

Identification of mutations responsible for improved xylose utilization in an adapted xylose isomerase expressing *Saccharomyces cerevisiae*

Ronald E. Hector*, Jeffrey A. Mertens, Nancy N. Nichols

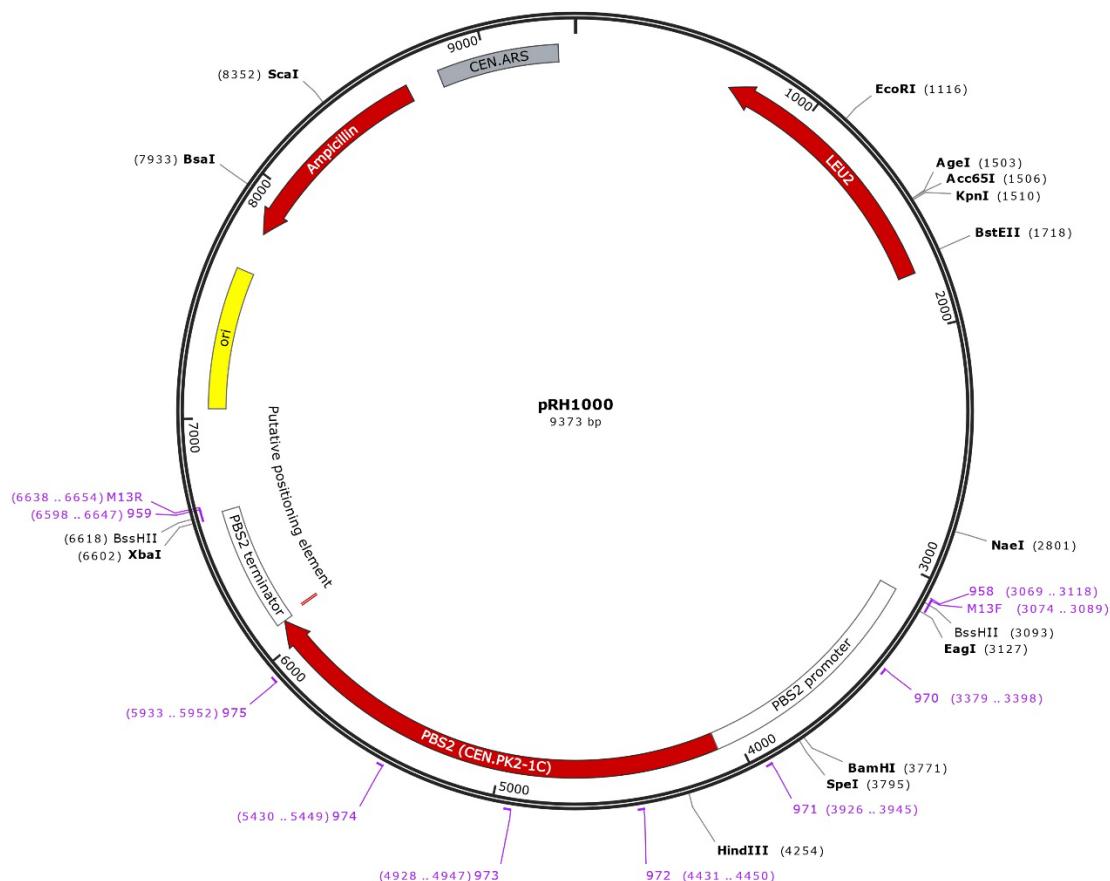
USDA, Agricultural Research Service, National Center for Agricultural Utilization Research,
Bioenergy Research Unit, 1815 North University Street, Peoria, IL 61604, USA;
jeffrey.mertens@usda.gov (J.A.M.); nancy.nichols@usda.gov (N.N.N.)

* Correspondence: ronald.hector@usda.gov

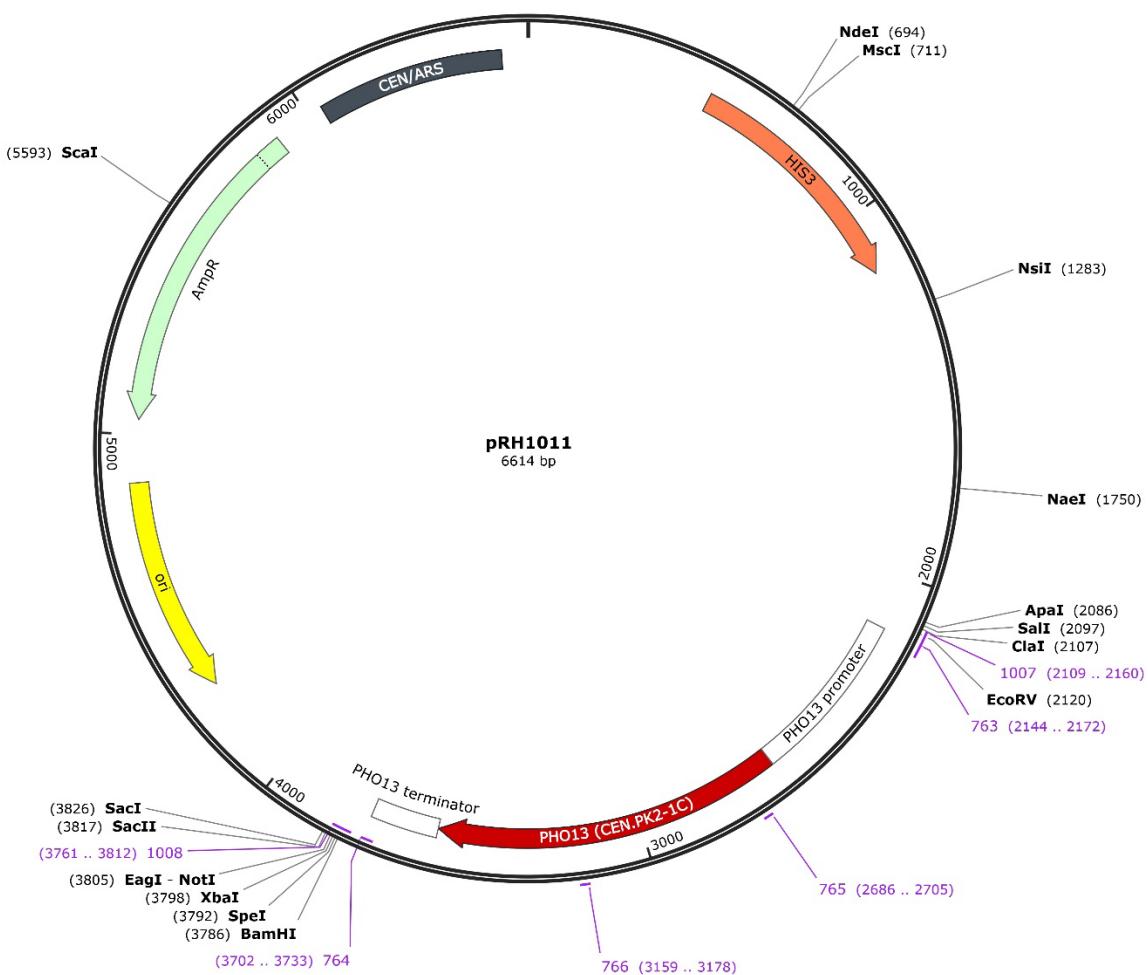
Supplemental materials:

Construction of plasmids for expressing PBS2 and PHO13

PBS2 DNA sequence, including PBS2 promoter and termination regions, was amplified from CEN.PK2-1C genomic DNA using Phusion polymerase and oligos 958 and 959. To generate pRH1000, the DNA fragment (bp -992/ORF/+520) was cloned into BssHII cut pRS415 using NEBuilder HiFi DNA assembly. DNA sequence homologous to the flanking BssHII sites of pRS415 was included in primers 958/959 to direct integration of the P_{PBS2} -PBS2-T $_{PBS2}$ fragment. Prior to transformation into *S. cerevisiae*, plasmid pRH1000 was sequenced using the primers shown below to confirm that no mutations were present.



PHO13 DNA sequence, including *PHO13* promoter and termination regions, was amplified from CEN.PK2-1C genomic DNA using Phusion polymerase and oligos 1007 and 1008. To generate pRH1011, the DNA fragment (bp -466/ORF/+180) was cloned into SmaI cut pRS413 using NEBuilder HiFi DNA assembly. DNA sequence homologous to the flanking SmaI site of pRS413 was included in primers 1007/1008 to direct integration of the P_{PHO13}-*PHO13*-T_{PHO13} fragment. Prior to transformation into *S. cerevisiae*, plasmid pRH1011 was sequenced using the primers shown below to confirm that no mutations were present.



Construction of PBS2 and PHO13 deletion strains

To delete *PBS2*, primers 989 and 990 were used to amplify the *LEU2* gene from plasmid pRS405. To direct integration of the *LEU2* gene to create *pbs2Δ::LEU2* strains, primers 989 and 990 also contained DNA sequence homologous to the sequence flanking the *PBS2* gene. Each *pbs2Δ::LEU2* strain was confirmed by PCR amplification of DNA fragments using primers that hybridize to sequences adjacent to the *PBS2* gene and within the *LEU2* gene. Hot-start Taq polymerase was used with primer pairs 991/36 and 992/35 to confirm gene deletion.

To delete *PHO13*, primers 761 and 762 were used to amplify the *HIS3* gene from plasmid pRS403. To direct integration of the *HIS3* gene to create *pho13Δ::HIS3* strains, primers 761 and 762 also contained DNA sequence homologous to the sequence flanking the *PHO13* gene. Each *pho13Δ::HIS3* strain was confirmed by PCR amplification of DNA fragments using primers that hybridize to sequences adjacent to the *PHO13* gene and within the *HIS3* gene. Hot-start Taq polymerase was used with primer pairs 763/59 and 764/60 to confirm gene deletion.

Supplementary Table S1. DNA oligonucleotides used in this study

Oligo#	Description/Use	Sequence (5' to 3')
35	LEU2 primer for gene deletion confirmation	CCAACGTGGTCACCTGGCAA
36	LEU2 primer for gene deletion confirmation	GTACCACCGAAGTCGGTGAT
761	PHO13 deletion oligo	AACTTCCGTTTTCTTTTCTGGTGAATGTTCTTCCGTTTAGTGAAGATTGACTGAGAGTGCAC
762	PHO13 deletion oligo	TATTTTCCCTTCAAAAAGTAATTCTACCCCTAGATTTGCATTGCTCCGTGCGGTATTCACACCG
763	PHO13 deletion confirmation oligo	AAAGTGGCTTGAGCTGTTGATAAGAAAAGC
764	PHO13 deletion confirmation oligo	TAATCGTCATCATTTTATTACACCTCCGGAT
765	PHO13 sequencing oligo	CACGTTCTGTTGATTGTG
766	PHO13 sequencing oligo	TGCAGAAGGATTCTGTTAC
958	PBS2-F2, for cloning P _{PBS2} -PBS2- T _{PBS2}	ACGTTGAAACGACGGCCAGTGAGCGCGCTTACTGCAGGGATTAACCTC
959	PBS2-R2, for cloning P _{PBS2} -PBS2- T _{PBS2}	CAGCTATGACCATGATTACGCCAACGCGCGCTAGTTCTGGTCTAGACTCC
970	PBS2 sequencing oligo	AATCTTATTGCGTACCACTC
971	PBS2 sequencing oligo	AGGGTAGCTGCTATTGTGAG
972	PBS2 sequencing oligo	TCGTGCAAGCGCTCCAAG
973	PBS2 sequencing oligo	AGCACATCCACCTCATCAAG
974	PBS2 sequencing oligo	ACGACGAATCATCTGAAATC
975	PBS2 sequencing oligo	GCAGCTTAACAGAGCATCC
981	SAS3-WT primer	GGTAACGTATCACTTGCATAGTG
982	SAS3-SNP-primer	GGTAACGTATCACTTGCATAGTG
983	PBS2-WT primer	CCATGACCCAGTTACATACA
984	PBS2-SNP-primer	CCATGACCCAGTTACATACT
989	PBS2 deletion oligo	TATAGATACATTATAATTAAAGCAGATCGAGACGTTAATTCTCAAAGAGATTGACTGAGAGTGCAC
990	PBS2 deletion oligo	TTGTTTATATTACCGTGCCTGGCTTTATTGGATATTACGCTACTGTGCGGTATTCACACCG
991	PBS2 deletion confirmation oligo	GATTCGTGAGGCCATACCGTC
992	PBS2 deletion confirmation oligo	GTCCACATCGCTTACATTGC
993	PHO13-WT primer	CCGAAAAGGGTTATACATTACG
994	PHO13-SNP primer	CCGAAAAGGGTTATACATTCACT
995	PHO13-R primer	CTCATTATTGGTAAGGTGTAGATGTCAC
996	HSP104-WT primer	AATTGGCTAAAAAAGTTGCTGGATTCTT
997	HSP104-SNP primer	AATTGGCTAAAAAAGTTGCTGGATTCTC
998	HSP104-R primer	GATAAATTCACTGACCTAGATTGAAAGTC
999	PHO81-SNP primer	CCTTAACTGGAAACAACCCAATTCCC
1000	PHO81-WT primer	CCTTAACTGGAAACAACCCAATTCCC
1001	PHO81-R primer	GTAGATCCGCTGTAACCTCCA
1002	STE24-WT primer	CAGAGGATCTACATTCTGGTGGACAG
1003	STE24-SNP primer	CAGAGGATCTACATTCTGGTGGACAA
1004	STE24-R primer	CCATGAAATCGGTACTGGCAA
1007	PHO13-F, for cloning P _{PHO13} -Pho13- T _{Pho13}	GATAAGCTTGTATCGAATTCTGCAGCCCGATAAGTGGCTGAGCTGTG
1008	PHO13-R, for cloning P _{PHO13} -Pho13- T _{Pho13}	GGCGGCCGCTAGAACTAGTGGATCCCCGTTCAAACGGCGAGAATTGAG