

Table 1 CytB

Position number based on alignment to reference sequence from *Zymoseptoria tritici* (NCBI gene accession number AY247413).

Amino acid substitution in archetype	Homologous position in other species
F129L	F129L in PHAKPA
	F129L in PLASVI
	F129L in PYRIOR
	F129L in PYRNTE
	F129L in PYRNTR
	F129L in RHIZSO
G137	G137R in PYRNTR
G143A	G143A in ALTEAL
	G143A in ALTELY
	G143A in ALTESO
	G143A in ALTETO
	G143A in BOTRCI
	G143A in CERCBE
	G143A in COLLGR
	G143A in ERYSGT
	G143A in LEPTNO
	G143A in MICDMA
	G143A in MONGNI
	G143A in MYCOFI
	G143A in MYCORA
	G143A in PLASVI
	G143A in PLEOAL
	G143A in PODOFU
	G143A in PSPECU
	G143A in PYRIOR
	G143A in PYRNTR
	G143A in RHIZSO
G143A in VENTIN	

Table 2 Cyp51A

Position number based on alignment to reference sequence from *Aspergillus fumigatus* (Cyp51A) (NCBI gene accession number AF338659).

Amino acid substitution in archetype	Homologous position in other species
N22D	NA
S52T	NA
G54E/K/R/V/W	G54W in ASPEPA
Y68	Y132N in ASPEFL
Q88H	NA
L98H	NA
V101F	NA
Y121F	Y136F in AJELCP
N125I	NA
K133	K197N in ASPEFL
G138C/R/S	NA
Q141H	NA
H147Y	NA
P216L	NA
F219S	NA
M220K/I/T/V	NA
D280	D282E in ASPEFL
M286	M288L in ASPEFL
T289A	NA
S297T	NA
P394L	NA
Y431C	NA
G432S	NA
G434C	NA
T440A	NA
G448S	NA
T470	T469S in ASPEFL
Y491H	NA
F495I	NA

Table 3 Cyp51B

Position number based on alignment to reference sequence from *Zymoseptoria tritici* (NCBI gene accession number AY253234).

Amino acid substitution in archetype	Homologous position in other species
T66	A61V in CANDAL
C80	S79T in ERYSGT
D107V	NA
L126	F120L in PHAKPA
D134G	NA
V136A/C/G	NA
Y137F	Y132F/H in CANDAL
	Y132F/H in PHAKPA
	Y134F in PUCCRT
	Y136F in ERYSGH
	Y136F in ERYSGT
	Y136F in MONIFC
	Y136F in MYCOFI
	Y136F in UNCNEC
Y145F in FILBNF	
M145L	NA
K148	K142R in PHAKPA
	K143E in CANDAL
	K147Q in ERYSGH
V151	I145F in PHAKPA
D176	K175N in ERYSGT
N178S	NA
S208T	NA
N284H	NA
E300	E297K in CERCBE
H303Y	NA
A311G	A313G in MYCOFI
G312A	NA
I333	I330T in CERCBE
A379G	A381G in MYCOFI
I381V	NA
P391	P394S in CERCBE
A410T	S405F in CANDAL
G412A	NA
H430	H399P in ASPEFL
A453	D411N in ASPEFL
Y459C/D/N/S/P/Δ	Y461D in MYCOFI
G460D/Δ	G462A in MYCOFI
Y461D/H/S	F449S in CANDAL
	Y463D/H/N in MYCOFI
G476	G464S in CANDAL
	G484S in FILBNF
R479	R467K in CANDAL

I483	I471T in CANDAL
	I475T in PHAKPA
V490L	NA
T496	T454P in ASPEFL
G510C	NA
S524T	S508T in PYRPBR
	S509T in ERYSGH

Table 4 b-Tubulin

Position number based on alignment to reference sequence from *Aspergillus nidulans* (benA) (NCBI gene accession number M17519).

Amino acid substitution in archetype	Homologous position in other species
H6L/Y	H6Y in LEPTNO
	H6Y in MONIFC
Y50N/S	Y50N in GIBBFU β_1 -tubulin
	Y50C in GIBBZE β_2 -tubulin
	Y50C in HYPMOD
M73	Q73R in GIBBZE β_2 -tubulin
Q134K	NA
A165V	NA
F167	F167Y in CERCBE
	F167Y in COCHHE
	F167Y in GIBBZE β_2 -tubulin
	F167Y in NEUSCR
	F167Y in PENIEX
E198D/K/Q	E198A/G/K/V in BOTRCI
	E198A in CERCBE
	E198V in GIBBFU β_2 -tubulin
	E198K/L/Q in GIBBZE β_2 -tubulin
	E198A/Q in HELMSO
	E198A/K in MONIFC
	E198G in NEUSCR
	E198A/K in PENIAU
	E198A/K/V in PENIEX
	E198K in PENIIT
	E198A/G in PYRPBR
	E198G/K in RHYNSE
	E198A/K in SCLEHO
	E198A in SCLESC
E198A/K in VENTIN	
F200Y	F200Y in BOTRCI
	F200Y in GIBBFU β_2 -tubulin
	F200Y in GIBBZE β_2 -tubulin
	F200Y in PENIAU
	F200Y in PENIIT
	F200Y in RHYNSE
	F200Y in VENTIN
L240	L240F in MONILA
	L240F in PYRPBR
	L240F in VENTIN
M257L	NA

Table 5 SdhB

Position number based on alignment to reference sequence from *Pyrenophora teres* f. sp. *teres* (NCBI gene accession number XM_003302513).

Amino acid substitution in archetype	Homologous position in other species
P230	P225F/L/T in BOTRCI
N235	N225I/T in SEPTTR
	N230I in BOTRCI
H277Y	H249L/N/Y in EUROOR
	H257L in USTIMA
	H267L/R/Y in SEPTTR
	H273Y in SCLESC
	H272L/R/V/Y in BOTRCI
	H277R/Y in ALTEAL
	H277R/Y in ALTESO
	H277R/Y in DIDYBR
	H278R/Y in CORYCA
	H->Y in PODOXA ^a
I279	I269V in SEPTTR

^aAmino acid position number for this substitution is unknown as only 176-bp fragment of SdhB gene has been sequenced in both sensitive and resistant isolates

Table 6 SdhC

Position number based on alignment to reference sequence from *Pyrenophora teres* f. sp. *teres* (NCBI gene accession number XM_003302752).

Amino acid substitution in archetype	Homologous position in other species
T68	T79I/N in SEPTTR
W69	W80S in SEPTTR
S73	S73P in CORYCA
	A84V in SEPTTR
	A85V in BOTRCI
N75S	N86K/S in SEPTTR
T78	T90I in EUROOR
G79R	G90R in SEPTTR
H134R	H134R in ALTEAL
	H146R in SCLESC
S135R	NA
H141	H152R in SEPTTR

Table 7 SdhD

Position number based on alignment to reference sequence from *Pyrenophora teres* f. sp. *teres* (NCBI gene accession number XM_003297196).

Amino acid substitution in archetype	Homologous position in other species
S118	S89P in CORYCA
D124E/N	NA
H134R	H132R in BOTRCI
	H132R in SCLESC
	H133R in ALTEAL
	H133R in ALTESO
G138	G109V in CORYCA
D145G	D124E in EUROOR
	D129E in SEPTTR

Table 8 CesA3

Position number based on alignment to reference sequence from *Phytophthora infestans* (NCBI gene accession number EF563995).

Amino acid substitution in archetype	Homologous position in other species
Q1077	Q1077K in PHYTCP
G1105A/V	G1105S/V in PLASVI
	G1105V/W in PSPECU
V1109L	V1109L/M in PHYTCP
	V1109L in PHYTDR

Table 9 OS-1

Position number based on alignment to reference sequence from *Botrytis cinerea* (Bos1) (NCBI gene accession number AF435964).

Amino acid substitution in archetype	Homologous position in other species
F250	F267L in PLEOAL
I273	L290S in PLEOAL
I365N/R/S	NA
V368F	NA
Q369H/P	NA
N373S	NA
G403	G420D in ALTELO
T447S	NA
E738	E753K in ALTEBI
T750	T765R in PLEOAL
Q762	Q777R in PLEOAL

Table 10 Abbreviations of Species Names

Abbreviation (EPPO code)	Name of pathogen
AJELCP	<i>Histoplasma capsulatum</i>
ALTEAL	<i>Alternaria alternata</i>
ALTEBI	<i>Alternaria brassicicola</i>
ALTELO	<i>Alternaria longipes</i>
ALTELY	<i>Alternaria arborescens</i>
ALTESO	<i>Alternaria solani</i>
ALTETO	<i>Alternaria tenuissima</i>
ASPEFL	<i>Aspergillus flavus</i>
ASPEFU	<i>Aspergillus fumigatus</i>
ASPEND	<i>Aspergillus nidulans</i>
ASPEPA	<i>Aspergillus parasiticus</i>
BOTRCI	<i>Botrytis cinerea</i>
CANDAL	<i>Candida albicans</i>
COCHHE	<i>Bipolaris maydis</i>
COLLGR	<i>Colletotrichum graminicola</i>
CORYCA	<i>Corynespora cassiicola</i>
CERCBE	<i>Cercospora beticola</i>
DIDYBR	<i>Stagonosporopsis cucurbitacearum</i>
ERYSGH	<i>Blumeria graminis</i> f. sp. <i>hordei</i>
ERYSGT	<i>Blumeria graminis</i> f. sp. <i>tritici</i>
EUROOR	<i>Aspergillus oryzae</i>
FILBNF	<i>Cryptococcus neoformans</i>
GIBBFU	<i>Fusarium fujikuroi</i>
GIBBZE	<i>Fusarium graminearum</i>
HELMSO	<i>Helminthosporium solani</i>
HYPMOD	<i>Hypomyces odoratus</i>
LEPTNO	<i>Parastagonospora nodorum</i>
MONGNI	<i>Microdochium nivale</i>
MONIFC	<i>Monilinia fructicola</i>
MONILA	<i>Monilinia laxa</i>
MICDMA	<i>Microdochium majus</i>
MYCOFI	<i>Mycosphaerella fijiensis</i>
MYCORA	<i>Didymella rabiei</i>
NEUSCR	<i>Neurospora crassa</i>
PENIAU	<i>Penicillium aurantiogriseum</i>
PENIEX	<i>Penicillium expansum</i>
PENIIT	<i>Penicillium italicum</i>
PHAKPA	<i>Phakopsora pachyrhizi</i>
PHYTCP	<i>Phytophthora capsici</i>
PHYTDR	<i>Phytophthora melonis</i>
PHYTIN	<i>Phytophthora infestans</i>
PLASVI	<i>Plasmopara viticola</i>
PLEOAL	<i>Stemphylium vesicarium</i>
PODOFU	<i>Podosphaera fusca</i>
PODOXA	<i>Podosphaera xanthii</i>
PSPECU	<i>Pseudoperonospora cubensis</i>
PUCCRT	<i>Puccinia triticina</i>
PYRIOR	<i>Magnaporthe grisea</i>

PYRNTE	<i>Pyrenophora teres</i>
PYRNTR	<i>Pyrenophora tritici-repentis</i>
PYRPBR	<i>Pyrenopeziza brassicae</i>
RHIZSO	<i>Rhizoctonia solani</i>
RHYNSE	<i>Rhynchosporium secalis</i>
SCLEHO	<i>Sclerotinia homoeocarpa</i>
SCLESC	<i>Sclerotinia sclerotiorum</i>
SEPTTR	<i>Zymoseptoria tritici</i>
UNCNEC	<i>Erysiphe necator</i>
USTIMA	<i>Ustilago maydis</i>
VENTIN	<i>Venturia inaequalis</i>

References for Tables and Figures

1, 23-25

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