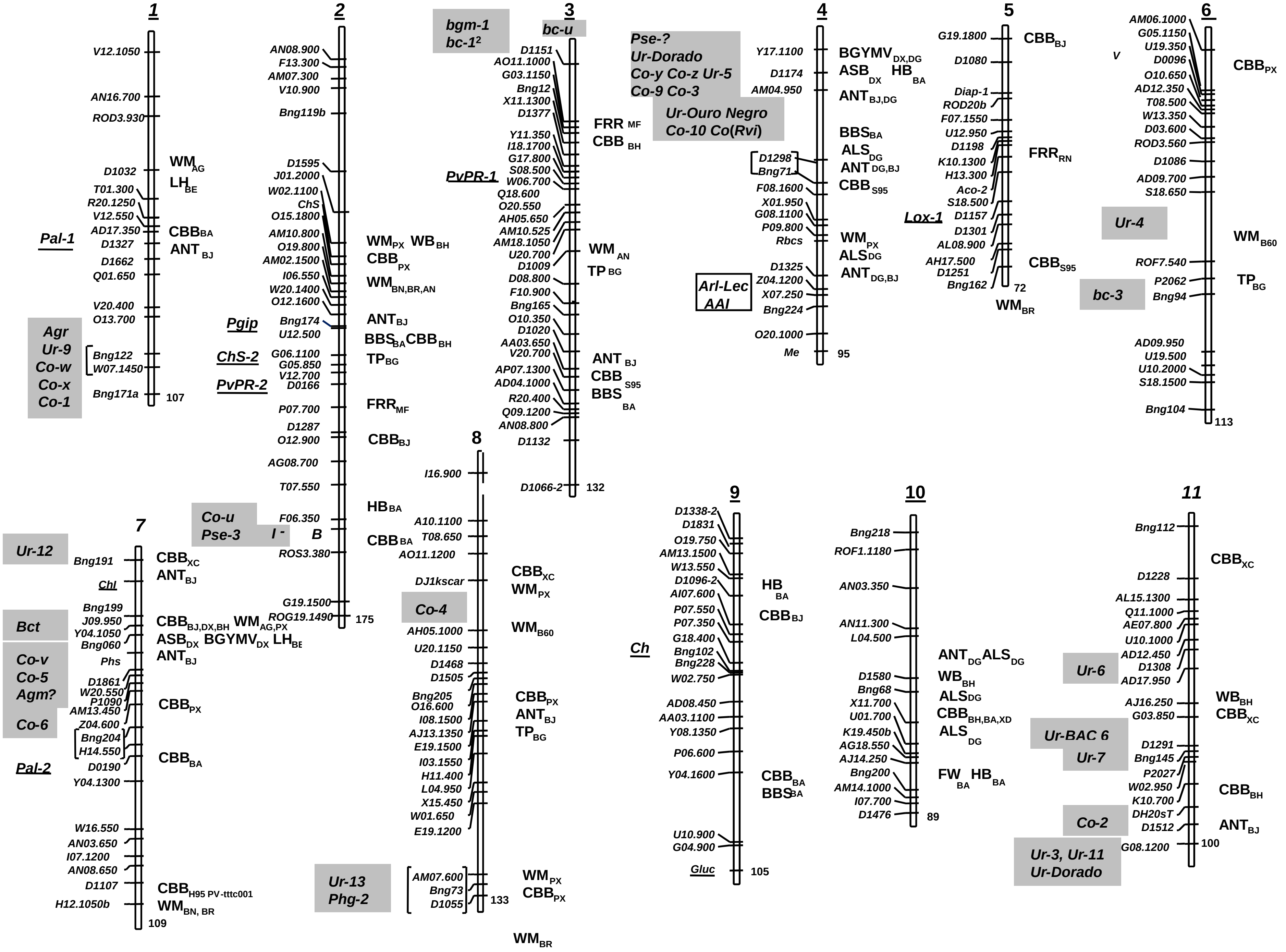
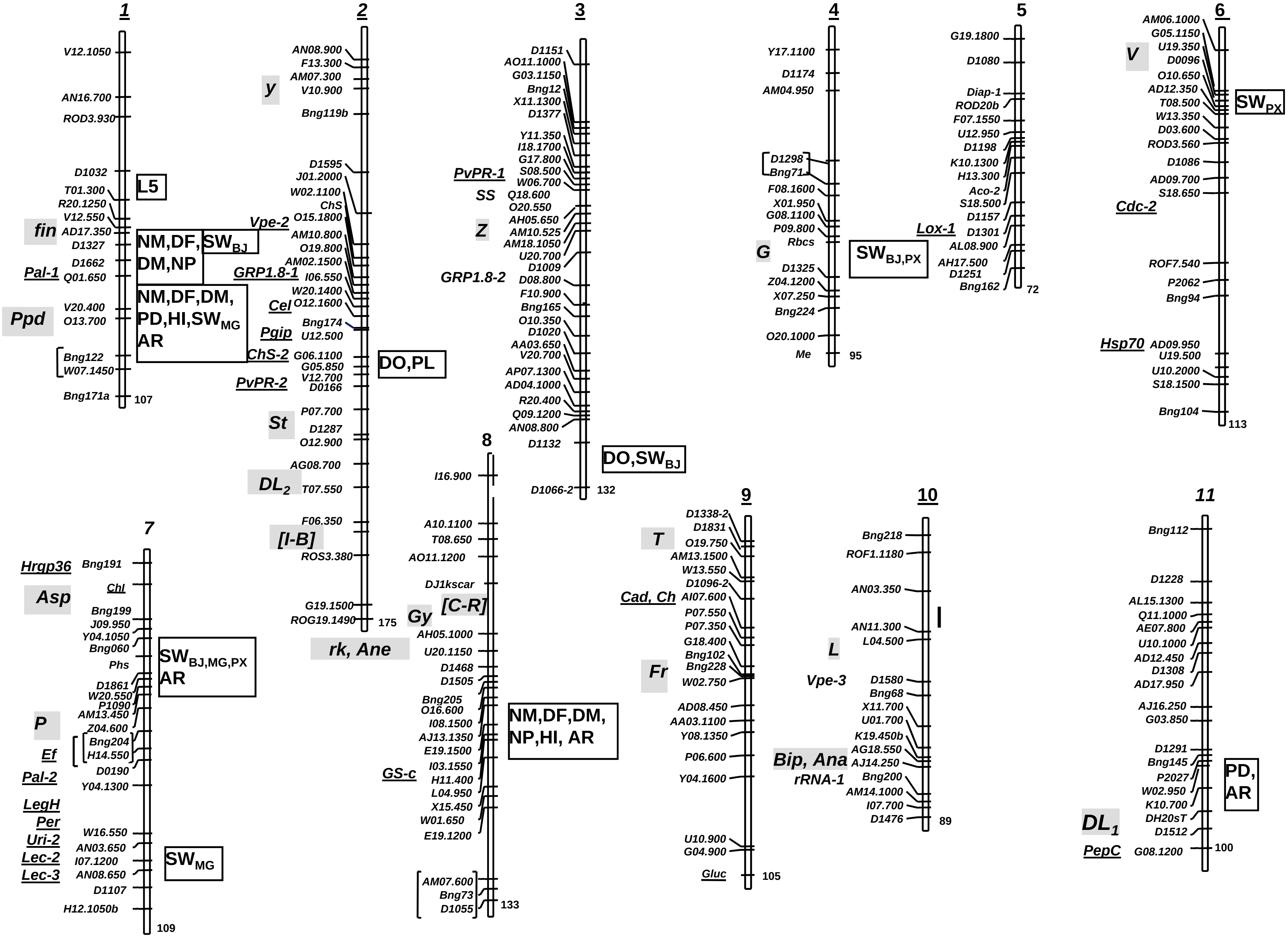

1
V12.1050
AN16.700
ROD3.930
D1032
T01.300
R20.1250
V12.550
AD17.350
D1327
D1662
Q01.650
V20.400
O13.700
Bng122
W07.1450
Bng171a
107
WM$_{AG}$
LH$_{BE}$
CBB$_{BA}$
ANT$_{BJ}$
Pal-1
Agr
Ur-9
Co-w
Co-x
Co-1
2
AN08.900
F13.300
AM07.300
V10.900
Bng119b
D1595
J01.2000
W02.1100
ChS
O15.1800
AM10.800
O19.800
AM02.1500
I06.550
W20.1400
O12.1600
Bng174
U12.500
G06.1100
G05.850
V12.700
D0166
P07.700
D1287
O12.900
AG08.700
T07.550
F06.350
B
ROS3.380
G19.1500
ROG19.1490
175
WM$_{PX}$ WB$_{BH}$
CBB$_{PX}$
WM$_{BN,BR,AN}$
ANT$_{BJ}$
BBS$_{BA}$ CBB$_{BH}$
TP$_{BG}$
FRR$_{MF}$
CBB$_{BJ}$
HB$_{BA}$
CBB$_{BA}$
Pgip
ChS-2
PvPR-2
Co-u
Pse-3
I -
bgm-1
bc-1^2
3
bc-u
D1151
AO11.1000
G03.1150
Bng12
X11.1300
D1377
Y11.350
I18.1700
G17.800
S08.500
W06.700
Q18.600
O20.550
AH05.650
AM10.525
AM18.1050
U20.700
D1009
D08.800
F10.900
Bng165
O10.350
D1020
AA03.650
V20.700
AP07.1300
AD04.1000
R20.400
Q09.1200
AN08.800
D1132
D1066-2
132
FRR$_{MF}$
CBB$_{BH}$
WM$_{AN}$
TP$_{BG}$
ANT$_{BJ}$
CBB$_{S95}$
BBS$_{BA}$
PvPR-1
Pse-?
Ur-Dorado
Co-y Co-z Ur-5
Co-9 Co-3
Ur-Ouro Negro
Co-10 Co(Rvi)
4
Y17.1100
D1174
AM04.950
D1298
Bng71
F08.1600
X01.950
G08.1100
P09.800
Rbcs
D1325
Z04.1200
X07.250
Bng224
O20.1000
Me
95
BGYMV$_{DX,DG}$
ASB$_{DX}$ HB$_{BA}$
ANT$_{BJ,DG}$
BBS$_{BA}$
ALS$_{DG}$
ANT$_{DG,BJ}$
CBB$_{S95}$
WM$_{PX}$
ALS$_{DG}$
ANT$_{DG,BJ}$
Arl-Lec
AAI
5
G19.1800
D1080
Diap-1
ROD20b
F07.1550
U12.950
D1198
K10.1300
H13.300
Aco-2
S18.500
D1157
D1301
AL08.900
AH17.500
D1251
Bng162
72
CBB$_{BJ}$
FRR$_{RN}$
CBB$_{S95}$
WM$_{BR}$
Lox-1
6
AM06.1000
G05.1150
U19.350
D0096
O10.650
AD12.350
T08.500
W13.350
D03.600
ROD3.560
D1086
AD09.700
S18.650
ROF7.540
P2062
Bng94
AD09.950
U19.500
U10.2000
S18.1500
Bng104
113
V
CBB$_{PX}$
WM$_{B60}$
TP$_{BG}$
Ur-4
bc-3
7
Bng191
Chl
Bng199
J09.950
Y04.1050
Bng060
Phs
D1861
W20.550
P1090
AM13.450
Z04.600
Bng204
H14.550
D0190
Y04.1300
W16.550
AN03.650
I07.1200
AN08.650
D1107
H12.1050b
109
CBB$_{XC}$
ANT$_{BJ}$
CBB$_{BJ,DX,BH}$ WM$_{AG,PX}$
ASB$_{DX}$ BGYMV$_{DX}$ LH$_{BE}$
ANT$_{BJ}$
CBB$_{PX}$
CBB$_{BA}$
CBB$_{H95\ PV\text{-}tttc001}$
WM$_{BN,\ BR}$
Ur-12
Bct
Co-v
Co-5
Agm?
Co-6
Pal-2
8
I16.900
A10.1100
T08.650
AO11.1200
DJ1kscar
AH05.1000
U20.1150
D1468
D1505
Bng205
O16.600
I08.1500
AJ13.1350
E19.1500
I03.1550
H11.400
L04.950
X15.450
W01.650
E19.1200
AM07.600
Bng73
D1055
133
CBB$_{XC}$
WM$_{PX}$
WM$_{B60}$
CBB$_{PX}$
ANT$_{BJ}$
TP$_{BG}$
WM$_{PX}$
CBB$_{PX}$
WM$_{BR}$
Co-4
Ur-13
Phg-2
9
D1338-2
D1831
O19.750
AM13.1500
W13.550
D1096-2
AI07.600
P07.550
P07.350
G18.400
Bng102
Bng228
W02.750
AD08.450
AA03.1100
Y08.1350
P06.600
Y04.1600
U10.900
G04.900
Gluc
105
HB$_{BA}$
CBB$_{BJ}$
CBB$_{BA}$
BBS$_{BA}$
Ch
10
Bng218
ROF1.1180
AN03.350
AN11.300
L04.500
D1580
Bng68
X11.700
U01.700
K19.450b
AG18.550
AJ14.250
Bng200
AM14.1000
I07.700
D1476
89
ANT$_{DG}$ ALS$_{DG}$
WB$_{BH}$
ALS$_{DG}$
CBB$_{BH,BA,XD}$
ALS$_{DG}$
FW$_{BA}$ HB$_{BA}$
11
Bng112
D1228
AL15.1300
Q11.1000
AE07.800
U10.1000
AD12.450
D1308
AD17.950
AJ16.250
G03.850
D1291
Bng145
P2027
W02.950
K10.700
DH20sT
D1512
G08.1200
100
CBB$_{XC}$
WB$_{BH}$
CBB$_{XC}$
CBB$_{BH}$
ANT$_{BJ}$
Ur-6
Ur-BAC 6
Ur-7
Co-2
Ur-3, Ur-11
Ur-Dorado

Legend

- Comprehensive genomic map of disease resistance genes and QTL in common bean [Abstracted from Miklas et al., 2006]. The standard common bean chromosome nomenclature is presented (chromosomes numbered 1-11) (Pedrosa-Harand et al., 2008) corresponding to the B1-B11 designation from the core map of Freyre et al. (1998), which was based on the original map (Nodari et al., 1993) and resembles maps previously presented by Kelly et al. (2003), Kelly and Vallejo (2004) and Blair et al. (2003; 2007). The chromosomes with underlined number designations have been rotated top to bottom from Freyre et al. (1998) in order for the short arm to be presented on top. The previous chromosome number (I –XI; Pedrosa et al., 2003) is shown at bottom of each chromosome. Directly to the left of each linkage group are the framework molecular markers (smaller font), the monogenic disease resistance genes (shaded boxes), defense related genes (underlined), and arcelin, lectin and alpha-amylase inhibitor genes (clear box). The *Co* are anthracnose resistance loci, *Ur* rust resistance loci (*Ur-Dorado*, *Ur-Ouro Negro,* and *Ur-BAC 6* refer to the line source of unnamed genes), *Pse* halo blight resistance loci, *I* and *bc* are dominant and recessive genes respectively for resistance to BCMV, *bgm-1* recessive resistance to BGYMV, *Phg* angular leaf spot resistance locus, *Bct* is a locus for resistance to BCTV, *Agr* and *Agm* independent genes for *Apion godmani* resistance (Garza et al., 1996; Blair et al., 2006). For further explanations on DNA markers and gene symbols see Gepts (1999) and Bassett (2004).

- To the right of each linkage group are QTL mapped in different populations: ALS resistance to angular leaf spot, ANT anthracnose, ASB ashy stem blight, BGYMV bean golden yellow mosaic virus, BBS bacterial brown spot, CBB common bacterial blight, FRR *Fusarium* root rot, HB halo blight, LH leaf hopper, TP thrips, WB web blight, and WM white mold resistance. Symbols in subscript represent the source population of the QTL: AG A55/G 122 (Miklas et al., 2001), AN Aztec/ND88-106-04 (Miklas et al., 2007), BA Belneb-RR-1/A55 (Ariyarathne et al., 1999; Fourie et al., 2004; Jung et al., 2003), BE Berna/EMP 419 (Murray et al., 2004), BG BAT 881/G 21212 (Frei et al., 2005), BJ BAT 93/Jalo EEP558 (Freyre et al., 1998; Gepts, 1999; Geffroy et al., 2000), BH BAC 6/HT 7719 (Jung et al., 1996), BN Bunsi/Newport (Kolkman & Kelly, 2003), BR Bunsi/Raven (Ender & Kelly, 2005), B60 Benton/NY6020-4 (Miklas et al., 2003), DG DOR 364/G 19833 (López et al., 2003), DX DOR 364/XAN 176 (Miklas et al., 2000), H95 HR67/OAC 95 (Yu et al., 2004), MF (Montcalm/FR266 (Schneider et al., 2001), PX PC50/XAN 159 (Jung et al., 1997, 1998; Park et al., 2001), RN Red Hawk/Negro San Luis (Román-Avilés &. Kelly, 2005), S95 Seaforth/OAC 95 (Tar'an et al., 2001), and XC XR-235-1-1/Calima (Yu et al., 1998). Gene and QTL locations are approximate because most were not directly mapped in the BAT 93/Jalo EEP558 population. The total distance of each linkage group is expressed in Kosambi cM (bottom-right).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V12.1050
AN16.700
ROD3.930
D1032
L5
T01.300
R20.1250
V12.550
fin
AD17.350
D1327
NM,DF,
DM,NP
SWBJ
D1662
Pal-1
Q01.650
NM,DF,DM,
PD,HI,SWMG
AR
Ppd
V20.400
O13.700
Bng122
W07.1450
Bng171a
107
2
AN08.900
F13.300
AM07.300
y
V10.900
Bng119b
D1595
J01.2000
W02.1100
ChS
Vpe-2
O15.1800
AM10.800
O19.800
AM02.1500
GRP1.8-1
I06.550
W20.1400
Cel
O12.1600
Bng174
Pgip
U12.500
ChS-2
G06.1100
G05.850
V12.700
PvPR-2
D0166
DO,PL
P07.700
St
D1287
O12.900
AG08.700
DL2
T07.550
F06.350
[I-B]
ROS3.380
G19.1500
ROG19.1490
175
rk, Ane
3
D1151
AO11.1000
G03.1150
Bng12
X11.1300
D1377
Y11.350
I18.1700
G17.800
PvPR-1
S08.500
W06.700
SS
Q18.600
O20.550
Z
AH05.650
AM10.525
AM18.1050
U20.700
D1009
GRP1.8-2
D08.800
F10.900
Bng165
O10.350
D1020
AA03.650
V20.700
AP07.1300
AD04.1000
R20.400
Q09.1200
AN08.800
D1132
DO,SWBJ
D1066-2
132
4
Y17.1100
D1174
AM04.950
D1298
Bng71
F08.1600
X01.950
G08.1100
P09.800
Rbcs
G
SWBJ,PX
D1325
Z04.1200
X07.250
Bng224
O20.1000
Me
95
5
G19.1800
D1080
Diap-1
ROD20b
F07.1550
U12.950
D1198
K10.1300
H13.300
Aco-2
S18.500
D1157
Lox-1
D1301
AL08.900
AH17.500
D1251
Bng162
72
6
AM06.1000
G05.1150
V
U19.350
D0096
O10.650
AD12.350
SWPX
T08.500
W13.350
D03.600
ROD3.560
D1086
AD09.700
S18.650
Cdc-2
ROF7.540
P2062
Bng94
Hsp70
AD09.950
U19.500
U10.2000
S18.1500
Bng104
113
7
Hrgp36
Bng191
Asp
Chl
Bng199
J09.950
Y04.1050
Bng060
SWBJ,MG,PX
AR
Phs
D1861
W20.550
P1090
AM13.450
P
Z04.600
Bng204
Ef
H14.550
D0190
Pal-2
Y04.1300
LegH
Per
W16.550
Uri-2
AN03.650
SWMG
Lec-2
I07.1200
Lec-3
AN08.650
D1107
H12.1050b
109
8
I16.900
A10.1100
T08.650
AO11.1200
DJ1kscar
[C-R]
Gy
AH05.1000
U20.1150
D1468
D1505
Bng205
O16.600
NM,DF,DM,
NP,HI, AR
I08.1500
AJ13.1350
E19.1500
GS-c
I03.1550
H11.400
L04.950
X15.450
W01.650
E19.1200
AM07.600
Bng73
D1055
133
9
D1338-2
D1831
T
O19.750
AM13.1500
W13.550
D1096-2
Cad, Ch
AI07.600
P07.550
P07.350
G18.400
Bng102
Fr
Bng228
W02.750
AD08.450
AA03.1100
Y08.1350
P06.600
Y04.1600
U10.900
G04.900
Gluc
105
10
Bng218
ROF1.1180
AN03.350
I
AN11.300
L04.500
L
Vpe-3
D1580
Bng68
X11.700
U01.700
K19.450b
AG18.550
Bip, Ana
AJ14.250
rRNA-1
Bng200
AM14.1000
I07.700
D1476
89
11
Bng112
D1228
AL15.1300
Q11.1000
AE07.800
U10.1000
AD12.450
D1308
AD17.950
AJ16.250
G03.850
D1291
Bng145
PD,
AR
P2027
W02.950
K10.700
DL1
DH20sT
D1512
PepC
G08.1200
100

Legend

Explanation: A second map is presented as it was not possible to fit all the genes and QTL on the first map due to space restrictions.

Comprehensive genomic map of the genes of known function for external phenotypic traits, and QTL in common bean, including genes with a biochemical function (mostly disease response genes), the domestication genes and color genes in common bean [Abstracted from Kelly et al., 2003]. Each linkage group is represented by its core map version (Freyre et al., 1998). To the left of each linkage group, are the framework molecular markers (smaller font) and the biochemical genes (larger font) and major phenotypic trait genes (shaded boxes). For explanations on marker and biochemical gene symbols, (Gepts, 1999); and the original map references (Vallejos et al., 1992; Nodari et al., 1993; Adam-Blondon et al., 1994) [α*AI*- *Arl*-*Lec*] is the main locus coding for the α-amylase inhibitor-arcelin-lectin multigene family. *Fin*, *Ppd*, *St* are genes for determinacy, sensitivity to photoperiod, and pod string formation (Koinange et al., 1996). *B, [C-R]*, *G*, *P*, and *rk* are seed color genes and *Ana*, *Ane*, *Bip*, *L*, *T* and *Z* are seed color pattern genes (McClean et al. 2002). *Asp* is a gene for seedcoat shininess (Arndt and Gepts 1989; Gepts 1999). *Fr* is a male fertility restorer gene (He et al. 1995). *SGou* and *Ms*-8 are genes controlling pod cross-section and male sterility (Adam-Blondon et al., 1994). DL_1 and DL_2 are the root and shoot expressed semidominant dosage-dependent lethal genes (Shii et al., 1980; Hannah et al., 2007).

To the right (boxed symbols), are QTLs mapped in different populations: AR: *Apion godmani* resistance (Blair et al., 2006), DF and DM: number of days to flowering and to maturity, DO: seed dormancy, HI: harvest index, HT: height, L5: length of the 5th internode, LDG: lodging, NM: number of nodes on the main stem, NN: *Rhizobium* nodulation, NP: number of pods, PD: photoperiod-induced delay in flowering, PL: pod length, SW: seed weight. Location of most genes is approximate, as most were not directly mapped in the BJ population.

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