

Development of high resolution mapping capabilities essential for trait elucidation and marker assisted breeding

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Drag And View - bpba001011HT.snp
File Edit View Options Zoom Filelist Window Help
[Icons] ASCII Text

QUERY 179 ctgccaggactgcattcagctggtaaccgacgtccaggaagctctgaggaccaactccac 238
991207BPBA001011HT 179 ..... 238
991217BPBA004750HT 179 ..... 238
991217BPBA004715HT 179 ..... 238
991217BPBA004511HT 179 ..... 238
991216BPBA003807HT 179 ..... 238
000218BOVB001382HT 147 ..n.....n..... 206
000217BOVB001207HT 189 ..... 248
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000208BCEB001161HT 57 ..... 116
000210BCEB002409HT 52 ..... 111
991217BPBA003943HT 179 ..... 184
000218BOVB001376HT 148 .....nm.....t.....n...t.....g.t. 207
991216BPBA003663HT 180 ...-..c..... 196

QUERY 239 cttcgttgaggccttggtagaccacgctaaggaggagtgc-nccgcctggggcctggcat 297
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991217BPBA004715HT 239 .....ga..... 298
991217BPBA004511HT 239 .....ga..... 298
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000217BOVB001207HT 249 .....c.....ga..... 308
000210BCEB002312HT 112 .....c.....ga..... 171
000208BCEB001161HT 117 .....c.....ga..... 176
000210BCEB002409HT 112 .....c.....ga..... 171
000218BOVB001376HT 208 ..... 213
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SNP discovery *in silico* (+Virtual Northern)

Allelic diversity

A fragment of a FAD2 gene amplified from the *Brassica oleracea* diversity collections which shows the presence of several polymorphisms. Knowledge of such polymorphisms in conjunction with the percentage of total fatty acids present within the seeds of a given variety opens up the possibilities of identifying novel alleles for modifying the amounts and ratios of the Omega 3 and Omega 6 oils which can be obtained from the crop

C05_BOW_FAD2_F.ab1(24>1002)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
G08_BoDIV_FAD2_F.ab1(25>974)	→	C-T t CCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
D04_BoDIV_FAD2_F.ab1(23>1017)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
E10_BoDIV_FAD2_F.ab1(32>979)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
D11_BoDIV_FAD2_F.ab1(20>1000)	→	C-T t CCGTTACGCCGCC s CGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
E04_BOW_FAD2_F.ab1(33>998)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT c -TACGGAGT-CCC G CTT y -TGA-TTGTC-AATG-G t TTCC
D07_BOW_FAD2_F.ab1(24>974)	→	C-TACCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
B04_BoDIV_FAD2_F.ab1(24>985)	→	C-TACCGTTAC s CC s CGCA a GGAGTGGCCTCGATGG y CTGCTT t -TACGGAGT-CCC G CTT t -TGA-tTG k C-AATG-G t TTCC
D05_BOW_FAD2_F.ab1(25>901)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC
E05_BOW_FAD2_F.ab1(29>997)	→	C-TACCGTTACGCCGCCGCGCA r GGAGTGGCCTCGATGGTCTGCTT t NTACGGAGT-CCC G TTT c TGA-TTGTC-AATG-G t TTCC
E08_BoDIV_FAD2_F.ab1(31>1041)	→	C-TACCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
D08_BoDIV_FAD2_F.ab1(26>980)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
D05_BoDIV_FAD2_F.ab1(31>1051)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
C07_BoDIV_FAD2_F.ab1(26>979)	→	C-T t CCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
B08_BoDIV_FAD2_F.ab1(28>981)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-TTGTC-AATG-G t TTCC
E10_BOW_FAD2_F.ab1(31>984)	→	C-T t CCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC
B02_BoDIV_FAD2_F.ab1(23>984)	→	C-TACCGTTACGCCGCCGCGCA a GGAGTGGCCTCGATGGTCTGCTT t -TACGGAGT-CCC G CTT t -TGA-w T GTC-AATG-G t TTCC
A07_BOW_FAD2_F.ab1(28>972)	→	C-TACCGTTACGCCGCCGCGCAGGGAGTGGCCTCGATGGTCTGCTTC-TACGGAGT-CCC G CTTC-TGA-TTGTC-AATG-G t TTCC

Approaches for SNP discovery

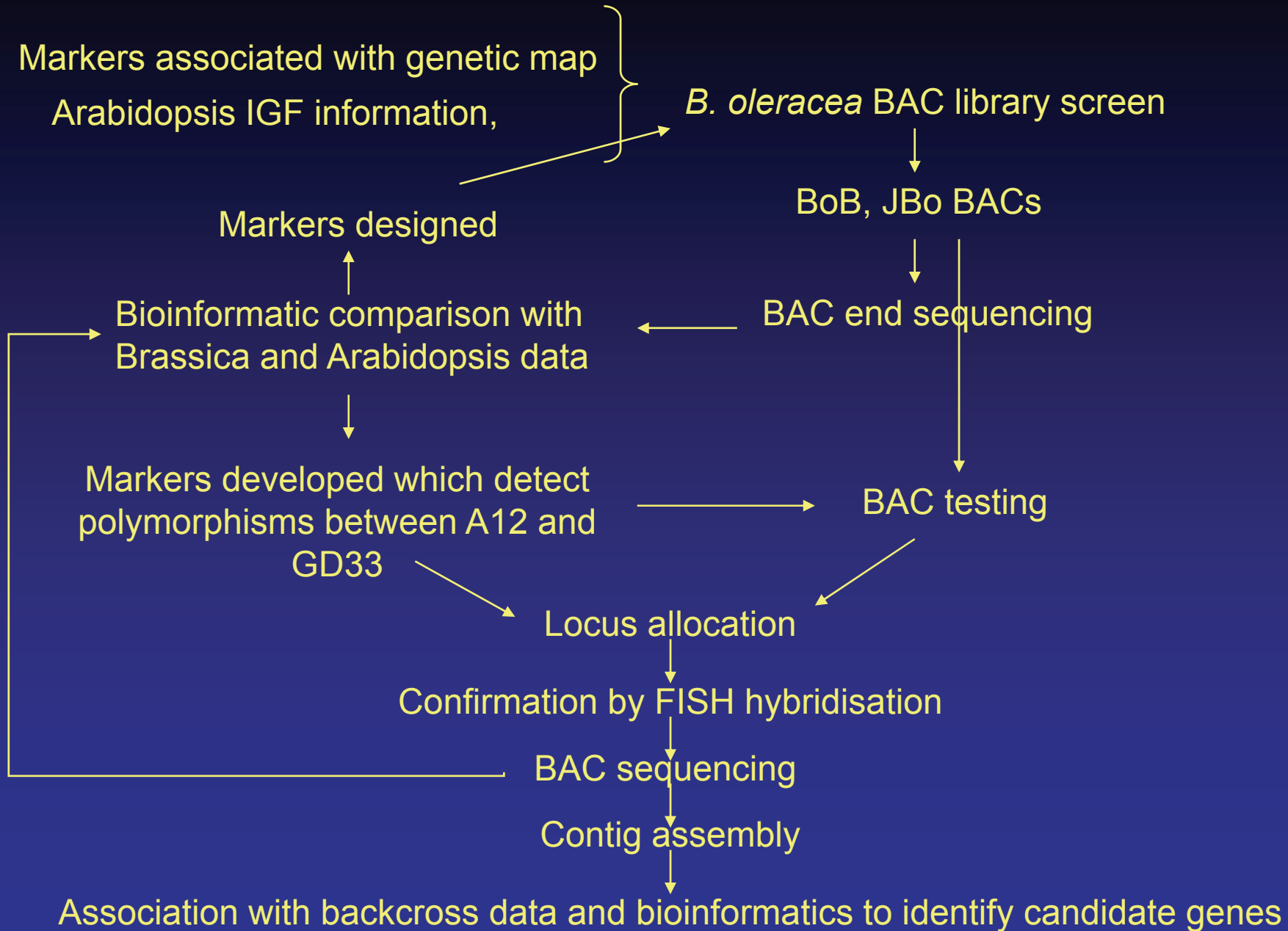
SNP detection

- Comparative sequencing
- Tiling arrays
- New generation sequencing

SNP screening

- GoldenGate assays
- Mass spec
- etc

Moving from QTL to candidate genes



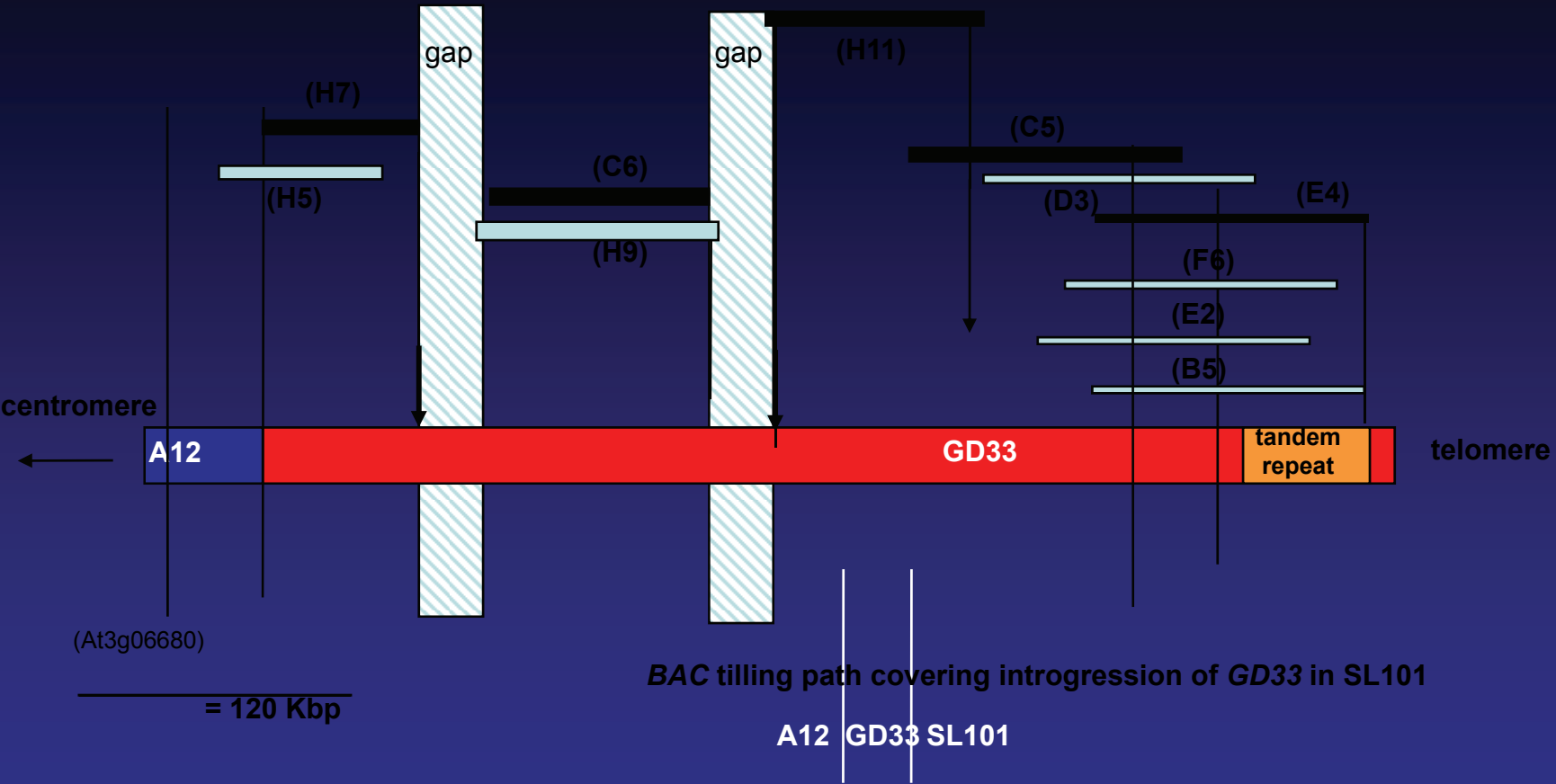


Seed Vigour in Brassica oleracea: Using Natural Variation to Identify Candidate Genes .

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Exploiting Brassica Diversity

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