THE PLANT CELL

Correction to: S Chopra, P Athma, T Peterson, Alleles of the maize P gene with distinct tissue specificities encode Myb-homologous proteins with C-terminal replacements., The Plant Cell, Volume 8, Issue 7, July 1996, Pages 1149–1158, and Peifen Zhang, Surinder Chopra, Thomas Peterson, A Segmental Gene Duplication Generated Differentially Expressed myb-Homologous Genes in Maize, The Plant Cell, Volume 12, Issue 12, December 2000, Pages 2311–2322

CORRECTION TO: S Chopra, P Athma, T Peterson, Alleles of the maize P gene with distinct tissue specificities encode Myb-homologous proteins with C-terminal replacements., *The Plant Cell*, Volume 8, Issue 7, July 1996, Pages 1149–1158, https://doi.org/10.1105/tpc.8.7.1149

AND: Peifen Zhang, Surinder Chopra, Thomas Peterson, A Segmental Gene Duplication Generated Differentially Expressed *myb*-Homologous Genes in Maize, *The Plant Cell*, Volume 12, Issue 12, December 2000, Pages 2311–2322, https://doi.org/10.1105/tpc.12.12.2311

We previously reported (Figure 5 in Chopra, Athma and Peterson, 1996) that the maize *P1-rr4B2* and *P1-wr* alleles encode proteins with distinct C-terminal sequences. However, Goettel and Messing (2009) reported that the *P1-rr-* and *P1-wr-* encoded proteins differ only at the fourth amino acid residue, and that the proteins are otherwise identical. We have checked these results by additional sequencing of genomic *P1-rr4B2* and *P1-wr* cDNA clones, and we agree that our original result is incorrect. This error was caused by a sequencing artifact due to high GC content in *P1* exon 3. As shown in Figure 1, the open reading frames of *P1-rr4B2* and *P1-wr* were shifted by this artifactual single nucleotide indel polymorphism (indicated by black arrow in Figure 1). There is an additional difference (A instead of C) in the previously-reported *P1-wr* sequence, located 40 bp downstream of the artifactual indel site (indicated by red arrow in Figure 1).

This single substitution does not alter the amino acid sequence. Based on the corrected sequence, the *P1-rr-* and *P1-wr*-encoded proteins have identical C-terminal sequences.

Based on the errors described above, we also reported erroneous alignments of maize and teosinte *p*-related genes (Figure 5 in Zhang, Chopra and Peterson, 2000). The corrected sequences indicate that the maize *P1-rr* and *P1-wr* alleles share high sequence similarity with a third maize *p1* allele (*P1-rw1077*; Zhang and Peterson 2005), the maize paralog *p2*, and a *p*-homologous gene from teosinte (*p2t* (over 96% at the nucleotide level; Figure 2). They all encode very similar C-terminal regions and differ only by a few amino acid substitutions and small indel polymorphisms (Figure 3). These sequence corrections do not affect the hypotheses or conclusions of Zhang et al. 2000. Sequence similarities were estimated using MEGA 2 software package.

We apologize for these errors and appreciate the opportunity to offer this correction. We thank Dr. Feng Zhang (zhangumn@umn.edu) for sequence analysis of maize and teosinte alleles, and Dr. Erich Grotewold (grotewol@msu.edu) for sequence data and discussions.

Sincerely,

Surinder Chopra, sic3@psu.edu

Peifen Zhang, pfzhang@yahoo.com

Thomas Peterson, thomasp@iastate.edu

(We regret that Co-Author Prasanna Athma is deceased)

```
P1-rr4B2_corrected_      ATGGGGAGGACGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
P1-rr4B2_former_         ATGGGGAGGACGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
P1-wr_corrected_         ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
P1-wr_former_            ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
                         ********* ***************************************************

P1-rr4B2_corrected_      GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
P1-rr4B2_former_         GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
P1-wr_corrected_         GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
P1-wr_former_            GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
                         ************************************************************

P1-rr4B2_corrected_      CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
P1-rr4B2_former_         CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
P1-wr_corrected_         CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
P1-wr_former_            CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
                         ************************************************************

P1-rr4B2_corrected_      CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
P1-rr4B2_former_         CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
P1-wr_corrected_         CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
P1-wr_former_            CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
                         ************************************************************

P1-rr4B2_corrected_      CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
P1-rr4B2_former_         CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
P1-wr_corrected_         CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
P1-wr_former_            CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
                         ************************************************************

P1-rr4B2_corrected_      GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
P1-rr4B2_former_         GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
P1-wr_corrected_         GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
P1-wr_former_            GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
                         ************************************************************

P1-rr4B2_corrected_      CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
P1-rr4B2_former_         CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
P1-wr_corrected_         CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
P1-wr_former_            CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
                         ************************************************************

P1-rr4B2_corrected_      AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
P1-rr4B2_former_         AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
P1-wr_corrected_         AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
P1-wr_former_            AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
                         ************************************************************

P1-rr4B2_corrected_      AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
P1-rr4B2_former_         AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
P1-wr_corrected_         AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
P1-wr_former_            AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
                         ************************************************************

P1-rr4B2_corrected_      GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
P1-rr4B2_former_         GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
P1-wr_corrected_         GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
P1-wr_former_            GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
                         ************************************************************

P1-rr4B2_corrected_      AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGAGCGGGCCG
```

Figure 1. Sequences of *P1-rr4B2* and *P1-wr* cDNA clones.

```
P1-rr4B2_former_       AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGAGCGGGCCG
P1-wr_corrected_       AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGAGCGGGCCG
P1-wr_former_          AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGAGCGGGCCG
                       ************************************************************


P1-rr4B2_corrected_    TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGAGGCCGACAGCGAGATG
P1-rr4B2_former_       TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGAGGCCGACAGCGAGATG
P1-wr_corrected_       TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGAGGCCGACAGCGAGATG
P1-wr_former_          TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGAGGCCGACAGCGAGATG
                       ************************************************************
                                                                  ↓
P1-rr4B2_corrected_    GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGC
P1-rr4B2_former_       GACGCCCTGATGCCTATCGGGCCCGGCGGC-ACGACTCGGCTGCCCTCGAAGGGCTTGGC
P1-wr_corrected_       GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGC
P1-wr_former_          GACGCCCTGATGCCTATCGGGCCCGGCGGC-ACGACTCGGCTGCCCTCGAAGGGCTTGGC
                       ****************************** *****************************


P1-rr4B2_corrected_    GCGGTCGGCTGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
P1-rr4B2_former_       GCGGTCGGCTGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
P1-wr_corrected_       GCGGTCGGCTGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
P1-wr_former_          GCGGTCGGCTGAGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
                       ***********↑************************************************

P1-rr4B2_corrected_    GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
P1-rr4B2_former_       GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
P1-wr_corrected_       GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
P1-wr_former_          GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
                       ************************************************************


P1-rr4B2_corrected_    GAGCCGCTGGAAGTTGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACCCCGGACGAT
P1-rr4B2_former_       GAGCCGCTGGAAGTTGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACCCCGGACGAT
P1-wr_corrected_       GAGCCGCTGGAAGTTGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACCCCGGACGAT
P1-wr_former_          GAGCCGCTGGAAGTTGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACCCCGGACGAT
                       ************************************************************


P1-rr4B2_corrected_    CGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA------------
P1-rr4B2_former_       CGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGACGGCTCCGGTCA
P1-wr_corrected_       CGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA------------
P1-wr_former_          CGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGACGGCTCCGGTCA
                       ************************************************


P1-rr4B2_corrected_    ------------------------------------------------------------
P1-rr4B2_former_       CCGGACCGATCAGACAGACCAAATAATTGGGTCACGTGTGCTCGCTCGCTCGCTGCCGTC
P1-wr_corrected_       ------------------------------------------------------------
P1-wr_former_          CCGGACCGATCAGACAGACCAACCAAGGTGGCC-----CGGCCATATGGTCGACGCCGCT


P1-rr4B2_corrected_    ------------------------------------------------------------
P1-rr4B2_former_       GCGTGGGTCTTGGTTCAGATGGCCAAATAATTGGGAAAAAAAATTCTACGGCCAGGGCCGT
P1-wr_corrected_       ------------------------------------------------------------
P1-wr_former_          A-GTAGGCGTTG-CTCGTGTGTACAGTTTTTTTTTCTT----TTTTGTAGATTTTGTTCT


P1-rr4B2_corrected_    -------------------------------------------------------------
P1-rr4B2_former_       AAAGCCACCACCGTGCGCTCCTGATGTCGATGCCTGCCGCGTGGAGCTCTTGCGTATCTAA
P1-wr_corrected_       -------------------------------------------------------------
P1-wr_former_          TAG----------------------------------------------------------
```

Figure 1. (Continued)

```
P1-rr4B2   ATGGGGAGGACGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
P1-wr      ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAA
p2t        ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGTGGGAGGTGGACGGCGGAG
p2         ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGGGCTCAAGCGAGGGAGGTGGACGGCGGAG
P1-rw1077  ATGGGGAGGGCGCCGTGCTGCGAGAAGGTGGAGCTCAAGCGAGGGAGGTGGACGGCGGAG

P1-rr4B2   GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
P1-wr      GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
p2t        GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
p2         GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG
P1-rw1077  GAGGACCAGTTACTTGCCAACTACATTGCGGAGCACGGCGAGGGGTCCTGGAGGTCGCTG

P1-rr4B2   CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
P1-wr      CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
p2t        CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
p2         CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC
P1-rw1077  CCCAAGAATGCAGGCCTGCTCCGGTGCGGCAAGAGCTGCCGGCTCCGGTGGATCAACTAC

P1-rr4B2   CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
P1-wr      CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
p2t        CTTCGGGCGGATGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
p2         CTCCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG
P1-rw1077  CTTCGGGCGGACGTCAAGAGGGGGAACATCTCCAAGGAGGAAGAAGACATCATCATCAAG

P1-rr4B2   CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
P1-wr      CTCCACGCCACCCTCGGCAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
p2t        CTCCACGCCACCCTCGGGAACAGGTGGTCCCTGATCGCCAGCCACCTGCCCGGCCGAACA
p2         CTCCACGCCACCCTCGGGAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA
P1-rw1077  CTCCACGCCACCCTCGGGAACAGGTGGTCCCTGATCGCCAGCCACCTCCCCGGCCGAACA

P1-rr4B2   GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
P1-wr      GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
p2t        GACAACGAGATCAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
p2         GACAACGAGATTAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC
P1-rw1077  GACAACGAGATTAAGAACTACTGGAACTCGCACCTCAGCCGGCAGATCCACACGTACCGC

P1-rr4B2   CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
P1-wr      CGGAAATACACCGCCGGGCCTGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
p2t        CGGAAATACACCGCCGGGCCGGAGGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG
p2         CGGAAATACACCGCCGGGCCGGACGATACCGCCATCGCCATCGACATGAGCAAGCTGCAG
P1-rw1077  CGGAAATACACCGCCGGGCCGGACGACACCGCCATCGCCATCGACATGAGCAAGCTGCAG

P1-rr4B2   AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
P1-wr      AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGGCTAGCGCCAGC
p2t        AGCACCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGACTAGCGCCAGC
p2         AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGACTAGCGCCAGC
P1-rw1077  AGCGCCGACAGGCGGCGCGGCGGCAGGACCCCGGGCCGGCCGCCGAAGACTAGCGCCAGC

P1-rr4B2   AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
P1-wr      AGGACCAAGCAGGCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGCCCGGCCGCGGCG
p2t        AGGACCAAGCAGCCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGC------GCGGCG
p2         AGGACCAAGCATTCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGC------GCGGCG
P1-rw1077  AGGACCAAGCATTCGGACGCCGATCAGCCCGGCGGCGAGGCGAAAGGC------GCGGCG
```

Figure 2. Alignment of maize *p1* and *p2* alleles.

```
P1-rr4B2    GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
P1-wr       GCGTCGAGCCCGCGGCACAGCGACGTGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
p2t         GCGTCGAGCCCGCGGCACAGCGACGCGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
p2          GCGTCGAGCCCGCGGCACAGCGACGCGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC
P1-rw1077   GCGTCGAGCCCGCGGCACAGCGACGCGGTGAACCCGGGCCCGAACCAGCCCAACAGCAGC

P1-rr4B2    AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGGAGCGGGCCG
P1-wr       AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGGAGCGGGCCG
p2t         AGCGGCAGCACGGGCACGGCCGAGGAGGAGGGGCCCAGCAGCGAGGACGCGGAGCGGGCCG
p2          AGCGGCAGCACGGGCACGGCCGAGGAGGAAGGGCCCAGCAGCGAGGACGCGGAGCGGGCCG
P1-rw1077   AGCGGCAGCACGGGCACGGCCGAGGAGGAAGGGCCCAGCAGCGAGGACGCGGAGCGGGCCG

P1-rr4B2    TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGGAGGCCGACAGCGAGATG
P1-wr       TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGGAGGCCGACAGCGAGATG
p2t         TGGGTGCTGGAGCCGATAGAGCTCGGGGACCTAGTCTGGGGGGGAGGCCGACAGCGAGATG
p2          TGGGTGCTGGAGCCGATAGAGCTCGGGGACCT---CTGGGGGGGAGGCCGACAGCGAGATG
P1-rw1077   TGGGTGCTGGAGCCGATAGAGCTCGGGGACCT---CTGGGGGGGAGGCCGACAGCGAGATG

P1-rr4B2    GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGC
P1-wr       GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGC
p2t         GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCGAAGGGCTTGGC
p2          GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCCAAGGGCTTGGC
P1-rw1077   GACGCCCTGATGCCTATCGGGCCCGGCGGCCACGACTCGGCTGCCCTCCAAGGGCTTGGC

P1-rr4B2    GCGGTCGGCTGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
P1-wr       GCGGTCGGCTGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
p2t         GCGGTCGGCTGCGAGGCCCAGGTGGATGACCTGTTCGACATGGACTGGGATGGCTTCGCG
p2          GCGGTCGGCGGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG
P1-rw1077   GCGGTCGGCGGCGAGGCCCAGGTGGACGACCTGTTCGACATGGACTGGGATGGCTTCGCG

P1-rr4B2    GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
P1-wr       GCCCATCTGTGGGGCGGGCCGGAGCAGGACGAGCACAGCGCGCAGCTGCGGCAGGCCGCC
p2t         GCCCATCTGTGGGGCGGGCCGGAGCAGGACGACCACAGCGCGCAGCTGCGGCAGGCCGCC
p2          GCCCATCTGTGGGGCGGGCCGGAGCAGGACGACCACAGCGCGCAGCTGCGGCAGGCCGCC
P1-rw1077   GCCCATCTGTGGGGCGGGCCGGAGCAGGACGACCACAGCGCGCAGCTGCGGCAGGCCGCC

P1-rr4B2    GAGCCGCTGGAAGT---------TGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACC
P1-wr       GAGCCGCTGGAAGT---------TGCTGCTGCTGCTGCTGCTGCGACGGCGGCCCGCACC
p2t         GAGCCGCTGGAAG------------------CTTCTGCCGCTGCGACGGCGGCCTGCACC
p2          GAGCCGATGGAAGCGGCTGCTGTTGCCGCTGCCGCTGCCGCTGCGACGGCGGCCTGCACC
P1-rw1077   GAGCCGATGGAAGCGGCTGCTGTTGCCGCTGCCGCTGCCGCTGCGACGGCGGCCTGCACC

P1-rr4B2    CCGGACGATCGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA
P1-wr       CCGGACGATCGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA
p2t         CCGGACGATCGCGAGCTGGAGGCGTTCGAGAATTGGCTCCTGTCCGACTCGTTCTGA
p2          CCGGACGATCGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA
P1-rw1077   CCGGACGATCGCGAGCTGGAGGCGTTCGAGACTTGGCTCCTGTCCGACTCGTTCTGA
```

```
Similarity matrix

          P1-rr4B2 P1-wr  p2t   p2  P1-rw1077
P1-rr4B2    ----
P1-wr       99.9  ----
p2t         96.8  96.9  ----
p2          96.2  96.3  96.2  ----
P1-rw1077   96.3  96.4  96.3  99.7  ----
```

Figure 2. (Continued)

```
P1-rr       MGRTPCCEKVGLKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINY
P1-wr       MGRAPCCEKVGLKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINY
P2t         MGRAPCCEKVGLKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINY
P1-rw1077   MGRAPCCEKVELKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINY
P2          MGRAPCCEKVGLKRGRWTAEEDQLLANYIAEHGEGSWRSLPKNAGLLRCGKSCRLRWINY
            1.........10........20........30........40........50........

P1-rr       LRADVKRGNISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNSHLSRQIHTYR
P1-wr       LRADVKRGNISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNSHLSRQIHTYR
P2t         LRADVKRGNISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNSHLSRQIHTYR
P1-rw1077   LRADVKRGNISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNSHLSRQIHTYR
P2          LRADVKRGNISKEEEDIIIKLHATLGNRWSLIASHLPGRTDNEIKNYWNSHLSRQIHTYR
            61.......70........80.......90........100......110........

P1-rr       RKYTAGPDDTAIAIDMSKLQSADRRRGGRTPGRPPKASASRTKQADADQPGGEAKGPAAA
P1-wr       RKYTAGPDDTAIAIDMSKLQSADRRRGGRTPGRPPKASASRTKQADADQPGGEAKGPAAA
P2t         RKYTAGPEDTAIAIDMSKLQSTDRRRGGRTPGRPPKTSASRTKQPDADQPGGEAKG--AA
P1-rw1077   RKYTAGPDDTAIAIDMSKLQSADRRRGGRTPGRPPKTSASRTKHSDADQPGGEAKG--AA
P2          RKYTAGPDDTAIAIDMSKLQSADRRRGGRTPGRPPKTSASRTKHSDADQPGGEAKG--AA
            121......130.......140.......150.......160.......170........

P1-rr       ASSPRHSDVVNPGPNQPNSSSGSTGTAEEEGPSSEDASGPWVLEPIELGDLVWGEADSEM
P1-wr       ASSPRHSDVVNPGPNQPNSSSGSTGTAEEEGPSSEDASGPWVLEPIELGDLVWGEADSEM
P2t         ASSPRHSDAVNPGPNQPNSSSGSTGTAEEEGPSSEDASGPWVLEPIELGDLVWGEADSEM
P1-rw1077   ASSPRHSDAVNPGPNQPNSSSGSTGTAEEEGPSSEDASGPWVLEPIELGDL-WGEADSEM
P2          ASSPRHSDAVNPGPNQPNSSSGSTGTAEEEGPSSEDASGPWVLEPIELGDL-WGEADSEM
            181......190.......200.......210.......220.......230........

P1-rr       DALMPIGPGGHDSAALEGLGAVGCEAQVDDLFDMDWDGFAAHLWGGPEQDEHSAQLRQAA
P1-wr       DALMPIGPGGHDSAALEGLGAVGCEAQVDDLFDMDWDGFAAHLWGGPEQDEHSAQLRQAA
P2t         DALMPIGPGGHDSAALEGLGAVGCEAQVDDLFDMDWDGFAAHLWGGPEQDDHSAQLRQAA
P1-rw1077   DALMPIGPGGHDSAALQGLGAVGGEAQVDDLFDMDWDGFAAHLWGGPEQDDHSAQLRQAA
P2          DALMPIGPGGHDSAALQGLGAVGGEAQVDDLFDMDWDGFAAHLWGGPEQDDHSAQLRQAA
            241......250.......260.......270.......280.......290........

P1-rr       EPLEVAA---AAAAATAARTPDDRELEAFETWLLSDSF
P1-wr       EPLEVAA---AAAAATAARTPDDRELEAFETWLLSDSF
P2t         EPLEAS-----AAATAACTPDDRELEAFENWLLSDSF
P1-rw1077   EPMEAAAVAAAAAAATAACTPDDRELEAFETWLLSDSF
P2          EPMEAAAVAAAAAAATAACTPDDRELEAFETWLLSDSF
            301......310.......320.......330......

similarity matrix
          P1-rr  P1-wr   P2t  P1-rw1077   P2
P1-rr      ----
P1-wr      99.7   ----
P2t        95.2   95.5   ----
P1-rw1077  94.7   95.0   94.9  ----
P2         95.0   95.3   95.2   99.7    ----
```

Figure 3. Alignment and comparison of proteins encoded by maize *p1* and *p2* alleles.