Main text: Population structure of Wilsonomyces carpophilus, the shot hole pathogen of stone fruits in Kashmir, India.

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Abstract

Background

Shot hole caused by Wilsonomyces carpophilus is one of the major fungal diseases of stone fruits. The population structure of this fungus has not been studied in detail. The objective of this work was to study the population differentiation of W.carpophilus associated with peach, plum, apricot and almond in three geographical regions using inter simple sequence repeats (ISSR) markers and DNA sequence of internal transcribed spacer (ITS1-5.8S-ITS2) region from fungal isolates.

Results

The geographical as well as host populations were homogenous with highest genetic diversity within the populations than among populations. Furthermore, the W.carpophilus population on plum host revealed minimal but considerable genetic difference from peach, apricot, and almond populations, suggesting that this pathogen may have speciated on plum host.

Conclusion

Gene flow is the main evolutionary process shaping the genetic structure of W.carpophilus in Kashmir. In addition, W.carpophilus population on plum host showed low but significant genetic differentiation with peach, apricot and almond population implicating the possibility of speciation of this pathogen on plum host.

1. Background

Coryneum blight or shot hole blight caused by *Wilsonomyces carpophilus* is one the most important fungal diseases of stone fruits worldwide. In India peaches, nectarines, plums, apricots and cherries are its main hosts. The disease is a serious threat to stone fruit industry in Kashmir, the north western Himalayas region, India. Under ideal climatic conditions, the disease was shown to cause 30 to 90 percent crop losses (Dar and Teng, 1979). The pathogen affects leaves, fruits, twigs, latent buds and flower calyxes (Abolfazl, 2018).

Symptoms of *W. carpophilus* include narrow circular purple lesions with pale center that gradually became larger and necrotic in the centre until the centre fell out, imitating a shot hole and on fruits sunken necrotic lesions are formed (Ye *et al*., 2020). Although the studies have been conducted on *W. carpophilus* morphology(Adaskaveg, 1995; Ahmadpour et al., 2009a), host inoculation and varietal response (Ahmadpour et al., 2012a), disease epidemiology (Adaskaveg, 1990b), disease control and genetic diversity (Ahmadpour et al., 2012b; Nabi et al., 2018), no information is available on its genetic structure. Recently, phylogentic analysis using large subunit (LSU) nuclear ribosomal RNA, internal transcribed spacer (ITS), and translation elongation factor 1-alpha (tef1) sequences identified *Wilsonomyces* as a separate genus and it has been placed in the *Dothidotthiaceae* family (Marin-Felix *et*

al., 2017). Seven ISSR (inter-simple sequence repeat) markers revealed a significant amount of polymorphism in various isolates of *W. carpophilus* in Kashmir, indicating that these markers were useful for examining the genetic diversity in shot-hole infections (Nabi *et al*., 2018). Morphological and cultural traits, as well as multilocus analysis utilizing the internal transcribed spacer (ITS) region, partial large subunit (LSU) nuclear ribosomal RNA (nrRNA) gene, and the translation elongation factor 1-alpha (tef1) gene, demonstrate substantial genetic variation in phylogentic analysis with 25 W. carpophilus isolates from *Prunus armeniaca* and *P. divaricadiata* (Ye *et al*., 2020).The knowledge of genetic structure provides insight into the evolutionary processes that shape the populations (Mc Donald and Linde, 2002). Thus, the objective of this study was to study the genetic structure of *W. carpophilus* from different geographic regions and different hosts by determining genetic diversity and genetic differentiation using ISSR markers and sequence information of ITS region of the fungus so as to analyse the possible disease management strategies.

2. Methods

2.1 Sampling and isolation of the pathogen

The infected leaves and fruits showing typical shot hole symptoms on different stone fruits such as peach, plum, apricot and almond, collected from three districts *viz.,* Srinagar, Ganderbal and Baramulla were brought to the laboratory for isolation of the pathogen. The pathogen was isolated using tissue bit method (Tuite, 1969). In all 25 isolates were collected and purified using single spore technique (Tuite, 1969). The pathogen was identified on the basis of the cultural and morphological characters.

2.2 Genomic DNA extraction

For genomic DNA extraction, all the pathogen isolates were cultured on potato dextrose broth in 150 ml Erlenmayer flasks for 10 days. Mycelia of different fungal isolates were filtered through a double layered sterilized filter paper, dried between two layers of filter paper in a laminar air flow cabinet and stored at -80^0C for further use. The total genomic DNA of each isolate was extracted with CTAB (Cetyl trimethyl ammonium bromide) method (Murray and Thompson, 1980) and diluted to a final concentration of 25 ng/µl.

2.3 Inter-Simple Sequence Repeat (ISSR) analysis

Seven primers *viz.,*(AG)5, (CA)5, (CCA)5, (CGA)5, (AG)5YC, (AG)5YA, (GA)5YCwere selected for genotyping of the pathogen isolates. PCR reaction was carried out in 0.2 ml PCR tube with 25 µl reaction volume containing 1X buffer (2.5 µl of 10 mM Tris-HCl pH 8.0; 50 mM KCl), 1.5 mM $MgCl_2$, 2.0 µl dNTP mix (0.2 mM), 1 U of Taq DNA polymerase (Fermentas Life Sciences, Genetix Biotech Asia Pvt. Ltd.), 5 U/µl), 2 µl of DNA template (25 ng), 1 µl of primer (0.4pmol) and 15.8 µl of sterilized distilled water. The reaction mixture was vortexed and centrifuged in a microfuge (Thermo Scientific, Thermo electron Corporation). Amplifications were performed using thermal cycler (Whatman Biometra, T-Gradient, Goettingen, Germany) programmed for initial denaturation at 94ºC for 5 minutes followed by 35/45 cycles with

denaturation at 94ºC for 1 minute, annealing for 1 minute at 47ºC for (AG)5 and (CA)5; 54ºC for (CCA)5 and (CGA)5; and 52ºC for (AG)5YC, (AG)5YA and (GA)5YC, extension at 72ºC for 2 minutes and a final extension of 10 minutes at72ºC. However, number of cycles were 45 for primers (AG)5YC, (AG)5YA and (GA)5YC and for rest of the primers there were 35 cycles. The amplified PCR products were resolved by electrophoresis using 1.2% (w/v) agarose gel in 0.5 X Tris acetate EDTA buffer and gels were stained with ethidium bromide (0.5 µg/ml). DNA ladders of 100 bp and Lambda DNA/EcoR1+HindIII Marker (Fermentas Life Sciences, Genetix Biotech Asia Pvt. Ltd.) were used as markers. The gel was run at 5 V/cm using Consort Power Pack system (Consort EV 215) and photographed using Alfa Imager gel documentation system (Alfa Imager EC, Protein Simple, USA).

The data from all the primers was recorded as 1 (band present) and 0 (band absent) in a binary matrix.

2.4 Internal Transcribed Spacer (ITS) sequence analysis

The ITS regions (5.8S) of rDNA were amplified using ITS1 and ITS4 (White *et al.,* 1990). PCR reaction was carried out in in 0.2 ml PCR tube with 25 µl reaction volume containing 1X buffer, 1.5 mM $MgCl_2$, 0.2 mM dNTP mix, 1 U of Taq DNA polymerase (Fermentas), 50 ngDNA template, 0.4 pmols of primers and 14.8 µl of sterilized distilled water. Amplifications were performed using thermal cycler (Whatman Biometra, T-Gradient, Goettingen, Germany) programmed for initial denaturation at 94ºC for 5 minutes followed by 35 cycles with denaturation at 94ºC for 1 minute, annealing at 58ºC for 1 minute, extension at 72ºC for 2 minutes and a final extension of 10 minutes at 72 ºC. PCR products were electrophoresed to ensure successful amplification and amplicons were lyophilized and sent for custom sequencing (Bioscience, Merck, Millipore Pvt. Ltd., New Delhi, India). The sequences were retrieved from chromatograms, trimmed and assembled using CLC Genomic Workbench version 7.5.1 (CLC Bio, Aarhus N, Denmark). Sequence alignment and editing was done with BioEdit Sequence Alignment program (Altschul *et al.,*1990) and compared with sequences already available in the databases using BLASTn programme (http://www.ncbi.nlm.nih.gov/BLAST). The consensus sequences were reconfirmed by comparing it with the original data output. The multiple sequences alignment was done using CLUSTALW software (Thompson *et al*., 1994). The processed sequences were submitted to GenBank, National Centre for Biotechnological Information (NCBI) database and the following Accession Numbers were allocated to them (Table-7).

2.5 Data analysis

Nucleotide diversity and haplotype diversity were estimated using DnaSP 5.0 (Libardo and Rozas, 2009). The population structure was evaluated using AMOVA in ARLEQUIN v. 3.0 software and fixation indices (F_{ST}) were estimated. In this analysis also, isolates belonging to hosts apricot, plum, peach and almond were considered as populations and isolates belonging to particular geographical area irrespective of their hosts were also considered as population. The statistical significance of the total and pair-wise fixation indices was estimated by comparing the observed distribution with the null distribution generated by 1023 permutations of data matrix. Using STRU CTURE 2.2, the spatial genetic structure of

W.carpophilus isolates was studied to determine the most likely number of populations (K) based on allele frequencies per locus using a Bayesian method (Pritchard *et al.*, 2000). Ten separate runs of K = 1–10 were carried out without any previous knowledge (location or host) of individual samples to determine the number of clusters (K). We employed a burn-in time of 50,000 iterations followed by run duration of 5, 00,000 iterations for each run, as well as a model with correlated allele frequencies and population admixture. The number of populations that best describe the observed data under the model applied was found by maximising the estimated ln likelihood of the data for various K values, and the Δk index is based on the rate of change in the ln likelihood of the data between successive K

3. Results

3.1. Isolation and identification of the pathogen

The pathogen was isolated on potato dextrose agar (PDA) medium using standard pathological procedures and purified using single spore technique (Tuite, 1969). The pathogen was identified as *W. carpophilus* (Lev.) Adaskaveg, Ogawa & Butler on the basis of morphological, pathological and molecular characteristics (Ellis, 1959; Adaskaveg, 1990; Sutton, 1997 and Tovar-Pedraza *et al.*, 2013). Twenty five isolates of *W. carpophilus* were obtained from different stone fruits grown in various districts and maintained at 24±1ºC (Table 1).

3.2Analysis of population structure of *W. carpophilus* based on ISSR data

3.2.1 Clustering of isolates according to their geographical distribution

All the 25 isolates were clustered into three groups *viz.,* Srinagar, Ganderbal and Baramulla on the basis of their geographical distribution. Gene diversity in each population was again 1.0, which indicated a high level of genetic diversity in *W. carpophilus* populations.

Analysis of molecular variance (AMOVA) revealed low genetic differentiation among populations as total $F_{ST}$is 0.006 ($p<0.35$, 1023 permutations) (Table 2). Genetic variability was more within population (99.33%) than among populations (0.67%), indicating that *W. carpophilus* is genetically diverse pathogen.

The estimates of pairwise F_{ST}between populations were very low (Table 3). Hence, there is no significant genetic differentiation among geographic populations as well.

3.2.2 Clustering of isolates based on their hosts

Clustering of *W. carpophilus* isolates according to their hosts grouped them into four populations *viz.,* apricot, peach, plum and almond. Gene diversity in each population was 1.0 depicting great genetic diversity in *W. carpophilus* populations.

Analysis of molecular variance (AMOVA) revealed low genetic differentiation (F_{ST} = 0.023, p<0.13, 1023 permutations) among populations (Table 2). Genetic variability was found to be high within population (97.6%) than among populations (2.40%), indicating that *W. carpophilus* is a diverse pathogen.

The values of pairwise F_{ST} between populations were very low except for plum and almond (Table 3). These results indicate that there is no significant genetic differentiation among populations except between plum and almond.

3.2.3 Assessment of population structure, regardless of host or geographical location

According to STRUCTU RE, the population in this research may be separated into two ancestral clusters, suggesting that samples have unequal proportions of membership in both clusters (Fig. 1a). Furthermore, STRUCTURE analysis revealed *W. carpophilus* isolates had Q admixture proportion (Fig. 1b).

3.3 Analysis of population structure based on sequence data

3.3.1 Clustering of sequences according to their geographical distribution:

Clustering of *W. carpophilus* sequences according to their geographical distribution grouped them into three populations *viz,* Srinagar, Ganderbal and Baramulla (Table 4). The numbers of sequences were 12, 6, 7 and the number haplotypes were 9, 6, 5 in Srinagar, Ganderbal and Baramulla populations respectively but some haplotypes were shared between populations. Haplotype diversity ranged from 0.86 to 1.0, depicting high genetic diversity in *W. carpophilus* populations. Nucleotide diversity ranged from 0.02-0.03.

Analysis of molecular variance (AMOVA) revealed low genetic differentiation (F_{ST} = 0.022, p<0.19, 1023 permutations), thus depicting frequent gene flow between populations (Table 5). The maximum variability was found within population (97.83%) than among populations (2.17%), indicating diverse nature of the pathogen.

Pairwise estimates of F_{ST} varied among populations (Table 6). The values were 0.02 between Srinagar and Ganderbal, 0.025 between Srinagar and Baramulla populations. These results indicate that there is less genetic differentiation between geographical populations as well and hence provide evidences of frequent gene flow between populations.

3.3.2 Clustering of sequences according to their hosts:

Clustering of *W. carpophilus* nucleotide sequences according to their hosts grouped them into four populations *viz.,* apricot, peach, plum and almond. The number of sequences were 7, 6, 6, 5 and number of haplotypes were 7, 6, 4 and 5 in apricot, peach, plum and almond, respectively (Table 4). Some haplotypes were shared between populations. Haplotype diversity in populations ranged from 0.8 to 1.0, thereby indicating a high level of genetic diversity in *W. carpophilus*. Nucleotide diversity varied from 0.02-

0.03 and was less owing to highly conserved regions within ITS sequences as there were only few variable sites among different isolates.

Analysis of molecular variance (AMOVA) showed low genetic differentiation ($F_{ST=}$ 0.038 p<0.09, 1023 permutations) among populations (Table 5). Genetic variability was 3.81per cent and 96.19 per cent among and within populations respectively.

Pairwise estimates of F_{ST} varied among populations (Table 6). The maximum values were 0.096 between plum and apricot, 0.095 between peach and plum, indicating that there is significant genetic differentiation between these populations. However F_{ST}values of 0.01 between apricot and peach, 0.03 between almond and plum, -0.01 between almond and apricot and 0.005 between almond and peach were observed. The lesser values of F_{ST} indicate that there is less genetic differentiation between populations and frequent gene flow occurs between them.

4. Discussion

Shot hole disease is an important fungal disease of stone fruits and a major threat to stone fruit industry in Kashmir. Lack of information on the genetic structure of shot hole pathogen has highlighted the need to carry out the present study. To the best of our knowledge, it is the first study on population structure of *W. carpophilus*.

The causal pathogen was isolated from diseased leaves of different hosts collected from different geographical regions. The isolates of the pathogen were identified as *W. carpophilus*(Lev.) Adaskaveg, Ogawa & Butler (Syn. *Thyrostroma carpophilum* (Lev.) B. Sutton) on the basis of morphological characters (Ellis, 1959., Adaskaveg, 1990 and Sutton, 1997). Ahmadpour *et al*. (2009b) also reported indirect hyphal penetration through stomata and direct penetration through the cuticle with the help of appresoria. Singh (2006) while inoculating *W. carpophilus* on different peach cultivars also found more per cent infection on injured leaves than on uninjured ones. Incubation period of different *W. carpophilus* isolates varied from 2-4 days when inoculated on their respective hosts.

Based on ISSR and ITS data *W. carpophilus* was found to exhibit high genetic diversity as reflected in high values of gene diversity and haplotype diversity. Nucleotide diversity being less (0.02-0.03) due to conserved nature of rDNA region. Mutation, recombination (sexual or parasexual), migration (gene flow), and adaptation to various hosts are all factors that contribute to high genetic diversity. Although Vuillemin (1888) reported the formation of a sexual stage of the shot hole pathogen (Ascospora beijerinckii Vuill.) on infected leaf debris, other researchers in California, Germany, and Australia were unable to find any sexual stage, leading to the conclusion that only the asexual stage is a source of inoculum (Samuel, 1927; Adaskaveg *et al*., 1990). More aspect on this topic is needed, both in the field and at the molecular level, to see if an undiscovered sexual stage contributes to shot hole pathogen diversity. For analysis of population structure, *W. carpophilus* sequences were clustered into three populations on regional basis and four populations based on their hosts.

In geographical populations, high genetic diversity was found within population than among populations. There was no significant genetic differentiation between populations owing to lesser values of pairwise F_{ST} and presence of shared haplotypes between populations. This indicated that there is frequent gene flow between populations, probably due to the movement of infected planting material from one region to another. There is no local quarantine for this pathogen in Kashmir valley and no certification of planting material. As a result, infected planting material moves to and fro between these geographical regions. Padder *et al*. (2013) has also reported frequent gene flow between *Venturia inaequalis* populations in Kashmir valley. According to Fisher's theorem, the evolutionary potential of a population is proportional to the amount of genetic diversity in it (Mc Donald, 1997). Therefore, high diversity in *W. carpophilus* populations categorises it as highly evolving fungus, that is able to overcome management strategies very quickly. The observed genetic structure of *W. carpophilus* poses a substantial risk for regional spread of mutant alleles like fungicide resistant strains or new races that enables the breakdown of host resistance.

In host populations, again high diversity was found within populations than among populations. There was no differentiation among host populations as reflected in low F_{ST} values, thus depicting frequent gene flow between populations. It is supported by the fact that *W. carpophilus* lacks host specificity (Ahmadpour *et al.,* 2009b; Ahmadpour *et al*., 2012a) and orchards sampled were planted with all the stone fruit trees, making it easy for the pathogen isolates of one host to infect the other.The coexistence of different pathogen haplotypes within the same host plant, as detected in this study, has diverse biological implications beyond the increased opportunities for sexual reproduction. Colonization of the host by different genotypes of the same pathogen leads to an increase of within-host competition and a selection of higher pathogen virulence (Read and Taylor, 2001). Estimates of pairwise F_{ST} (based on ISSR and ITS sequence data) were low in host populations, however, plum population showed low but significant genetic differentiation with peach, apricot and almond populations. Peever *et al*. (2000) reported that the populations of *Alternaria* spp. (causing brown spot of citrus) on grapefruit and 'Nova' in Florida are genetically distinct from isolates on other cultivars and genetic differentiation between populations were low but significant, suggesting that these populations are in the early stages of adaptation and to possible speciation on these hosts. According to the STRUCTURE software, the *W. carpophilus* population can be divided into two ancestral clusters, implying that samples have unequal proportions of membership in both clusters and both populations have admixtures, indicating weak population structure or no substructure in *W. carpophilus*. In present study, plum populations also showed low but significant genetic differentiation with almond, peach and apricot. We suggest in present case also, plum population is at early stage of adaptation and there is possibility of speciation of *W. carpophilus* on plum host.

Conclusion

Gene flow is mainly responsible in shaping or structuring populations of *W. carpophilus* in Kashmir valley. If gene flow continues, it will be difficult to manage the disease on regional basis and durability of

management programme will be questioned. Thus, there is need to have local quarantine and nurseries that provide certified planting material in order to restrict gene flow between geographical populations. Similarly, gene flow between host populations can be restricted by avoiding the planting of different stone fruit trees in the same orchard.

Declarations

Ethics approval and consent to participate

Not applicable.

Consent for publication

All authors agreed to publish this paper. The data have not been published partially or completely in any other journal.

Availability of Data and Material:

All the data generated and analyzed for current study are presented in this manuscript, and the corresponding authors have no objection to the availability of data and material.

Competing interests

Authors declare that they have no competing interests

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Authors Contributions

A.N and M.D.S performed experiments, analyzed and interpreted the data of work and prepared the original manuscript; B.A.P and M.A. S.A.D analysed the data, reviewed and edited the writing. R.T.N., M., S.K and also helped in editing the manuscript .The authors read and approved the final manuscript.

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Tables

Table – 1 ***Wilsonomyces carpophilus*** **isolates obtained from different geographical regions and hosts**

District	Location	Isolate Number	Host
Srinagar	Shalimar	WcS1	Apricot
	Zakoora	WcS2	
	Shalimar	WcS3	Peach
	Boelvard	WcS4	
	Boelvard	WcS5	
	Shalimar	WcS6	Plum
	Boelvard	WcS7	
	Harwan	WcS8	
	Shalimar	WcS9	Almond
	Shalimar	WcS10	
	Boelvard	WcS11	
	Boelvard	WcS12	
Ganderbal	Repora	WcG1	Apricot
	Lar	WcG2	
	Dangerpora	WcG3	
	Haran	WcG4	Plum
	Haran	WcG5	Peach
	Dangerpora	WcG6	Almond
Baramulla	Pattan	WcB1	Apricot
	Pattan	WcB2	
	Pattan	WcB3	Peach
	Tangmarg	WcB4	
	Wadura	WcB5	
	Pattan	WcB6	Plum
	Pattan	WcB7	Cherry

Table – 2 Analysis of molecular variance (AMOVA) based on ISSR data of four *W. carpophilus* populations isolated from different hosts

Host Populations					
Source of variation	**Df**	**Variance component**	**Percentage variation**	**F_{ST}**	**P value**
Among populations	2	0.06208	0.67	0.006	0.355
Within population	22	9.26569	99.33		
Geographical regions					
Source of variation	**Df**	**Variance component**	**Percentage variation**	**F_{ST}**	**P value**
Among populations	3	0.22573	2.40	0.0239	0.1309
Within population	20	9.18286	97.60		

Table – 3:Pairwise genetic differentiation (F_{ST}) based on ISSR data between four *Wilsonomyces carpophilus* populations

Population	Apricot	Peach	Plum	Population	Srinagar	Ganderbal
Peach	-0.00686			Ganderbal	-0.009	
Plum	0.02687	-0.00669		Baramulla	0.014	0.017
Almond	0.03624	0.00041	0.10858*			

Table – 4: Polymorphism survey of *Wilsonomyces carpophilus* populations based on ITS sequences

Population	No. of sequences	No. of haplotypes	Shared haplotypes	Haplotype diversity	Nucleotide diversity
Apricot	7	7	2	1± 0.08	0.03 ± 0.02
Peach	6	6	2	1 ± 0.09	0.02 ± 0.01
Plum	6	4	3	0.8 ± 0.17	0.02 ± 0.01
Almond	5	5	1	1 ± 0.13	0.02 ± 0.01
Srinagar	12	9	2	0.95± 0.47	0.03± 0.01
Ganderbal	6	6	1	1.0± 0.10	0.03± 0.02
Baramulla	7	5	1	0.86± 0.14	0.02± 0.01

Table – 5 Analysis of molecular variance (AMOVA) of four *Wilsonomyces carpophilus* populations isolated from different hosts based ITS sequence data

Source of variation	Df	Variance component	Percentage variation	F_{ST}	P value
Host populations					
Among populations	3	0.226	3.81	0.038	0.09286
Within Population	20	5.709	96.19		
Different regions					
Among populations	2	0.126	2.17	0.022	0.198
Within populations	22	5.674	97.83		

Table – 6 Pairwise genetic differentiation (F_{ST}) between four *Wilsonomyces carpophilus* populations based ITS sequence data

Population	Plum	Apricot	Peach	Population	Srinagar	Ganderbal
Apricot	0.096*			Ganderbal	0.0200	
Peach	0.095*	0.01		Baramulla	0.02569	0.01848
Almond	0.030	-0.011	0.005			

*Significant

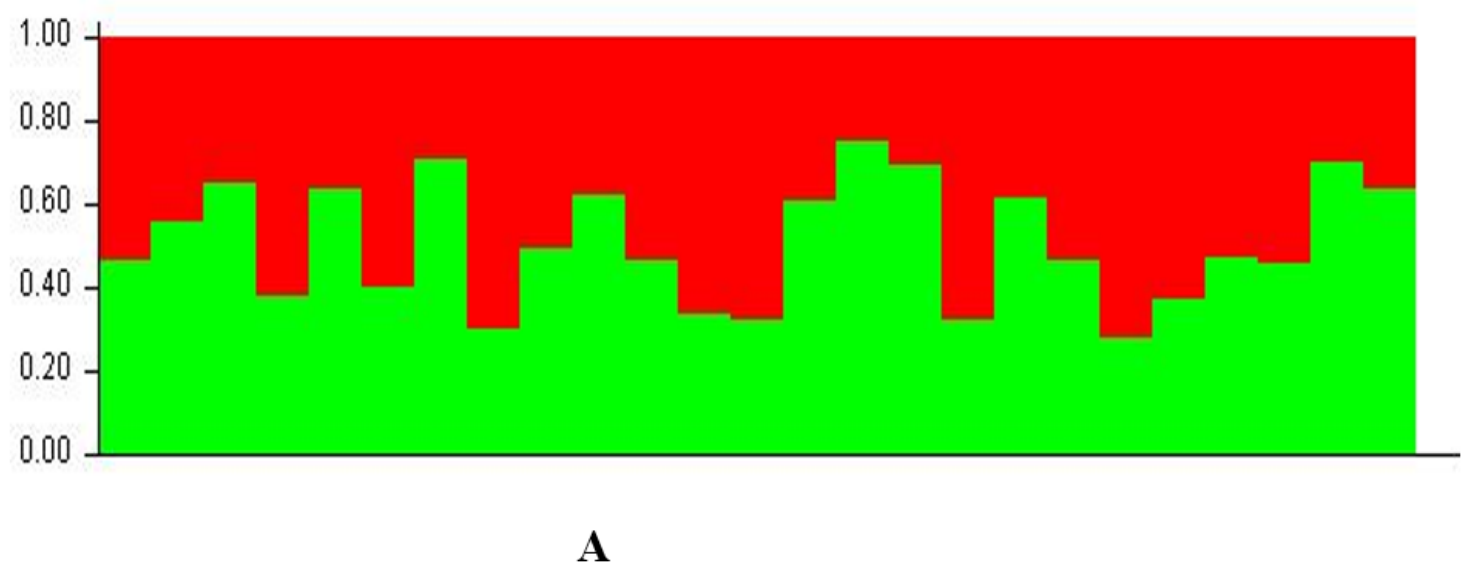
Table-7: Allotted Accession numbers to *W. carpophilus* isolates

Anamorph	Host	Isolate code	Accession No.	Origin
Wilsonomyces carpophilus	Plum	WcS6	KC815886	India
Wilsonomyces carpophilus	Apricot	WcS2	KC815887	India
Wilsonomyces carpophilus	Apricot	WcG3	KC815888	India
Wilsonomyces carpophilus	Peach	WcG5	KC815889	India
Wilsonomyces carpophilus	Plum	WcB6	KC815890	India
Wilsonomyces carpophilus	Peach	WcS5	KC815891	India
Wilsonomyces carpophilus	Peach	WcS3	KC815892	India
Wilsonomyces carpophilus	Plum	WcS7	KC815893	India
Wilsonomyces carpophilus	Apricot	WcG1	KC815894	India
Wilsonomyces carpophilus	Peach	WcB3	KC815895	India
Wilsonomyces carpophilus	Plum	WcG4	KC815896	India
Wilsonomyces carpophilus	Apricot	WcB2	KC815897	India
Wilsonomyces carpophilus	Cherry	WcB7	KC815898	India
Wilsonomyces carpophilus	Peach	WcB4	KC815899	India
Wilsonomyces carpophilus	Apricot	WcG2	KC815900	India
Wilsonomyces carpophilus	Almond	WcG6	KC815901	India
Wilsonomyces carpophilus	Almond	WcS9	KC815902	India
Wilsonomyces carpophilus	Plum	WcS8	KC815903	India
Wilsonomyces carpophilus	Plum	WcB5	KC815904	India
Wilsonomyces carpophilus	Apricot	WcB1	KC815905	India
Wilsonomyces carpophilus	Peach	WcS4	KC815906	India
Wilsonomyces carpophilus	Almond	WcS10	KC815907	India
Wilsonomyces carpophilus	Apricot	WcS1	KC815908	India
Wilsonomyces carpophilus	Almond	WcS11	KC815909	India
Wilsonomyces carpophilus	Almond	WcS12	KC815910	India

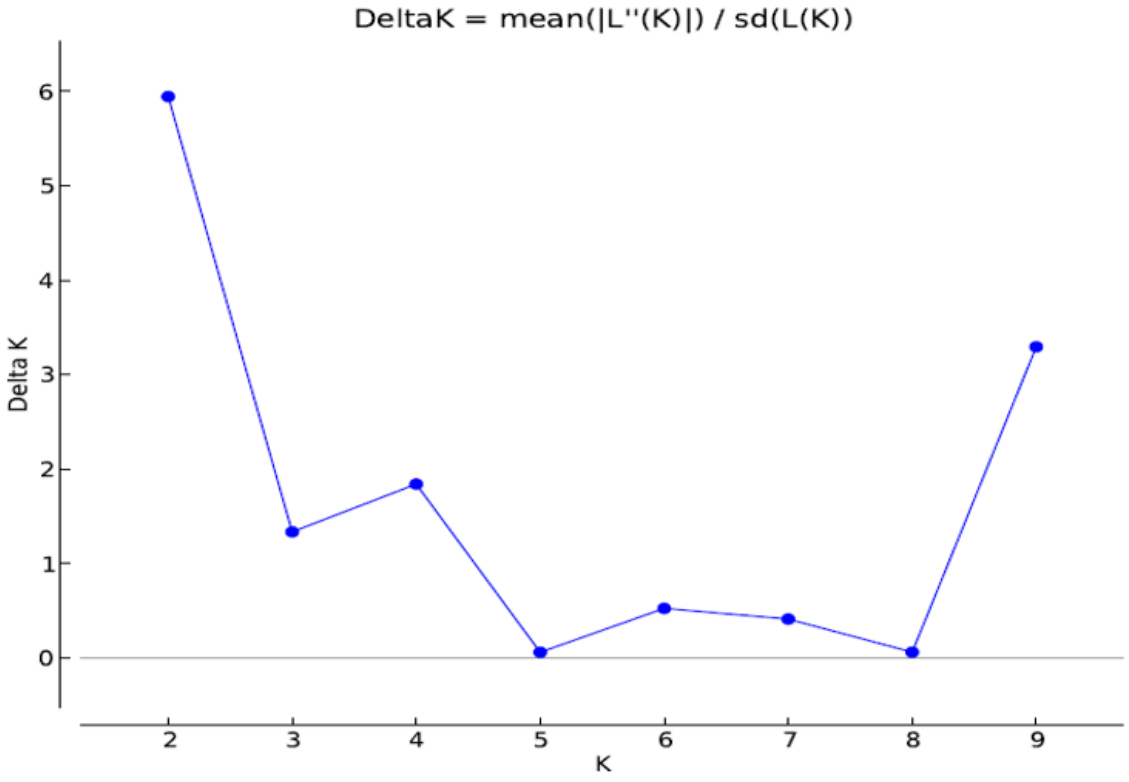
Plate

Plate 1 is available in the Supplementary Files section

Figures



A



B

Figure 1

The Structure bar plot (K = 2; a) depicts the ancestry coefficients of *W. carpophilus* in the Kashmir valley. The parameters reflecting the number of populations in the Bayesian clustering algorithm of the STRU

CTU RE program are represented in the ln likelihood plot. At least 10 separate runs of the programme were used to average the Ln likelihood values (b).

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Plate1.png