Occurrence and diversity of endophytic colonization of *Taraxacum officinale* by *Botrytis* species: A preliminary study

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Date: August 2014

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Abstract

The genus *Botrytis* (sexual form *Botryotinia* Whetzel) contains renowned plant pathogenic species with a necrotrophic lifestyle in which kill and feed on its hosts. Recent reports of symptomless endophytic colonization by *Botrytis cinerea* in cultivated plants of lettuce (*Lactuca sativa*) and *Botrytis* spp. in the wild plants dandelion (*Taraxacum agg*) and spotted knapweed *(Centaura stoebe*) reveal a different "side" of *Botrytis* spp. These findings, expose additional strategies of *Botrytis* species to disseminate and grow in wild plants and also highlight the possibility that there exist (novel?) *Botrytis* species lacking virulence factors or with novel adaptations which could include some benefits to its hosts. In this work, the occurrence of endophytic colonization by *Botrytis* spp. in dandelion plants was investigated. The results, confirmed that symptomless dandelion plants were infected with *Botrytis* spp.. From these plants, 23 Botrytis isolates were obtained. By sequencing based on the genes *HSP60* (Heat-shock Protein 60), *G3PDH* (Glyceraldehyde-3-Phosphate Dehydrogenase) and *RPB2* (DNA-dependent RNA polymerase subunit II), 6 different genotypes were identified 3 of them showed the strongest phylogenetic association with *B. cinerea* whereas the other 3 were associated with *B. pseudocinerea*. Importantly, a pathogenicity test showed the capability of these isolates to cause disease lesions in tomato and *Nicotiana benthamiana*. In this report, the implications of the ecology of *Botrytis* species are discussed.

1. Introduction

The genus *Botrytis* (sexual form *Botryotinia* Whetzel) contains renowned plant pathogenic species with worldwide distribution which includes both host generalists and specialists. *Botrytis cinerea*, a generalist species, affects more than 200 eudicots whereas the others are specialized species which affect a single or closely related hosts (Staats et al., 2005). *Botrytis* species are important pathogens in fruits, vegetables, bulbous monocotyledons (members of the families *Liliaceae, Amaryllidacea*, and *Iridaceae*) and green house crops (Jarvis, 1977).

Commonly, *Botrytis* species are known as pathogens with a necrotrophic lifestyle which kill and then feed on the dead cells of plants using in this process a variety of toxic molecules and lytic enzymes (van Kan et al., 2014). For example, in *Botrytis cinerea* host penetration is attributed more to the secretion of H_2O_2 and the degrading enzymes such as lipases, cutinases and oxidases rather than the physical pressure by the pathogen (van Kan et al., 2014). Then, for successful infection, cell dead is induced using toxins that are effective against a large spectrum of plants in the case of *Botrytis cinerea* (Choquer et al, 2007). In this species, the toxins botrydial and botcinic acid have been identified as virulence factors (Choquer et al., 2007). In addition, secretion of H_2O_2 by both, the pathogen and the host (hypersensitive response), in response to the pathogen attack, contribute to the pathogen growth (van Kan, 2006; Choquer et al., 2007).

Recent reports of symptomless endophytic colonization by *Botrytis cinerea* in cultivated plants of lettuce (*Lactuca sativa*) (Sowley et al., 2010) and *Botrytis* spp. in wild plants such as dandelion (*Taraxacum agg*) (Shafia, 2009) and spotted knapweed (*Centaura stoebe*) (Shipunov et al, 2008) provide evidence of the flexibility of *Botrytis* species to establish unnoticeable associations with plants. Although, this finding exposes the additional strategies of pathogenic *Botrytis* species to disseminate and grow in wild plants also highlights the possibility that there exist (novel?) *Botrytis* species lacking virulence factors or with novel adaptations which could include some benefits to its hosts.

In this work, the occurrence of endophytic colonization by *Botrytis* spp. in dandelion plants was investigated and we tried to answer the following research questions:

- How many different *Botrytis* genotypes are detected?
- To which species do these fungi belong?
- Are they novel species or isolates of a known species?

- The plants from which the isolates are sampled are not diseased, but are these isolates capable of causing disease?

2. Materials and methods

2.1 Plant sampling

Dandelion plants were sampled from 4 sites in Wageningen (The Netherlands) (Figure 1, Appendix 1) in May 2014. Sampling sites differed in soil composition and the surrounding vegetation. From each site 22-25 symptomless plants were collected and in total 97 plants were sampled.

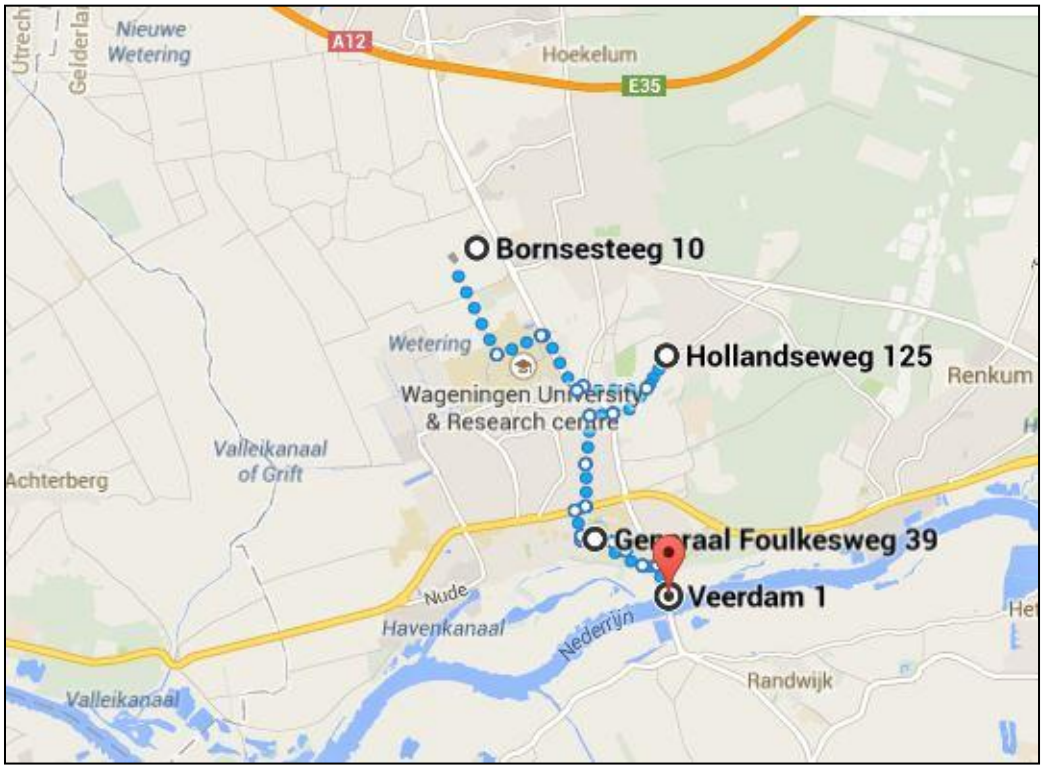


Figure 1. Sampling sites of *Taraxacum officinale* for *Botrytis* isolation in Wageningen

2.2 *Botrytis* isolation

Botrytis spp. were isolated from stems, leaves and flowers tissues after surface sterilization. Plant tissues were treated 30 s in a bleach solution (2%), 30 s in an ethanol solution (48%) and finally rinsed with water; 4 to 5 pieces from leaves, stems and flowers were plated separately in selective media for *Botrytis* (SBM, supplemented basal medium) (Kerssies, 1990). The media consisted of the following components (g/L distilled water): $NaNO_3$, 1.0; K_2HPO_4, 1.2; $MgSO_4.7H_20$, 0.2; KCl, 0.15; glucose, 20.0 and agar, 25.0. The medium was sterilized, cooled

to 65 °C and supplemented with the following ingredients (g/1 distilled water): terrachlor (PCNB, pentachlorobenzene 75%WP), $15x10^{-3}$; tetracycline, $2x10^{-2}$; chloramphenicol (antibiotic), 5×10^{-2}; CuSO4, 1.0; tannic acid, 5.0. The pH of the supplemented basal medium (SBM) was adjusted to 4.5 with 5.0 N NaOH.

A total of 291 SBM plates were employed for isolation of *Botrytis* sp. from the different plant tissues. Fungal cultures appeared after 7-10 days of plating and they were screened for the production of dark pigments in the medium due to the degradation of tannic acid, a characteristic property of *Botrytis* spp. Cultures were purified by transferring hyphae from the primary culture with minimal agar onto a fresh sterile plate with the selective media (SBM). Pure cultures were grown on MEA (Malt Extract Agar, DIFCO) plates over a cellophane membrane (1 cm^2) which facilitated the sampling of mycelium without agar.

An immunoassay test, using a kit QuickStix strips for *Botrytis* (Envirologix, catalog Number AS 049 GP 25) was employed to identify *Botrytis* colonies among the cultures. For the test, a small sample of mycelium (around 0.5 mm^2) was immersed in a eppendorf tube containing 300 µl of a buffer provided with the kit. The mycelium was mixed with the buffer by vortex and then the QuickStix strip for *Botrytis* was placed into the prepared suspension. Positive detection for *Botrytis* sp. was indicated by strips displaying two blue lines (control line and test line).

2.3 Species identification

2.3.1 DNA extraction and sequencing

Mycelial tissue (10-20 mg) from the pure cultures grown over the cellophane membrane was harvested, lyophilized and finely ground to extract DNA, using a modified protocol of Puregene DNA Purification Kit (Gentra Systems Inc./Biozym systems. Landgraaf, The Netherlands). The ground mycelium was placed in a 1.5 ml eppendorf tube (kept in ice) containing 600 µl of cell lysis solution and 3 µl of proteinase K solution (20mg/ml) and mixed by vortexing. Then, the cell lysate was incubated at 55°C for 1.5 h and vortexed periodically every 20 min. Tubes containing the cell lysate were cooled to room temperature and then 200µl of a protein precipitation solution were added and mixed thoroughly. Tubes were incubated on ice for 10-15 min and then centrifuged at 16000 x g for 3 min. 500µl of the supernatant were poured into a new 1.5 ml eppendorf tube containing 500µl of 100% isopropanol. The solution was mixed gently by inverting the tube. The mixture was centrifuged at 16000 x g for 1 min to obtain a DNA pellet, which was then, washed twice

using 600 µl of 70% ethanol. The ethanol was discarded after centrifugation at 16000 x g for 1 min. The DNA was dried in an oven at 37°C around 1 min and then rehydrated and dissolved in 60µl of sterile ultrapure water.

Amplification of regions of the three nuclear genes *HSP60* (Heat-shock Protein 60), *G3PDH* (Glyceraldehyde-3-Phosphate Dehydrogenase) and *RPB2* (DNA-dependent RNA polymerase subunit II) described by Staats et al. (2005) was done using the primers described in the Table 1.

Table 1. Primers employed for PCR amplification of regions of the genes *HSP60,G3PDH* and *RPB2* in *Botryti*s spp.

Primer name	Target region	Primer Sequence (5′-3′)
G3PDHfor+	G3PDH	GTTTTCCCAGTCACGACATTGACATCGTCGCTGT
G3PDHrev+		CAGGAAACAGTCATGACACCCACATCGTTGTCGT
HSP60for+	HSP60	GTTTTCCCAGTCACGACCAACAATTGAGATTTCCCCACAAG
HSP60rev+		CAGGAAACAGCTATGACGATGGATCCAGTGGTACCGAGCAT
RPB2for+	RPB2	GTTTCCCAGTCAGGACGATGATCGTGATCATTT
RPB2rev+		CAGGAAACAGTCATGACCCCATAGCTTGCTTACC

PCR amplification was carried out in a 25 µl reaction mixture containing 30-50 ng of DNA, 5X Colorless GoTaq Reaction Buffer (Promega, The Netherlands), 200µM each deoxynucleoside triphosphate (Promega, The Netherland.), 0.2 pmol of each primer (Amersham Pharmacia Biotech), and 1.0 U of GoTaq G2 DNA polymerase (Promega, The Netherlands). PCR conditions for *HSP60* and *RPB2* gene fragment amplification were as follows: 94°C for 5 min (1 cycle); 94°C for 30 s, 55°C for 30 s, and 72°C for 90 s (35 cycles), and then 72°C for 10 min (1 cycle). The same program with an annealing temperature of 64°C was used for *G3PDH* gene. The purified amplified fragments were sequenced by Macrogen Inc. (The Netherlands).

2.3.2 Phylogenetic analysis

From the collection of isolates obtained, initially 12 were sequenced based on *HSP60* gene. The sequence data obtained were employed to perform multiple alignments and sequence comparisons across isolates to select a set representing probably different genotypes or species. Then, the selected isolates were sequenced based on *G3PDH* and *RPB2* genes.

Sequence data of fragments of the genes *HSP60, G3PDH* and *RPB2* were analysed, assembled and consensus sequences were obtained using BioEdit sofware (Biological sequence alignment editor). Multiple sequences alignments and comparisons across isolates were performed by using Clustalw2 (http://www.ebi.ac.uk/Tools/msa/clustalw2/) .

HSP60, G3PDH and *RPB2* sequences of 26 *Botrytis* species were downloaded from TreeBASE (http://treebase.org/treebase-

web/home.html;jsessionid=B0D9A31750551B6430F2C506C36EF512) and phylogenetic trees based on *HSP60, RPB2, G3PDH* and all three genes were reconstructed by Maximum-likelihood with MEGA 6 (Tamura et al., 2013). *Sclerotinia sclerotiorum* and/or *Monilinia fructigena* were included in the phylogenetic analysis as out groups.

2.4 Pathogenicity assay

Pathogenicity tests with five of the *Botrytis* sp. isolates (V18F, V17S, B1LA, A7LA, B18F, A25SB) were carried out on detached leaves of tomato (*Solanum lycopersicum*, cv. Moneymaker) and *Nicotiana benthamiana* plants as described by Zhang and van Kan (2012).

In order to test each selected isolate, two composite tomato leaves and two *N. benthamiana* plants 5-week old were employed. Leaves were cut from tomato plants and stacked in horizontal position with their backsides down in strips of soak oasis placed in petri dishes containing a layer of water. The detached leaves were maintained in plastic trays with a lid to create a humid chamber. Similar moisture conditions were provided for *N. benthamiana* plants in pots.

For leaf inoculation, sporulating *Botrytis* sp. isolates grown for 8-10 days on malt extract agar plates at 18-20°C were flooded with 20 ml of sterile distilled water; the spores were gently removed using a Drigalski spatula and filtered through a glass fibre to eliminate fungi debris. The spore suspension obtained was adjusted to 10^6 spores /ml using a haemocytometer and a diluted (1:2) potato dextrose solution. Three 2-µl drops of the spore suspension were inoculated on the front side of tomato leaflets and *N. benthamiana* leaves.

One of the tomato detached leaves and one of the *N. benthamiana* plants was inoculated with *Botrytis cinerea* strain B05.10 (control) and with one of the testing *Botrytis* isolates. Each of these was inoculated on one-half of a leaflet/leaf. The other detached tomato leaf and *N. benthamiana* plant was inoculated with the testing isolate alone.

Infective developing lesions were monitored after 24 h and expanding lesions were measured (mm) using a calliper after 48 h.

3. Results

3.1 *Botrytis* isolates

Colonization in dandelion plants (*Taraxacum officinale*) by *Botrytis* sp. isolates was detected in 21% of the plants sampled (N=97) based on the visual observation of dark pigments in the selective medium (an indication of tannic acid degradation, a property of *Botrytis* spp.) and

the immunoassay test. From the 291 SBM plates containing the plant tissues sampled in the 4 sites for isolation, 23 fungal cultures were identify as *Botrytis* by the immunoassay test (Table 2). The percentage of isolates obtained from flowers, stems and leaves were 48%, 39% and 13% respectively (Figure 2). 5 additional fungal cultures identified as *Botrytis* by the immunoassay were not considered (Table 2, Figure 3). In these isolates, formation of sclerotia and conidiphores was absent, they presented slow growth and their morphology was quite distinct to the majority of isolates obtained and identified as *Botrytis.*

Table 2. *Botrytis* cultures identified by immunoassay test (kit QuickStix strips for *Botrytis* spp.) isolated from symptomless dandelion plants (*Taraxacum officinale).*

#	Isolate name	#	Isolate name
1	B1LA	15	A14L
2	B1FA	16	A25SA
3	B13F	17	A25SB
4	B14FA	18	A12F
5	B18F	19	A24FA
6	B21F	20	H17SA
7	B24F	21	H23SA
8	B25F	22	H23SB
9	V8S	23	H24S
10	V9S	24	A1LA*
11	V17S	25	A11FA*
12	V5F	26	B2L*
13	V18F	27	H1L*
14	A7LA	28	H15S*

*Unlikely *Botrytis* isolates

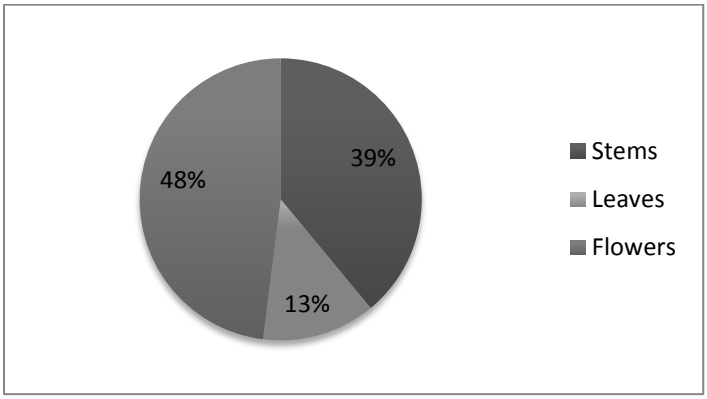


Figure 2. Percentage of *Botrytis* isolates obtained from different tissues of symptomless *Taraxacum officinale plants* (N=23).

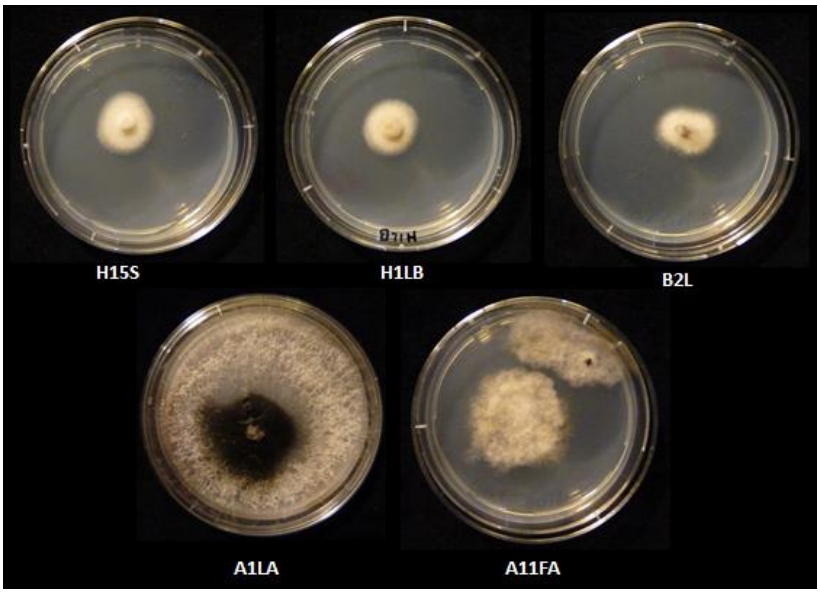


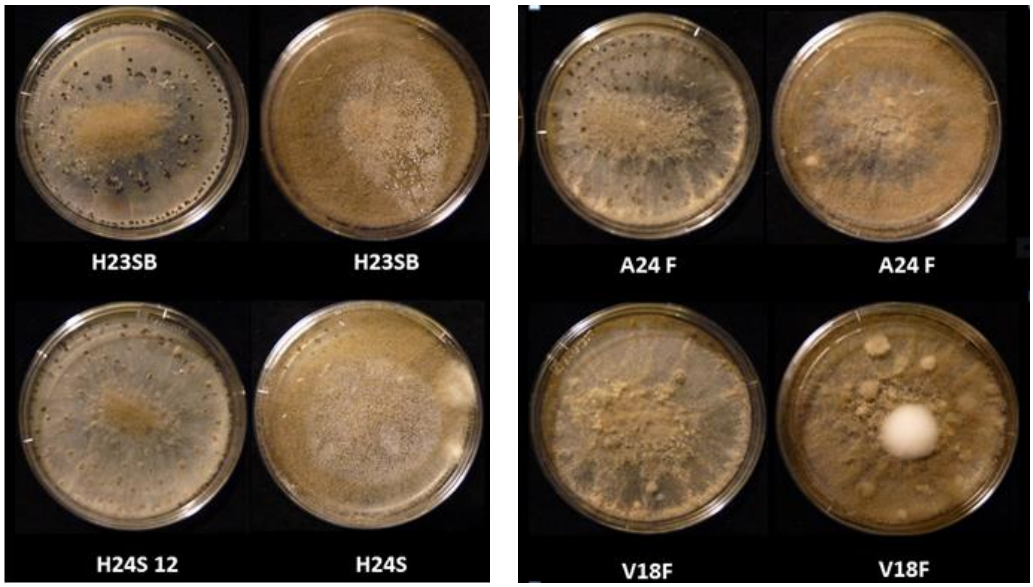
Figure 3. Morphology of unlikely *Botrytis* cultures (7 days old) on PDA with a positive identification by using QuickStix strips immunoassay test for *Botrytis* spp (Envirologix).

3.2 *Botrytis* species associated to *Taraxacum officinale*

The immunoassay test detected 23 isolates as *Botrytis* sp.. The phylogenetic analysis based on the *HSP60* gene of 12 of these isolates namely, B1LA, V17S, H24S, H23SA, H23SB, V5F, V9S, B24F, A24F, V18F, A14L and A25SA clustered them in the clade containing members; 3 different genotypes were found that showed the strongest phylogenetic association with *B. cinerea;* the genotype B1LA clustered closest to *B. pelargonii* strain 459.50; whereas V17S and a group of 5 strains (H24S, H23SA, H23SB, V5F, V9S) clustered as different genotypes together with *B. cinerea* strain MUCL87 (Figure 4, 5). Three other genotypes were distinguished that were associated with *B. pseudocinerea* they were B24F, A24F and a cluster of 3 isolates (V18F, A14L and A25SA) (Figure 4, 5). A set of 5 genotypes was chosen for further phylogenetic analysis.

The phylogenetic analysis based on *G3PDH* showed similar results; 4 of the genotypes clustered together with the species *B. cinerea* and 1 genotype was clustered with the species *B. pseudocinerea* (Figure 6). These results, were consistent with the phylogenetic analysis based *RPB2* and on all 3 genes (Figures 6, 7, 8). Unfortunately, for the phylogenetic analyses based on *RPB2* and all 3 genes the genotype V18F identified as *B. pseudocinerea* was excluded due to the low quality of the sequence data generated.

A B



B. cinerea *B. pseudocinerea*

Figure 4. Cultures of *Botrytis* species *pseudocinerea* (A) and *cinerea* (B) on malt extract agar isolated from symptomless dandelion plants (*Taraxacum officinale*). Sclerotia in cultures of 12 days old grown in darkness (left side in the pictures) and sporulating cultures of 15 days old (right side of the pictures).

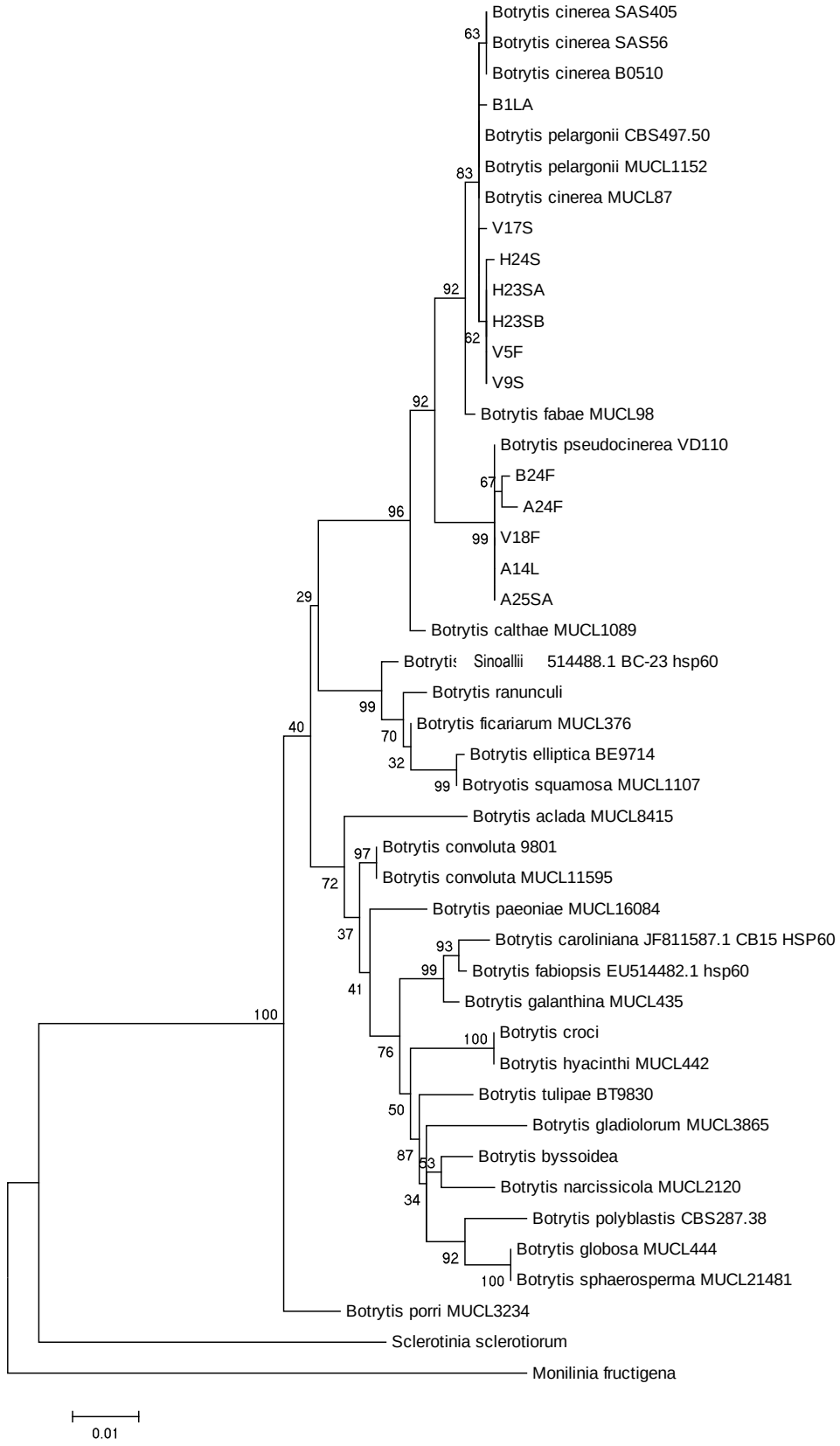


Figure 5. Phylogenetic tree based on *HSP60* gene for *Botrytis* species isolated from symptomless dandelion plants (*Taraxacum officinale)*

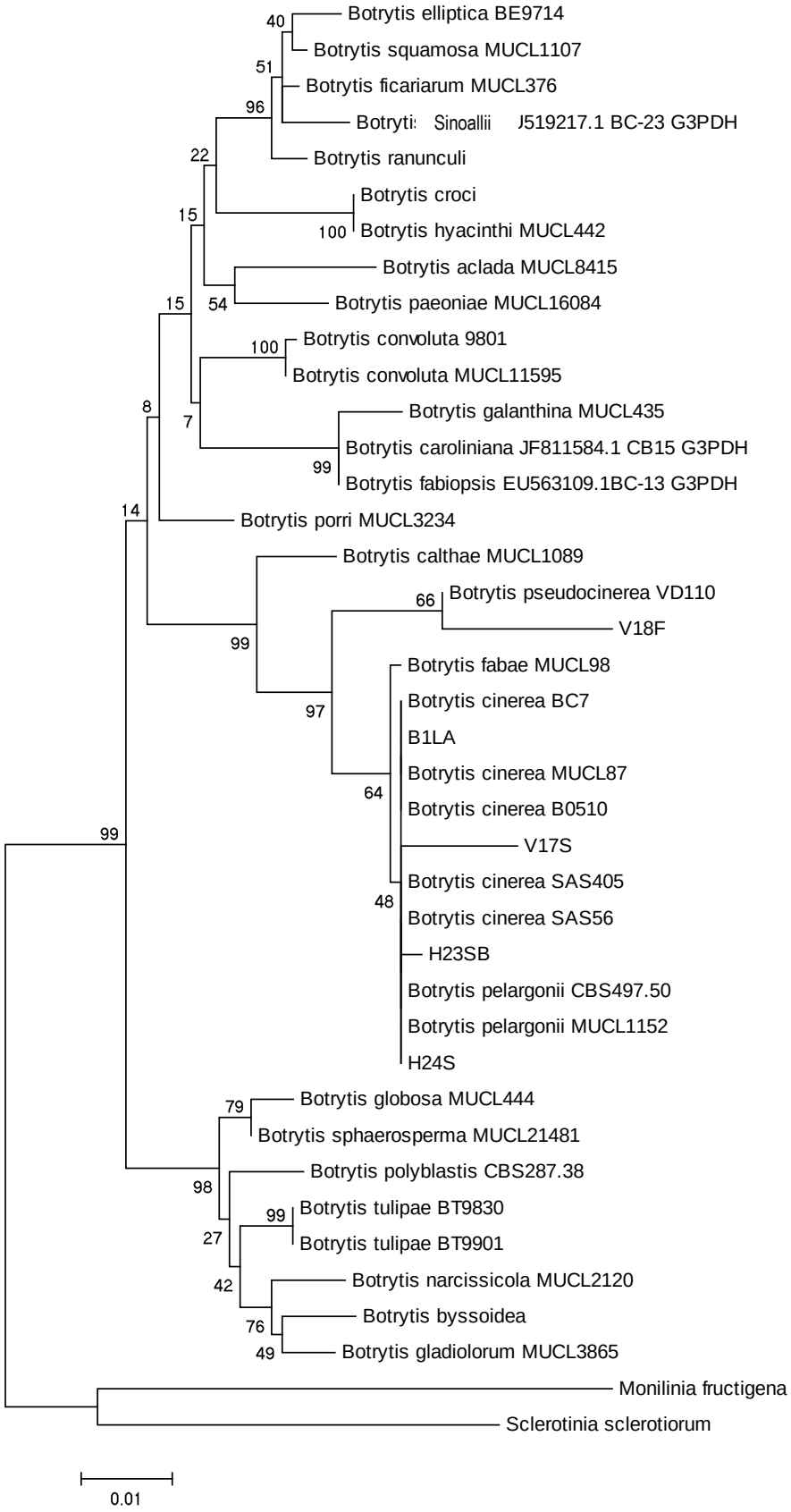


Figure 6. Phylogenetic tree based on *G3PDH* gene for *Botrytis* species isolated from symptomless dandelion plants (*Taraxacum officinale)*

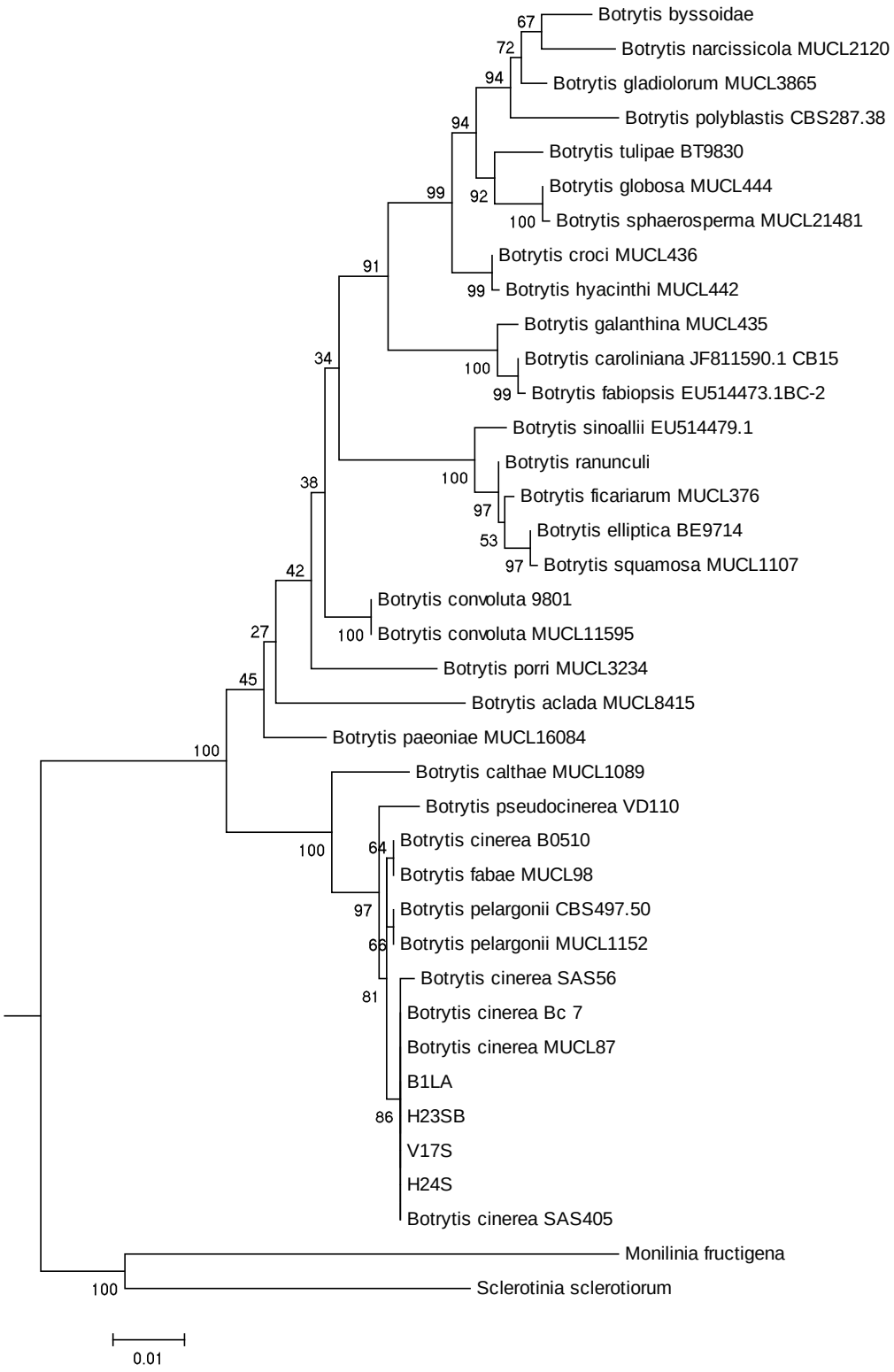


Figure 7. Phylogenetic tree based on *RPB2* gene for *Botrytis* species isolated from symptomless dandelion plants (*Taraxacum officinale)*

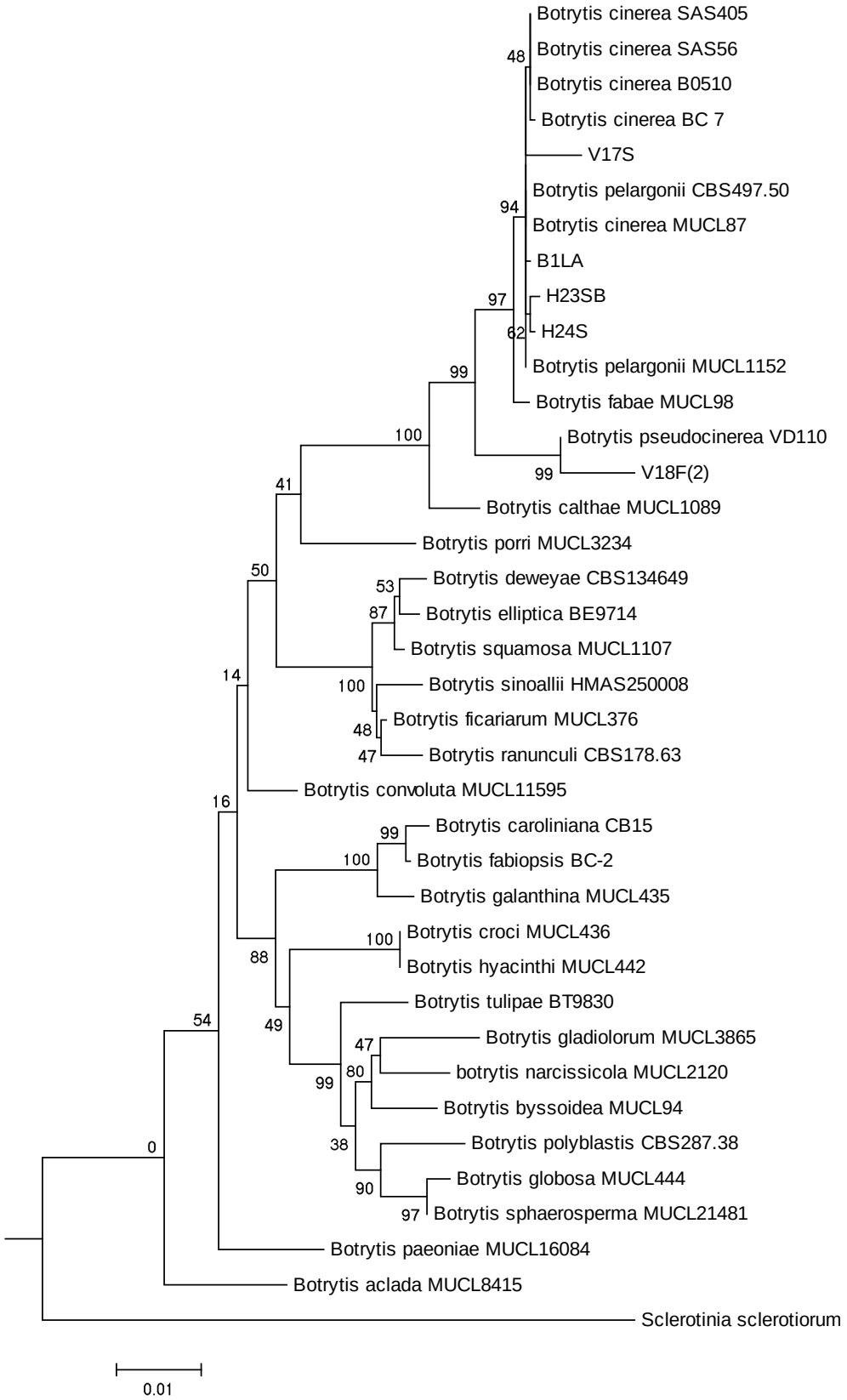


Figure 8. Phylogenetic tree based on *HSP60 and G3PDH* genes of *Botrytis* species isolated from symptomless dandelion plants (*Taraxacum officinale).*

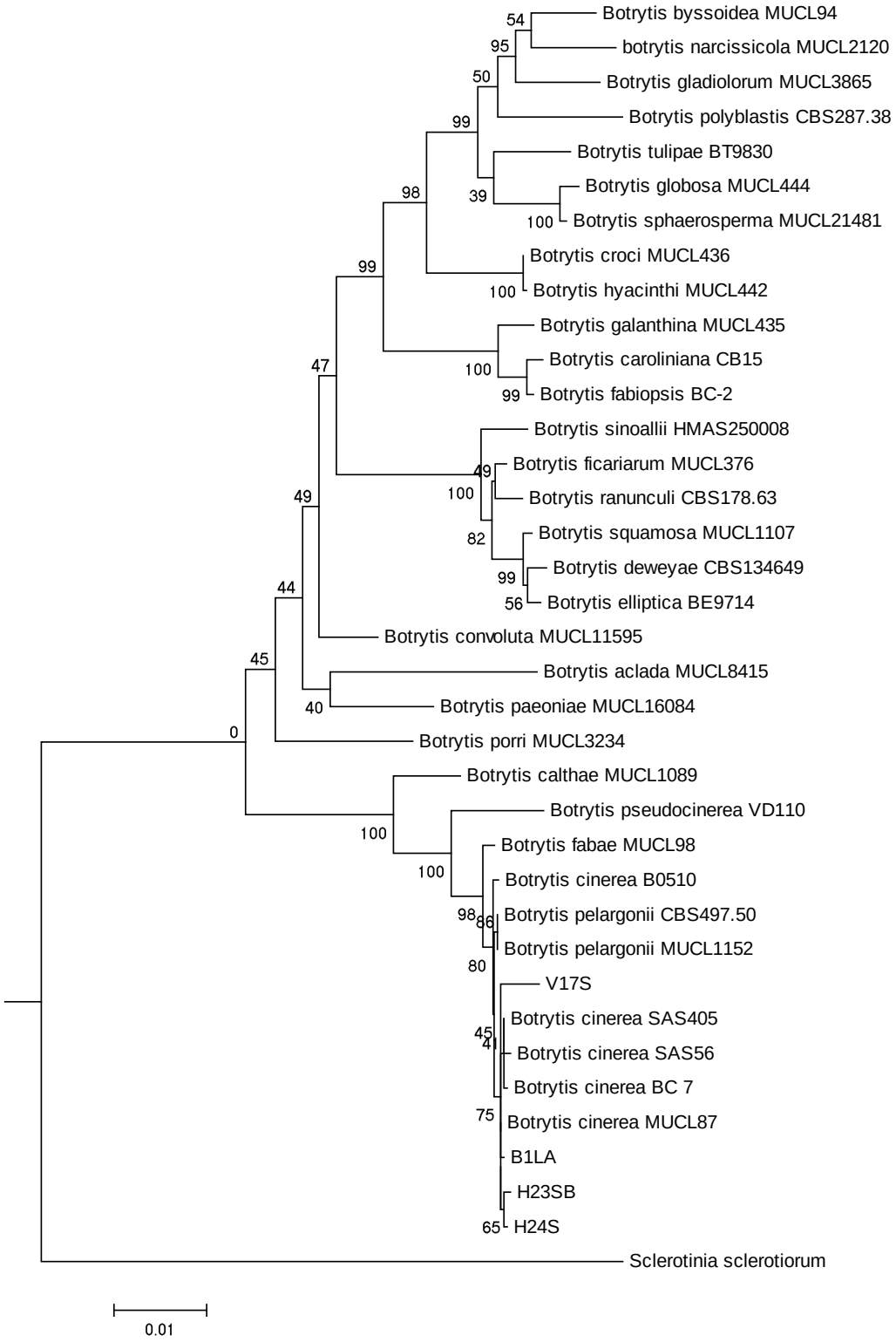
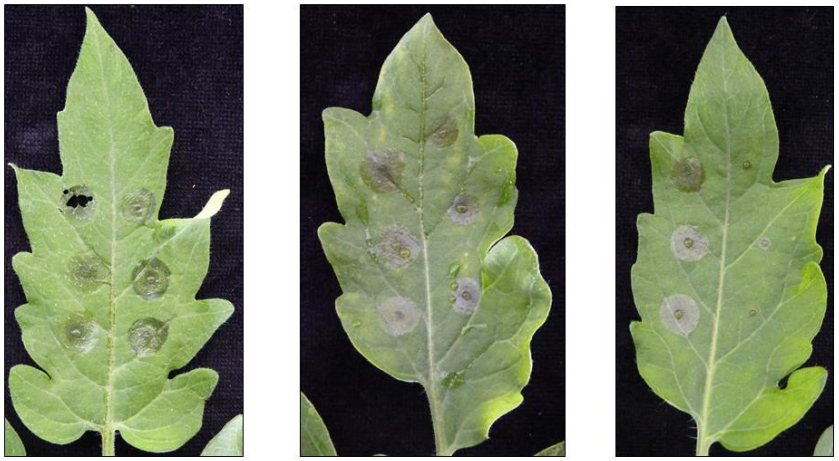


Figure 9. Phylogenetic tree based on *HSP60, G3PDH and RPB2* genes of *Botrytis* species isolated from symptomless dandelion plants (*Taraxacum officinale)*

Pathogenicity assay

Inoculation of tomato leaves and *N. benthamiana* plants demonstrated that 5 of the 6 testing *Botrytis* sp. isolates had the capacity to cause infective expanding lesions. In some of the isolates, lesions were comparable to those caused by *Botrytis cinerea* strain B05.10 employed as control (Figure 10, Table 3). Among the *Botrytis* isolates tested, inoculations with A25SB resulted in smaller lesions which developed slower compared with the other isolates inoculated.

A



B

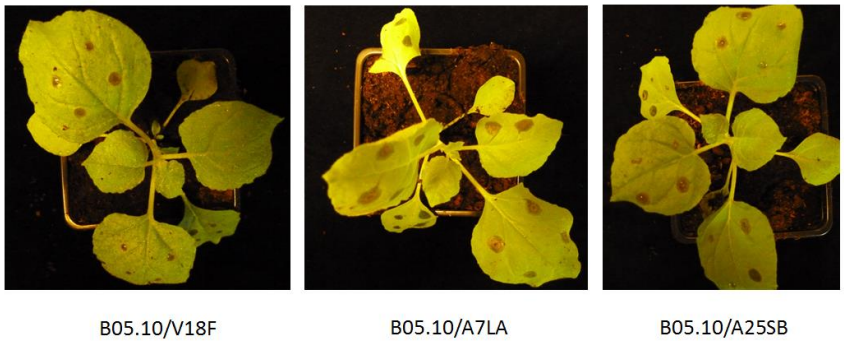


Figure 10. Lesion development (24hpi) on (A) tomato leaflets (cv. Moneymaker) and (B) *N. benthamiana* leaves inoculated (10^6 spores/ml) with *Botrytis cinerea* B05.10 (control) (leaf left side) and *Botrytis* sp. (leaf right side) isolated from symptomless *Taraxacum officinale* plants.

Table 3. Infective lesions (mm) on tomato (*S. lycopersicum)* and *N. benthamiana* leaves, produced by *Botrytis* spp. isolated from symptomless *Taraxacum officinale* plants.

Botrytis isolates	Tomato	*N. benthamiana*
	Lesion diameter (mm)	Lesion diameter (mm)
B. cinerea strain B05.10 (control)	18	14
Botrytis pseudocinerea (V18F)	16	10
Botrytis cinerea (V17S)	15	14
Botrytis cinerea (B1LA)	13	12
Botrytis sp A7LA	13	12
Botrytis sp B18F	12	13
Botrytis sp A25SB	10	7

Discussion

Botrytis cinerea is known as a polyphagous necrotrophic pathogen of plants which kills the host's cells by secreting toxic compounds and degrading enzymes, and inducing a programmed cell death by the host itself (van Kan, 2006; Choquer et al., 2007; Shlezinger et al., 2011). However, recent studies show a different "side" of this pathogen, in which it behaves as an endophyte and causes symptomless systemic infections in some plants (Sowley et al., 2010; Shipunov et al., 2008). Our results confirm the flexibility of this pathogen to behave as an endophyte. Dandelion plants investigated for endophytic colonization by *Botrytis* species resulted in isolation of different strains, which were identified by sequencing as *B. cinerea* and *B. pseudocinera*. In this study, the limited set of isolates sequenced made it difficult to elucidate if *Botrytis* species less related to *B. cinerea* were also present.

The flexible behaviour by *Botrytis* species agrees with a phylogenetic study of some fungal lineages in which it was determined that an interchangeable switch between a necrotrophic and endophytic behaviour occurred multiple times (Delaye et al., 2013). In contrast, a biotrophic condition in pathogen fungi was considered a more stable trait (Delaye et al., 2013).

Endophytes have commonly been defined as organisms which live inside plants without causing symptoms of disease (Carroll, 1988). However, this definition should be considered as a temporary status which includes a variety of microorganisms with different life history strategies (Schulz and Boyle, 2006). Endophytes can display variable associations which range from mutualism, commensalism, latent pathogenicity, and exploitation (Saikkonen et al.,

1998; Schulz and Boyle, 2006). The flexibility of these associations depends on the genetic dispositions of the two partners, their developmental stage and nutritional status as well as environmental factors (Schulz and Boyle 2006). For example, van Kan et al. (2014) suggest that a reduced genetic diversity in cultivated *Hemerocallis* hybrids could be a significant factor in the abrupt occurrence of a foliar disease called "spring sickness" that emerged from a switch of *B. deweyae* from endophytic to pathogenic infections in these plants. In grape, kiwi, strawberry and other hosts, *B. cinerea* may produce dormant infections which are then activated by the onset of senescence or stress of the host tissue (Sowley et al., 2010).

In the present study, the pathogenicity tests carried out on tomato and *N. benthamiana* with 5 of the 6 strains isolated from symptomless dandelion plants revealed that these strains were able to degrade plant tissues and cause the typical expanding disease lesions observed in aggressive infections by *Botrytis* pathogens. These results were similar to those reported by Sowley et al. 2010 in which *Botrytis cinerea* isolated from symptomless lettuce plants and later drop-inoculated on detached lettuce leaf pieces developed typical disease lesions. Endophytes and pathogens can have many of the same virulence factors which are required to infect and colonize the host (Schulz and Boyle, 2006). However, if the fungal virulence and the defensive response (which could include defensive metabolites and a general defence) by the plant are balanced, this interaction is asymptomatic (Schulz and Boyle, 2006). The conditions under which endophytic symptomless colonization by *Botrytis* species occurs have not yet been elucidated (Sowley et al. 2010; van Kan et al., 2014). Sowley et. al. (2010) suggest that during endophytic colonization by *B. cinerea* in lettuce, toxic compounds are not produced or are maintained at low levels to minimize host plant defence responses, and also mentions that active and aggressive infections by *B. cinerea* are only found in ripened fruits and wounded plant tissues. Van Kan et al. (2014) suggest that the switch from one lifestyle to another as described in *Botrytis sp*. is controlled by a mechanism which prevents or induce the expression of toxic compounds and degrading enzymes.

Overall this work we consider some information from some of the isolates is still lacking. Among the cultures identified as *Botrytis* by the immunoassay 5 isolates were considered unlikely members of the *Botrytis* genus due to their distinct morphology. However, the immunoassay test employed in this work is thought to be highly specific, therefore, obtaining information of these isolates by sequencing and a morphological description could confirm our assumption. Similarly, information by sequencing of the isolate A25SB could contribute

to explain if its reduced aggression to produce disease lesions is due to its adaptation as an endphyte or due to species particularities.

This study supports previous research in which the flexibility of *Botrytis* species to behave as necrotrophic pathogens or endophytes was established (Shipunov et al., 2008; Sowley et al. 2010), and highlights the necessity to generate new knowledge about the complex interactions which *Botrytis* species display with plants as well as the need to elucidate what could be the key factors capable of modulating such contrasting behaviours in these fungal species.

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Appendices

Appendix 1.

Table 1. Sampling sites of *Taraxacum officinale* for *Botrytis* isolation in Wageningen

	Sites	Latitude	Longitude
1	Bornsesteeg 6721 Bennekom	51.995452	5.653710
2	Hollandseweg 6705 BC Wageningen	51.985182	5.689045
3	Arboretum de Dreijen 6703 BL Wageningen	51.967068	5.677716
4	Veerdam 6703 PA, Wageningen	51.963223	5.688082

Appendix 2.

Multiple sequence alignment (Clustal 2.1) of *Botrytis* spp. based on consensus sequences of *HSP60,G3PDH, RPB2* genes

HSP60

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CLUSTAL 2.1 multiple sequence alignment


V17S            ------------------------------TTTAAGATACGACATGGATATCTGGTGATT 30
B1LA            ------------------------------------------------------TGGTGATT 8
H23SA           ----------------------CCACGTCGCTCTAAGATACGACATGGATATCTGGTGATT 39
V9S             ------------------------------GCTCTAAGATACGACATGGATATCTGGTGATT 32
H24S            --------------------TCCACGTCGCTCTAAGATACGACATGGATATCTGGTGATT 40
V5F             ------------------------------------------------------------ATT 3
H23SB           -----------------CAGTCCACGTCGCTTTAAGATACGACATGGATATCTGGTGATT 43
V18F            CTATGTGTGGGTTGACTTCAGTCCCATCGCTCTAAGATACGACATAGATATTTGGTGATT 60
A24F            ------------------------------------------------------------
B24F            ------------------------------------------------------------
A14L            ------------------------------------------------------------
A25SA           ------------------------------------------------------------


V17S            GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 90
B1LA            GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 68
H23SA           GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 99
V9S             GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 92
H24S            GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 100
V5F             GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 63
H23SB           GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 103
V18F            GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 120
A24F            ------TGAACCTGTGTTTAATTTATGAGCTCAAATTCCGGGTTGAGGGCAGAGCAGCTC 54
B24F            ----ACTGATCATGTTTTTAATTTAGGAGCTCGAATTCGGGGTTGAGGGCAGAGCAGCTC 56
A14L            GTAAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 60
A25SA           --AAACTGATCATGTTTTTAATTTAGGAGCTCAAATTCGGTGTTGAGGGCAGAGCAGCTC 58
                      ***:*.*** ********* ******.***** * ********************


V17S            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 150
B1LA            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 128
H23SA           TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 159
V9S             TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 152
H24S            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 160
V5F             TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 123
H23SB           TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 163
V18F            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 180
A24F            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 114
B24F            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 116
A14L            TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 120
A25SA           TTCTTGCTGGTGTTGAGACTTTGGCAAAAGCTGTTGCTACAACCTTGGGTCCCAAAGGCC 118
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V17S            GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 210
B1LA            GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 188
H23SA           GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 219
V9S             GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 212
H24S            GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 220
V5F             GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 183
H23SB           GAAATGTTCTTATTGAGTCAGCATATGGCTCCCCAAAGATCACTAAAGGTTTGCAAAACT 223
V18F            GAAATGTTCTTATTGAGTCAGCATATGGCTCTCCAAAGATCACTAAAGGTTTGTGAAACT 240
A24F            GAAATGTTCTTATTGAGTCAGCATATGGCTCTCCAAAGATCACTAAAGGTTTGTGAAACT 174
B24F            GAAATGTTCTTATTGAGTCAGCATATGGCTCTCCAAAGATCACTAAAGGTTTGTGAAACT 176
A14L            GAAATGTTCTTATTGAGTCAGCATATGGCTCTCCAAAGATCACTAAAGGTTTGTGAAACT 180
A25SA           GAAATGTTCTTATTGAGTCAGCATATGGCTCTCCAAAGATCACTAAAGGTTTGTGAAACT 178
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V17S            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 270
B1LA            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 248
H23SA           CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 279
V9S             CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 272
H24S            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 280
V5F             CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 243
H23SB           CCCGGCTACCTAGTTTCAAGATTCTAATTATTGGTGAATAGATGGTGTAACCGTTGCCAG 283
V18F            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGATGAATAGATGGTGTAACCGTTGCCAG 300
A24F            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGATGAATAGATGGTGTAACCGTTGCCAG 234
B24F            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGATGAATAGATGGTGTAACCGTTGCCAG 236
A14L            CCCGGCTACCTAGTTTCAAGATTCTAATTATTGATGAATAGATGGTGTAACCGTTGCCAG 240
A25SA           CCCGGCTACCTAGTTTCAAGATTCTAATTATTGATGAATAGATGGTGTAACCGTTGCCAG 238
                *********************************.************************

V17S            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 330
B1LA            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 308
H23SA           AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 339
V9S             AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 332
H24S            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 340
V5F             AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 303
H23SB           AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 343
V18F            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 360
A24F            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 294
B24F            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 296
A14L            AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 300
A25SA           AGCTATTTCCCTCAAGGACAAATTCGAGAACCTCGGTGCTAGACTTATCCAAGATGTTGC 298
                ************************************************************

V17S            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 390
B1LA            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 368
H23SA           CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 399
V9S             CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 392
H24S            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 400
V5F             CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 363
H23SB           CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 403
V18F            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 420
A24F            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 354
B24F            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 356
A14L            CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 360
A25SA           CTCGAAAACCAACGAGACCGCTGGTGATGGAACCACAACCGCTACTGTCCTTGCTAAATC 358
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V17S            TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 450
B1LA            TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 428
H23SA           TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 459
V9S             TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 452
H24S            TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 460
V5F             TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 423
H23SB           TATTTTCTCCGAGACCGTAAAGAACGTCGCCGCAGGATGCAACCCAATGGACTTGCGCAG 463
V18F            TATTTTCTCCGAGACCGTAAAGAACGTGGCCGCAGGATGCAACCCAATGGACTTGCGCAG 480
A24F            TATTTTCTCCGAGACCGTAAAGAACGTGGCCGCAGGATGCAACCCAATGGACTTGCGCAG 414
B24F            TATTTTCTCCGAGACCGTAAAGAACGTGGCCGCAGGATGCAACCCAATGGACTTGCGCAG 416
A14L            TATTTTCTCCGAGACCGTAAAGAACGTGGCCGCAGGATGCAACCCAATGGACTTGCGCAG 420
A25SA           TATTTTCTCCGAGACCGTAAAGAACGTGGCCGCAGGATGCAACCCAATGGACTTGCGCAG 418
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V17S            AGGTACTCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 510
B1LA            AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 488
H23SA           AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 519
V9S             AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 512
H24S            AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 520
V5F             AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 483
H23SB           AGGTACCCAAGCTGCCGTGGAGGCCGTTGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 523
V18F            AGGTACCCAAGCTGCCGTGGAGGCCGTAGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 540
A24F            AGGTACCCAAGCTGCCGTGGAGGCCGTAGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 474
B24F            AGGTACCCAAGCTGCCGTGGAGGCCGTAGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 476
A14L            AGGTACCCAAGCTGCCGTGGAGGCCGTAGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 480
A25SA           AGGTACCCAAGCTGCCGTGGAGGCCGTAGTTGAGTTTTTGCAAAAGAACAAGCGTGATAT 478
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V17S            CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 570
B1LA            CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 548
H23SA           CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 579
V9S             CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 572
H24S            CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 580
V5F             CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 543
H23SB           CACAACAAGCGAGGAAATCGCACAAGTTGCGACTATCAGTGCAAACGGTGATACCCACAT 583
V18F            CACAACCAGCGAGGAAATCGCACAAGTTGCGACTATTAGTGCAAACGGTGATACCCACAT 600
A24F            CACAACCAGCGAGGAAATCGCACAAGTTGCGACTATTAGTGCAAACGGTGATACCCACAT 534
B24F            CACAACCAGCGAGGAAATCGCACAAGTTGCGACTATTAGTGCAAACGGTGATACCCACAT 536
A14L            CACAACCAGCGAGGAAATCGCACAAGTTGCGACTATTAGTGCAAACGGTGATACCCACAT 540
A25SA           CACAACCAGCGAGGAAATCGCACAAGTTGCGACTATTAGTGCAAACGGTGATACCCACAT 538
                ******.***************************** ***********************

V17S            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 630
B1LA            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 608
H23SA           CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 639
V9S             CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 632
H24S            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 640
V5F             CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 603
H23SB           CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 643
V18F            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 660
A24F            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 594
B24F            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 596
A14L            CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 600
A25SA           CGGAAAATTGATTGCCAACGCTATGGAAAAGGTTGGAAAGGAAGGTGTTATCACAGTTAA 598
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V17S            GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 690
B1LA            GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 668
H23SA           GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 699
V9S             GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 692
H24S            GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 700
V5F             GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 663
H23SB           GGAAGGAAAGACCATGGAGGACGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 703
V18F            GGAAGGTAAGACCATGGAGGATGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 720
A24F            GGAAGGTAAGACCATGGAGGATGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 654
B24F            GGAAGGTAAGACCATGGAGGATGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 656
A14L            GGAAGGTAAGACCATGGAGGATGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 660
A25SA           GGAAGGTAAGACCATGGAGGATGAACTCGATATTACCGAGGGAATGAGATTTGACCGCGG 658
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V17S            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 750
B1LA            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 728
H23SA           TTATGTTTCTCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 759
V9S             TTATGTTTCTCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 752
H24S            TTATGTTTCTCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 760
V5F             TTATGTTTCTCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 723
H23SB           TTATGTTTCTCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 763
V18F            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 780
A24F            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 714
B24F            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 716
A14L            TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 720
A25SA           TTATGTTTCCCCATACTTCATCACCGATACCAAGTCGCAAAAGGTGGAATTCGAGAAGCC 718
                ********* **************************************************

V17S            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 810
B1LA            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 788
H23SA           ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 819
V9S             ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 812
H24S            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGACATTATCCCAGCACTTGA 820
V5F             ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 783
H23SB           ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 823
V18F            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 840
A24F            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 774
B24F            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 776
A14L            ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 780
A25SA           ATTGATTCTCCTTTCTGAGAAGAAGATTTCAAACGTCCAAGATATTATCCCAGCACTTGA 778
                **************************************** *****************

V17S            GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 870
B1LA            GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATCGCTGAAGATATCGATGGAGAAGC 848
H23SA           GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 879
V9S             GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 872
H24S            GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 880
V5F             GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 843
H23SB           GGCGTCTACTCAACTTCGTCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 883
V18F            GGCGTCTACTCAACTTCGCCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 900
A24F            GGCGTCTACTCAACTTCGCCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 834
B24F            GGCGTCTACTCAACTTCGCCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 836
A14L            GGCGTCTACTCAACTTCGCCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 840
A25SA           GGCGTCTACTCAACTTCGCCGTCCTTTGGTCATCATTGCTGAAGATATCGATGGAGAAGC 838
                ****************** ***************** ************************

V17S            TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 930
B1LA            TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 908
H23SA           TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 939
V9S             TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 932
H24S            TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 940
V5F             TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 903
H23SB           TCTCGCAGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 943
V18F            TCTCGCTGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 960
A24F            TCTCGCTGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 894
B24F            TCTCGCTGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 896
A14L            TCTCGCTGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 900
A25SA           TCTCGCTGTATGCATTCTTAACAAGCTCCGTGGTCAACTCCAAGTTGCCGCTGTCAAGGC 898
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V17S            CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 990
B1LA            CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 968
H23SA           CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 999
V9S             CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 992
H24S            CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 1000
V5F             CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 963
H23SB           CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 1003
V18F            CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTTGACCAATGC 1020
A24F            CCCCGG---------------------------------------------------- 900
B24F            CCCCGG---------------------------------------------------- 902
A14L            CCCCGGTTTCGGTGATAACCGAAAGTTCATCCTCGGCGATCTCGGTATCTTGACCAATG- 959
A25SA           CCCCGGTTTCGGTGATAACCGAAAGTCCATCCTCGGCGATCTCGGTATCTT--------- 949
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V17S            TACCGTCTTCACTGACGAGCTTGATCTCAA------ 1020
B1LA            TACCGTCTTCACTGACGA------------------ 986
H23SA           TACCGTCTTCACTGACGAGCTTGATCTCA------- 1028
V9S             TACCGTCTTCACTGACGAGCTTGATCTCAA------ 1022
H24S            TACCGTCTTCACTGACGAGCTTGATCTCAAGCTCGA 1036
V5F             TACCGTCTTCACTGACGAGCTTGATCTCAAGCTCGA 999
H23SB           TACCGTCTTCACTGACGAGCTTGATCTCAAGCTCG- 1038
V18F            TACCGTCTTCACTGACGAGCTTGATCTCAAG----- 1051
A24F            ------------------------------------
B24F            ------------------------------------
A14L            ------------------------------------
A25SA           ------------------------------------
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G3PDH

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CLUSTAL 2.1 multiple sequence alignment


H24S            ------------TTTCCGCTATCGGAGCTCCCGCAGATATCAAGGACCCGAGCTAATTTA 48
B1LA            --ATGCCGTAAGTTTCCGCTATCGGAGCTCCCGCAGATATCAAGGACCCGAGCTAATTTA 58
V17S            --ATGCCGTAAGTTTCCGCTATCGGAGCTCCCGCAGATATCAAGGACCCGAGCTAATTTA 58
H23SB           --ATGCCGTAAGTTTCCGCTATCGGAGCTCCCGCAGATATCAAGGACCCGAGCTAATTTA 58
V18F            ATATGCCGTAAGTTTCCGCTATCGGACTTCCCGCAGATATTACGGACCCGAGCTAATTTA 60
                             **************  ************ *.*****************

H24S            TGTTTTGCACAGGCATACATGTTGAAGTATGATTCCACCCACGGTCAATTCAAGGGTGAC 108
B1LA            TGTTTTGCACAGGCATACATGTTGAAGTATGATTCCACCCACGGTCAATTCAAGGGTGAC 118
V17S            TGTTTTGCACAGGCATACATGTTGAAGTATGATTCCACCCACGGTCAATTCAAGGGTGAC 118
H23SB           TGTTTTGCACAGGCATACATGTTGAAGTATGATTCCACCCACGGTCAATTCAAGGGTGAC 118
V18F            TATTTTGCACAGGCATACATGTTGAAGTATGATTCCACCCACGGTCAATTCAAGGGTGAC 120
                *.************************************************************

H24S            ATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCAAGTTCTACACCGAG 168
B1LA            ATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCAAGTTCTACACCGAG 178
V17S            ATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCAAGTTCTACACCGAG 178
H23SB           ATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCAAGTTCTACACCGAG 178
V18F            ATCAAGGTCCTTGCCGATGGATTGGAGGTCAATGGCAAGAAGGTCAAGTTCTACACCGAG 180
                ************************************************************

H24S            AGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACC 228
B1LA            AGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACC 238
V17S            AGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACC 238
H23SB           AGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACC 238
V18F            AGAGACCCAGCCAACATCCCATGGGCTGAGTCTGAGGCATACTACGTCGTCGAGTCCACC 240
                ************************************************************

H24S            GGTGTTTTCACCACCACCGAGAAGGCCAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTT 288
B1LA            GGTGTTTTCACCACCACCGAGAAGGCCAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTT 298
V17S            GGTGTTTTCACCACCACCGAGAAGGCCAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTT 298
H23SB           GGTGTTTTCACCACCACCGAGAAGGCCAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTT 298
V18F            GGTGTTTTCACCACCACCGAGAAGGCTAAGGCACATTTGAAGGGTGGTGCCAAGAAGGTT 300
                ************************* ********************************

H24S            GTTATCTCTGCTCCTTCTGCCGATGCCCCAATGTACGTTATGGGTGTCAACAACGAGACC 348
B1LA            GTTATCTCTGCTCCTTCTGCCGATGCCCCAATGTACGTTATGGGTGTCAACAACGAGACC 358
V17S            GTTATCTCTGCTCCTTCTGCCGATGCCCCAATGTACGTTATGGGTGTCAACAACGAGACC 358
H23SB           GTTATCTCTGCTCCTTCTGCCGATGCCCCAATGTACGTTATGGGTGTCAACAACGAGACC 358
V18F            GTTATCTCTGCTCCTTCTGCCGACGCCCCAATGTACGTTATGGGTGTCAACAACGAGACC 360
                ********************** ***********************************

H24S            TACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACAACCAACTGCTTGGCTCCT 408
B1LA            TACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACAACCAACTGCTTGGCTCCT 418
V17S            TACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACAACCAACTGCTTGGCTCCT 418
H23SB           TACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACAACCAACTGCTTGGCTCCT 418
V18F            TACACTGGTGATGTTGATGTTATCTCCAACGCCTCTTGCACAACCAACTGCTTGGCTCCT 420
                ************************************************************

H24S            CTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGTTTGATGACCACCATCCAC 468
B1LA            CTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGTTTGATGACCACCATCCAC 478
V17S            CTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGTTTGATGACCACCATCCAC 478
H23SB           CTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGGTTGATGACCACCATCCAC 478
V18F            CTCGCCAAGGTCATCAACGATGAGTTCACCATCATTGAAGGTTTGATGACCACCATCCAC 480
                ************************************** ******************

H24S            TCCTACACCGCTACCCAAAAGACCGTTGATGGTCCATCCGCTAAGGATTGGCGTGGAGGA 528
B1LA            TCCTACACCGCTACCCAAAAGACCGTTGATGGTCCATCCGCTAAGGATTGGCGTGGAGGA 538
V17S            TCCTACACCGCTACCCAAAAGACCGTTGATGGTCCATCCGCTAAGGATTGGCGTGGAGGA 538
H23SB           TCCTACACCGCTACCCAAAAGACCGTTGATGGTCCATCCGCTAAGGATTGGCGTGGAGGA 538
V18F            TCCTACACCGCTACCCAAAAGACCGTTGACGGTCCATCCGCTAAGGATTGGCGTGGAGGA 540
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H24S            CGTACCGCTGCTCAAAACATCATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAG 588
B1LA            CGTACCGCTGCTCAAAACATCATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAG 598
V17S            CGTACCGCTGCTCAAAACATCATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAG 598
H23SB           CGTACCGCTGCTCAAAACATCATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAG 598
V18F            CGTACCGCTGCTCAAAACATCATCCCATCGAGCACCGGTGCTGCCAAGGCTGTCGGAAAG 600
                ************************************************************

H24S            GTCATCCCAGTCCTTAACGGCAAACTCACCGGAATGTCCATGCGTGTTCCAACTGCCAAC 648
B1LA            GTCATCCCAGTCCTTAACGGCAAACTCACCGGAATGTCCATGCGTGTTCCAACTGCCAAC 658
V17S            GTCATCCCAGTCCTTAACGGCAAACTCACCGGAATGTCCATGCGTGTTCCAACTGCCAAC 658
H23SB           GTCATCCCAGTCCTTAACGGCAAACTCACCGGAATGTCCATGCGTGTTCCAACTGCCAAC 658
V18F            GTCATCCCAGTGCTTAACGGCAAACTCACCGGAATGTCCATGCGTGTTCCAACTGCCAAC 660
                *********** ************************************************

H24S            GTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTACGATGAGATCAAG 708
B1LA            GTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTACGATGAGATCAAG 718
V17S            GTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTACGATGAGATCAAG 718
H23SB           GTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTACGATGAGATCAAG 718
V18F            GTCTCAGTTGTTGACTTGACTGTCCGCATTGAGAAGGGTGCTTCTTATGATGAGATTAAG 720
                ********************************************* ******** ***

H24S            GCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGTAAGTTACTCCATTACTCTTTC 768
B1LA            GCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGTAAGTTACTCCATTACTCTTTC 778
V17S            GCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGTAAGTTACTCCATTACTCTTTC 778
H23SB           GCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGTAAGTTACTCCATTACTCTT-- 776
V18F            GCCGTCATCAAGAAGGCTGCTGATGGTCCTCTCAAGGGCAGGTTACTCCATCACTCTTTC 780
                ************************************ *.********** ******

H24S            TTCGGCTCTAATTTGCTAATCGTAACACAGGCATATTGGCTTACACTGAGGACGATGTTG 828
B1LA            TTCGGCTCTAATTTGCTAATCGTAACACAGGCATATTGGCTTACACTGAGGACGATGTTG 838
V17S            TTCGGCTCTAATTTGCTAATCGTAACACAGGCATATTGGCTTACACTGAGGACGATGTTG 838
H23SB           -TCGGCTCTAATTTGCTAATCGTAACACAGGCATATTGGCTTACACTGAGGACGATGTCG 835
V18F            TTTGGCTCTAATTTACTAATCATAATACAGGCATATTGGCTTACACTGAGGACGATGTTG 840
                 * ***********.******.*** ******************************** *

H24S            TCTCCACTGACATGAACGG-TGACAACCA-CTCCTCCATCTT-CGATGCCA-AGGCTGGT 884
B1LA            TCTCCACTGACATGAACGG-TGACAACCA-CTCCTCCATCTT-CGATGCCA-AGGCTGGT 894
V17S            TCTCCACTGACATGAACGGT-GACAACCA-CTCCTCCATCTTCTGATGCCATAGGCTGGT 896
H23SB           TCTCCACTGACATGAACGGT-GACAACCA-CTCCTCCATCTT-CGATGCCA-AGGCTGGT 891
V18F            TCTCCACTGACATGAACGG-TGACAACCA-CTCCTCCATTCTTCGATGCCCAAGGCCGGT 898
                ******************  ******** *********  *  ******. **** ***

H24S            ATCTCCCTCAACGCAAACTTCGT------- 907
B1LA            ATCTCCCTCAACGCAAACTTCGTCAAGTTG 924
V17S            ATCTCC----------------------- 902
H23SB           ATCTCCCTCA------------------- 901
V18F            ATCTCCC---------------------- 905
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RPB2

CLUSTAL 2.1 multiple sequence alignment

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V17S            -----CCGCAGATTGACAACAGACGTGTACAGATACTTGCAACGTTGCGTGGAAAACAAC 55
H24S            ------------------ACAGACGTGTACAGATACTTGCAACGTTGCGTGGAAAACAAC 42
B1LA            CCGGTCCGCAGATTGACAACAGACGTGTACAGATACTTGCAACGTTGCGTGGAAAACAAC 60
H23SB           CCTGTCCGCAGATTGACAACAGACGTGTACAGATACTTGCAACGTTGCGTGGAAAACAAC 60
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V17S            CGAGAGTTTAATTTGACTTTGGGTGTGAAATCAACAACAATCACCAACGGTCTGAAATAT 115
H24S            CGAGAGTTTAATTTGACTTTGGGTGTGAAATCAACAACAATCACCAACGGTCTGAAATAT 102
B1LA            CGAGAGTTTAATTTGACTTTGGGTGTGAAATCAACAACAATCACCAACGGTCTGAAATAT 120
H23SB           CGAGAGTTTAATTTGACTTTGGGTGTGAAATCAACAACAATCACCAACGGTCTGAAATAT 120
                ************************************************************

V17S            TCTTTGGCCACAGGTAACTGGGGTGACCAGAAGAAGGCAGCAAGTTCTACCGCCGGAGTG 175
H24S            TCTTTGGCCACAGGTAACTGGGGTGACCAGAAGAAGGCAGCAAGTTCTACCGCCGGAGTG 162
B1LA            TCTTTGGCCACAGGTAACTGGGGTGACCAGAAGAAGGCAGCAAGTTCTACCGCCGGAGTG 180
H23SB           TCTTTGGCCACAGGTAACTGGGGTGACCAGAAGAAGGCAGCAAGTTCTACCGCCGGAGTG 180
                ************************************************************

V17S            TCTCAAGTGTTGAACAGATATACCTTTGCATCCACACTTTCTCATTTGCGCCGAACCAAT 235
H24S            TCTCAAGTGTTGAACAGATATACCTTTGCATCCACACTTTCTCATTTGCGCCGAACCAAT 222
B1LA            TCTCAAGTGTTGAACAGATATACCTTTGCATCCACACTTTCTCATTTGCGCCGAACCAAT 240
H23SB           TCTCAAGTGTTGAACAGATATACCTTTGCATCCACACTTTCTCATTTGCGCCGAACCAAT 240
                ************************************************************

V17S            ACACCCATTGGACGTGATGGAAAGATCGCCAAACCTAGACAGCTGCATAATACCCATTGG 295
H24S            ACACCCATTGGACGTGATGGAAAGATCGCCAAACCTAGACAGCTGCATAATACCCATTGG 282
B1LA            ACACCCATTGGACGTGATGGAAAGATCGCCAAACCTAGACAGCTGCATAATACCCATTGG 300
H23SB           ACACCCATTGGACGTGATGGAAAGATCGCCAAACCTAGACAGCTGCATAATACCCATTGG 300
                ************************************************************

V17S            GGCTTGGTCTGTCCGGCAGAGACGCCCGAAGGACAAGCTTGTGGTTTGGTTAAGAATTTG 355
H24S            GGCTTGGTCTGTCCGGCAGAGACGCCCGAAGGACAAGCTTGTGGTTTGGTTAAGAATTTG 342
B1LA            GGCTTGGTCTGTCCGGCAGAGACGCCCGAAGGACAAGCTTGTGGTTTGGTTAAGAATTTG 360
H23SB           GGCTTGGTCTGTCCGGCAGAGACGCCCGAAGGACAAGCTTGTGGTTTGGTTAAGAATTTG 360
                ************************************************************

V17S            GCTCTGATGTGTTACGTTACAGTCGGTACGCCAAGTGATCCAATCGTTGAGTTCATGATT 415
H24S            GCTCTGATGTGTTACGTTACAGTCGGTACGCCAAGTGATCCAATCGTTGAGTTCATGATT 402
B1LA            GCTCTGATGTGTTACGTTACAGTCGGTACGCCAAGTGATCCAATCGTTGAGTTCATGATT 420
H23SB           GCTCTGATGTGTTACGTTACAGTCGGTACGCCAAGTGATCCAATCGTTGAGTTCATGATT 420
                ************************************************************

V17S            CAACGAAATATGGAAGTATTGGAGGAGTATGAACCACTCCGAGCCCCCAATGCAACAAAG 475
H24S            CAACGAAATATGGAAGTATTGGAGGAGTATGAACCACTCCGAGCCCCCAATGCAACAAAG 462
B1LA            CAACGAAATATGGAAGTATTGGAGGAGTATGAACCACTCCGAGCCCCCAATGCAACAAAG 480
H23SB           CAACGAAATATGGAAGTATTGGAGGAGTATGAACCACTCCGAGCCCCCAATGCAACAAAG 480
                ************************************************************

V17S            GTTTTCGTCAATGGTGTTTGGGTTGGTATTCATCGAGATCCTGCTCATTTGGTCAAATGT 535
H24S            GTTTTCGTCAATGGTGTTTGGGTTGGTATTCATCGAGATCCTGCTCATTTGGTCAAATGT 522
B1LA            GTTTTCGTCAATGGTGTTTGGGTTGGTATTCATCGAGATCCTGCTCATTTGGTCAAATGT 540
H23SB           GTTTTCGTCAATGGTGTTTGGGTTGGTATTCATCGAGATCCTGCTCATTTGGTCAAATGT 540
                ************************************************************

V17S            GTCCAAGATCTTCGTAGATCACACTTGATCTCTCATGAAGTTTCACTTATTCGAGAAATT 595
H24S            GTCCAAGATCTTCGTAGATCACACTTGATCTCTCATGAAGTTTCACTTATTCGAGAAATT 582
B1LA            GTCCAAGATCTTCGTAGATCACACTTGATCTCTCATGAAGTTTCACTTATTCGAGAAATT 600
H23SB           GTCCAAGATCTTCGTAGATCACACTTGATCTCTCATGAAGTTTCACTTATTCGAGAAATT 600
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V17S            CGTGATAGAGAATTCAAGATTTTCACAGATGCAGGACGAGTGTGCAGACCTCTATTGGTT 655
H24S            CGTGATAGAGAATTCAAGATTTTCACAGATGCAGGACGAGTGTGCAGACCTCTATTGGTT 642
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B1LA            CGTGATAGAGAATTCAAGATTTTCACAGATGCAGGACGAGTGTGCAGACCTCTATTGGTT 660
H23SB           CGTGATAGAGAATTCAAGATTTTCACAGATGCAGGACGAGTGTGCAGACCTCTATTGGTT 660
                ************************************************************

V17S            ATTGACAATGATCCTGACAGCGCAAACAAAGGTAACTTGGTGTTGAACAAGGATCACATT 715
H24S            ATTGACAATGATCCTGACAGCGCAAACAAAGGTAACTTGGTGTTGAACAAGGATCACATT 702
B1LA            ATTGACAATGATCCTGACAGCGCAAACAAAGGTAACTTGGTGTTGAACAAGGATCACATT 720
H23SB           ATTGACAATGATCCTGACAGCGCAAACAAAGGTAACTTGGTGTTGAACAAGGATCACATT 720
                ************************************************************

V17S            CGCCGTCTGGAGGATGATCAGTTGCTACCAGCAAACATGGATAAGGATGAGAAAGTAAGA 775
H24S            CGCCGTCTGGAGGATGATCAGTTGCTACCAGCAAACATGGATAAGGATGAGAAAGTAAGA 762
B1LA            CGCCGTCTGGAGGATGATCAGTTGCTACCAGCAAACATGGATAAGGATGAGAAAGTAAGA 780
H23SB           CGCCGTCTGGAGGATGATCAGTTGCTACCAGCAAACATGGATAAGGATGAGAAAGTAAGA 780
                ************************************************************

V17S            AACGGATACTATGGATTCCAAGGTTTGATTAATGACGGTGTGGTTGAGTACCTGGATGCC 835
H24S            AACGGATACTATGGATTCCAAGGTTTGATTAATGACGGTGTGGTTGAGTACCTGGATGCC 822
B1LA            AACGGATACTATGGATTCCAAGGTTTGATTAATGACGGTGTGGTTGAGTACCTGGATGCC 840
H23SB           AACGGATACTATGGATTCCAAGGTTTGATTAATGACGGTGTGGTTGAGTACCTGGATGCC 840
                ************************************************************

V17S            GAGGAAGAAGAGACTGTCATGATTACAATGACACCTGAAGATCTGGACATCTCCCGACAG 895
H24S            GAGGAAGAAGAGACTGTCATGATTACAATGACACCTGAAGATCTGGACATCTCCCGACAG 882
B1LA            GAGGAAGAAGAGACTGTCATGATTACAATGACACCTGAAGATCTGGACATCTCCCGACAG 900
H23SB           GAGGAAGAAGAGACTGTCATGATTACAATGACACCTGAAGATCTGGACATCTCCCGACAG 900
                ************************************************************

V17S            CTTCAGGCTGGTTACCAAATTCGTCCTGACGAAAGTGGTGATTTGAACAAGCGTGTTAAG 955
H24S            CTTCAGGCTGGTTACCAAATTCGTCCTGACGAAAGTGGTGATTTGAACAAGCGTGTTAAG 942
B1LA            CTTCAGGCTGGTTACCAAATTCGTCCTGACGAAAGTGGTGATTTGAACAAGCGTGTTAAG 960
H23SB           CTTCAGGCTGGTTACCAAATTCGTCCTGACGAAAGTGGTGATTTGAACAAGCGTGTTAAG 960
                ************************************************************

V17S            GCACCTATCAATCCAACTGCTCATGTCTGGACTCATTGTGAAATTCATCCAAGTATGATC 1015
H24S            GCACCTATCAATCCAACTGCTCATGTCTGGACTCATTGTGAAATTCATCCAAGTATGATC 1002
B1LA            GCACCTATCAATCCAACTGCTCATGTCTGGACTCATTGTGAAATTCATCCAAGTATGATC 1020
H23SB           GCACCTATCAATCCAACTGCTCATGTCTGGACTCATTGTGAAATTCATCCAAGTATGATC 1020
                ************************************************************

V17S            TTGGGTATCTGCGCAAGCATTATTCCCTTCCCGGATCACAATCAGGTAAGCTTTAAGTTC 1075
H24S            TTGGGTATCTGCGCAAGCATTATTCCCTTCCCGGATCACAATCAGGTAAGCTTTA----- 1057
B1LA            TTGGGTATCTGCGCAAGCATTATTCCCTTCCCGGATCACAATCAGGTAAGCTTTAAGTTC 1080
H23SB           TTGGGTATCTGCGCAAGCATTATTCCCTTCCCGGATCACAATCAGGTAAGCTTTAAGTTC 1080
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V17S            AATGAATTTATTTG 1089
H24S            -------------
B1LA            AATGAATTTAT--- 1091
H23SB           AATGAA-------- 1086
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