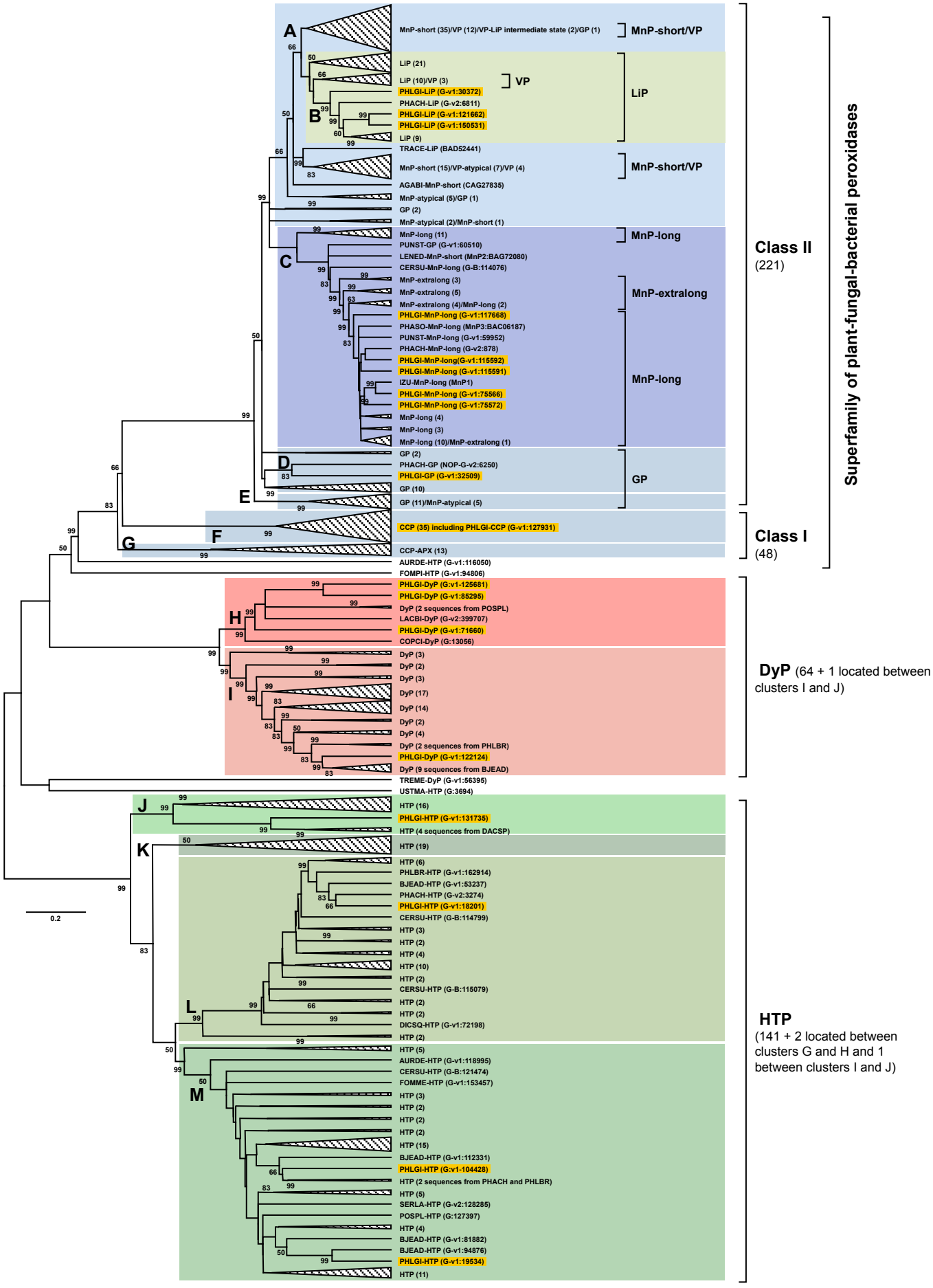
A
B
C
D
E
F
G
H
I
J
K
L
M
MnP-short (35)/VP (12)/VP-LiP intermediate state (2)/GP (1)
MnP-short/VP
LiP (21)
LiP (10)/VP (3)
VP
PHLGI-LiP (G-v1:30372)
PHACH-LiP (G-v2:6811)
PHLGI-LiP (G-v1:121662)
PHLGI-LiP (G-v1:150531)
LiP (9)
LiP
TRACE-LiP (BAD52441)
MnP-short (15)/VP-atypical (7)/VP (4)
MnP-short/VP
AGABI-MnP-short (CAG27835)
MnP-atypical (5)/GP (1)
GP (2)
MnP-atypical (2)/MnP-short (1)
MnP-long (11)
MnP-long
PUNST-GP (G-v1:60510)
LENED-MnP-short (MnP2:BAG72080)
CERSU-MnP-long (G-B:114076)
MnP-extralong (3)
MnP-extralong (5)
MnP-extralong
MnP-extralong (4)/MnP-long (2)
PHLGI-MnP-long (G-v1:117668)
PHASO-MnP-long (MnP3:BAC06187)
PUNST-MnP-long (G-v1:59952)
PHACH-MnP-long (G-v2:878)
PHLGI-MnP-long(G-v1:115592)
PHLGI-MnP-long (G-v1:115591)
IZU-MnP-long (MnP1)
MnP-long
PHLGI-MnP-long (G-v1:75566)
PHLGI-MnP-long (G-v1:75572)
MnP-long (4)
MnP-long (3)
MnP-long (10)/MnP-extralong (1)
GP (2)
PHACH-GP (NOP-G-v2:6250)
PHLGI-GP (G-v1:32509)
GP (10)
GP
GP (11)/MnP-atypical (5)
CCP (35) including PHLGI-CCP (G-v1:127931)
CCP-APX (13)
AURDE-HTP (G-v1:116050)
FOMPI-HTP (G-v1:94806)
PHLGI-DyP (G:v1-125681)
PHLGI-DyP (G-v1:85295)
DyP (2 sequences from POSPL)
LACBI-DyP (G-v2:399707)
PHLGI-DyP (G-v1:71660)
COPCI-DyP (G:13056)
DyP (3)
DyP (2)
DyP (3)
DyP (17)
DyP (14)
DyP (2)
DyP (4)
DyP (2 sequences from PHLBR)
PHLGI-DyP (G-v1:122124)
DyP (9 sequences from BJEAD)
TREME-DyP (G-v1:56395)
USTMA-HTP (G:3694)
HTP (16)
PHLGI-HTP (G-v1:131735)
HTP (4 sequences from DACSP)
HTP (19)
HTP (6)
PHLBR-HTP (G-v1:162914)
BJEAD-HTP (G-v1:53237)
PHACH-HTP (G-v2:3274)
PHLGI-HTP (G-v1:18201)
CERSU-HTP (G-B:114799)
HTP (3)
HTP (2)
HTP (4)
HTP (10)
HTP (2)
CERSU-HTP (G-B:115079)
HTP (2)
HTP (2)
DICSQ-HTP (G-v1:72198)
HTP (2)
HTP (5)
AURDE-HTP (G-v1:118995)
CERSU-HTP (G-B:121474)
FOMME-HTP (G-v1:153457)
HTP (3)
HTP (2)
HTP (2)
HTP (2)
HTP (15)
BJEAD-HTP (G-v1:112331)
PHLGI-HTP (G:v1-104428)
HTP (2 sequences from PHACH and PHLBR)
HTP (5)
SERLA-HTP (G-v2:128285)
POSPL-HTP (G:127397)
HTP (4)
BJEAD-HTP (G-v1:81882)
BJEAD-HTP (G-v1:94876)
PHLGI-HTP (G-v1:19534)
HTP (11)
0.2
Class II
(221)
Class I
(48)
Superfamily of plant-fungal-bacterial peroxidases
DyP (64 + 1 located between clusters I and J)
HTP
(141 + 2 located between clusters G and H and 1 between clusters I and J)