.912	0.904	0.906	0.912	0.890	0.901	0.903	0.520	0.589	0.477
Uv11	0.949	0.988	0.941	0.982	0.963	0.982	0.930	0.969	0.935	0.904	ID	0.735	0.974	0.921	0.896	1.000	0.921	0.930	0.927	0.918	0.872	0.966	0.924	0.980	0.957	0.963	0.974	0.921	0.935	0.951	0.535	0.607	0.491
Uv12	0.729	0.732	0.743	0.735	0.729	0.735	0.743	0.724	0.745	0.707	0.735	ID	0.737	0.756	0.702	0.735	0.737	0.744	0.746	0.713	0.847	0.736	0.753	0.735	0.733	0.728	0.735	0.735	0.740	0.740	0.518	0.588	0.475
Uv13	0.958	0.971	0.935	0.974	0.952	0.974	0.933	0.969	0.941	0.899	0.974	0.737	ID	0.918	0.891	0.974	0.924	0.927	0.936	0.912	0.870	0.980	0.930	0.971	0.974	0.960	0.966	0.924	0.938	0.952	0.535	0.606	0.491
Uv14	0.911	0.918	0.921	0.921	0.903	0.921	0.918	0.908	0.921	0.898	0.921	0.756	0.918	ID	0.885	0.921	0.913	0.910	0.919	0.915	0.890	0.910	0.916	0.921	0.921	0.910	0.921	0.913	0.916	0.921	0.547	0.620	0.502
Uv15	0.891	0.901	0.878	0.901	0.883	0.903	0.891	0.891	0.886	0.904	0.896	0.702	0.891	0.891	ID	0.896	0.887	0.893	0.888	0.906	0.836	0.891	0.880	0.903	0.891	0.888	0.901	0.885	0.888	0.895	0.516	0.584	0.473
Uv16	0.949	0.988	0.941	0.982	0.963	0.982	0.930	0.969	0.935	0.904	1.000	0.735	0.974	0.921	0.896	ID	0.921	0.930	0.927	0.918	0.872	0.966	0.924	0.980	0.957	0.963	0.974	0.921	0.935	0.951	0.535	0.607	0.491
Uv17	0.938	0.921	0.943	0.921	0.927	0.924	0.954	0.908	0.952	0.890	0.921	0.737	0.924	0.913	0.887	0.921	ID	0.938	0.944	0.896	0.872	0.919	0.946	0.924	0.933	0.910	0.923	0.994	0.943	0.932	0.535	0.607	0.491
Uv18	0.939	0.935	0.944	0.927	0.928	0.930	0.963	0.919	0.963	0.904	0.930	0.744	0.927	0.910	0.893	0.930	0.938	ID	0.952	0.910	0.883	0.933	0.955	0.930	0.933	0.924	0.924	0.935	0.957	0.935	0.544	0.616	0.499
Uv19	0.955	0.927	0.952	0.930	0.930	0.930	0.969	0.925	0.963	0.899	0.927	0.746	0.936	0.919	0.888	0.927	0.944	0.952	ID	0.915	0.883	0.938	0.961	0.930	0.944	0.919	0.924	0.941	0.961	0.952	0.544	0.616	0.499
Uv20	0.910	0.918	0.910	0.912	0.905	0.912	0.913	0.899	0.916	0.917	0.918	0.713	0.912	0.915	0.906	0.918	0.896	0.910	0.915	ID	0.853	0.910	0.913	0.912	0.924	0.901	0.909	0.896	0.924	0.929	0.524	0.594	0.481
Uv21	0.865	0.869	0.882	0.872	0.865	0.872	0.880	0.860	0.885	0.843	0.872	0.847	0.870	0.890	0.836	0.872	0.872	0.883	0.883	0.853	ID	0.867	0.893	0.872	0.870	0.865	0.872	0.869	0.880	0.877	0.612	0.693	0.561
Uv22	0.958	0.963	0.938	0.971	0.952	0.966	0.933	0.963	0.944	0.904	0.966	0.736	0.980	0.910	0.891	0.966	0.919	0.933	0.938	0.910	0.867	ID	0.933	0.969	0.971	0.960	0.963	0.919	0.938	0.941	0.535	0.606	0.491
Uv23	0.939	0.929	0.955	0.927	0.928	0.929	0.957	0.914	0.974	0.891	0.924	0.753	0.930	0.916	0.880	0.924	0.946	0.955	0.961	0.913	0.893	0.933	ID	0.929	0.938	0.916	0.924	0.943	0.966	0.944	0.547	0.620	0.502
Uv24	0.960	0.991	0.932	0.997	0.955	0.997	0.929	0.974	0.941	0.912	0.980	0.735	0.971	0.921	0.903	0.980	0.924	0.930	0.930	0.912	0.872	0.969	0.929	ID	0.963	0.982	0.994	0.921	0.938	0.949	0.535	0.607	0.491
Uv25	0.958	0.963	0.944	0.963	0.944	0.966	0.947	0.958	0.952	0.904	0.957	0.733	0.974	0.921	0.891	0.957	0.933	0.933	0.944	0.924	0.870	0.971	0.938	0.963	ID	0.952	0.957	0.935	0.949	0.952	0.535	0.606	0.491
Uv26	0.949	0.974	0.919	0.980	0.944	0.980	0.922	0.969	0.927	0.906	0.963	0.728	0.960	0.910	0.898	0.963	0.910	0.924	0.919	0.901	0.865	0.960	0.916	0.982	0.952	ID	0.982	0.908	0.924	0.935	0.533	0.604	0.489
Uv27	0.955	0.985	0.930	0.991	0.949	0.991	0.929	0.971	0.935	0.912	0.974	0.735	0.966	0.921	0.901	0.974	0.923	0.924	0.924	0.909	0.872	0.963	0.924	0.994	0.957	0.982	ID	0.921	0.932	0.943	0.535	0.607	0.491
Uv28	0.936	0.921	0.946	0.918	0.925	0.924	0.952	0.908	0.955	0.890	0.921	0.735	0.924	0.913	0.885	0.921	0.994	0.935	0.941	0.896	0.869	0.919	0.943	0.921	0.935	0.908	0.921	ID	0.946	0.932	0.534	0.605	0.490
Uv29	0.947	0.941	0.960	0.935	0.930	0.941	0.957	0.928	0.977	0.901	0.935	0.740	0.938	0.916	0.888	0.935	0.943	0.957	0.961	0.924	0.880	0.938	0.966	0.938	0.949	0.924	0.932	0.946	ID	0.952	0.540	0.612	0.496
Uv30	0.946	0.957	0.941	0.949	0.941	0.951	0.941	0.935	0.946	0.903	0.951	0.740	0.952	0.921	0.895	0.951	0.932	0.935	0.952	0.929	0.877	0.941	0.944	0.949	0.952	0.935	0.943	0.932	0.952	ID	0.539	0.611	0.494
Uv31	0.537	0.534	0.542	0.535	0.535	0.535	0.540	0.533	0.544	0.520	0.535	0.518	0.535	0.547	0.516	0.535	0.535	0.544	0.544	0.524	0.612	0.535	0.547	0.535	0.535	0.533	0.535	0.534	0.540	0.539	ID	0.882	0.894
Uv32	0.609	0.605	0.614	0.607	0.606	0.607	0.612	0.604	0.616	0.589	0.607	0.588	0.606	0.620	0.584	0.607	0.607	0.616	0.616	0.594	0.693	0.606	0.620	0.607	0.6								

#### 4. DISCUSSION

The thirty isolates of *U. virens* showed well defined colonies on PSA medium. The maximum colony diameter found 85.68 mm with growth rate of 2.85 mm in Uv23 isolate and minimum colony diameter found 10.14 mm with growth rate of 0.33 mm was observed in Uv15 isolate. However, thirty isolates exhibit various cultural and morphological characters like, colony color, growth pattern, elevation and chlamydospores formation. Similar morphological characteristics of the pathogen were described by [5]. Meanwhile, maximum (n=25) isolates showed flat elevation, only five isolates was exhibit raised elevation, likewise sixteen isolates produced irregular margin and remaining (n=14) were exhibited circular margin after 30 days of incubation. These results are agreement with [5; 8]. In cluster analysis, two major groups (I), (II) were formed, first major group I contain Uv15 isolate and second major group II contain 29 *U. virens* isolates, further which were divided into two subgroups which are subgroup Ila contain 22 isolates and I Ib contain 7 isolates. The results of the experiment were in accordance with the finding of [8; 9], who studied 35 isolates and 12 isolates respectively and observed different characters like growth pattern, growth rate, colony color., and grouped them in different clusters. The PCR amplification was done with species specific primers which were yielded products of 380 bp and 230 bp respectively. Similar results were observed, [5], who studied 9 isolates and confirmed as *U. virens* using the specific primers of US1-5/US3-3 and US2-5/US4-3. In phylogenetic tree analysis results revealed that, cluster (I) contain 5 isolates whereas cluster (II) contain 28 isolates includes china and japan isolates. Similar results were observed by [25], who studied 71 *U. virens* isolates for phylogenetic analysis among them, 54 isolates was grouped into clusters (I) and 7 isolates were grouped in cluster (II). The MAT1-1-1 primer was amplified a product of 250 bp and contain 18 isolates. Whereas, MAT1-2-1 primer was yielded a product of 220 bp and contain 12 isolates. Our findings were similar with [21; 25], who studied mating type of analysis using the MAT1-1-1 and MAT1-2-1 locus primers. The nucleotide divergence analysis results revealed that numbers of polymorphic sites (s) were found 7, mutations (*Eta*) found 10, nucleotide diversity (*k*) was found 0.76515, tajimas test value was -2.13885. The experiment results were accordance with [25], who studied 61 isolates and observed nucleotide diversity (*k*) of 0.9163. Likewise, for haplotype analysis revealed that total haplotype groups were found (*h*) 10, with haplotype diversity was found (*hd*) 0.4773. Among them, hap\_1 was the major group and contained 24 isolates. Similar results were observed by [25], who studied 61 isolates and observed 42 haplotypes. Similarly, clear nucleotide variations were observed between Indian isolates and China as well as Japanese isolates. The genetic similarity coefficient matrix revealed that thirty Indian isolates showed maximum similarity (0.9). whereas the Uv32 isolate showed 0.6, the Uv31 isolate exhibited 0.5, and the UA33 isolate found 0.4

#### 5. CONCLUSION

We conclude that this study revealed cultural, morphological, nucleotide diversity, and population divergence among *U. virens* Indian isolates and *U. virens* isolates from other countries. This study was very useful for understanding the diversity of the rice false smut pathogen in different geographical areas and, meanwhile, adapting better management strategies to control the rice false smut disease in the rice ecosystem

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#### COMPETING INTERESTS

Authors have declared that no competing interests exist

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