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Supplementary Material

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Identification of *Klebsiella Variicola* T29A Genes Involved In Tolerance To Desiccation

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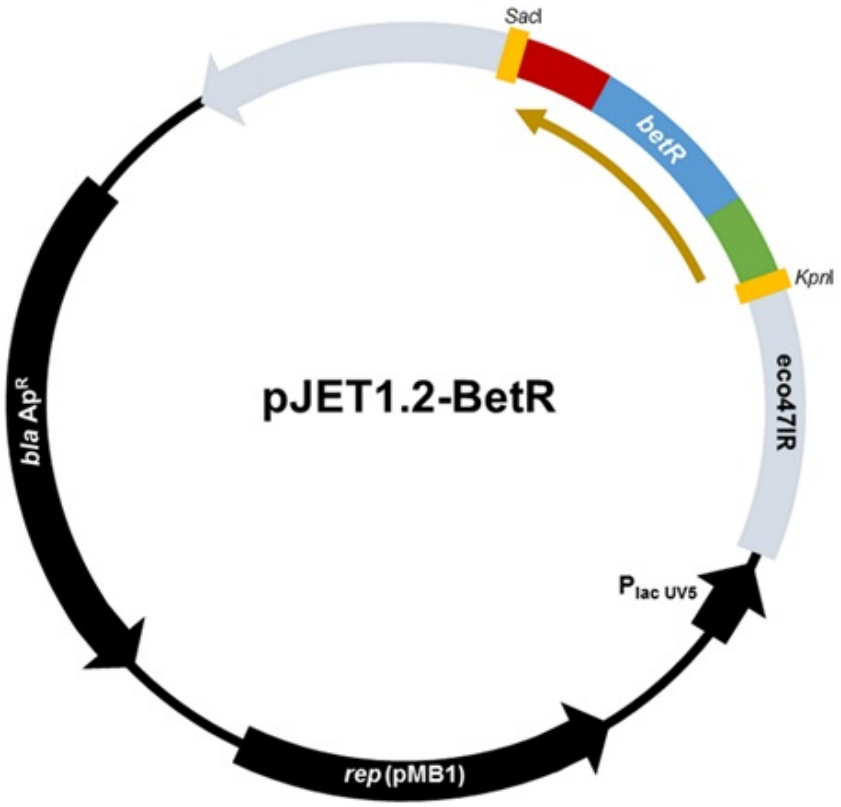
SUPPLEMENTARY TABLES AND FIGURES

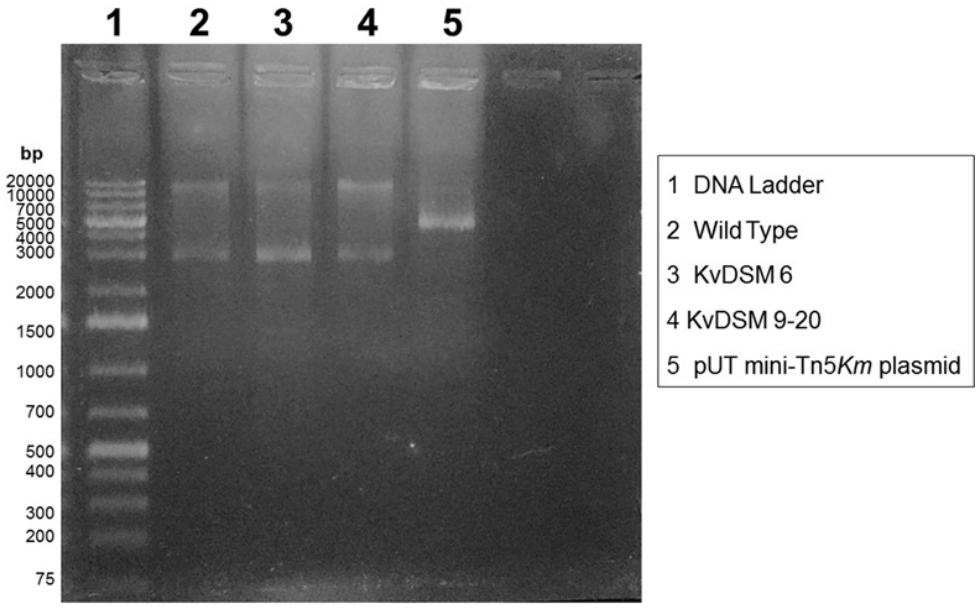
Supplementary Table 1. Nucleotidic sequences of the *BetR* gene fragments interrupted by the mini-Tn5Km transposon in the KvDSM 6 mutant. The pair of oligonucleotides: Mut 6 start-Rv/Tn5-Fw, allowed to amplify a region of 490 base pairs between the transposon and a region of 223 base pairs upstream of the start of the *BetR* gene, while the pair: Mut 6 stop-Fw/Tn5-Rv, allowed to amplify a region of 695 base pairs between the transposon and the end of the *BetR* gene.

PCR Product	Sequence
DNA fragment amplified with the oligonucleotides: Mut 6 start-Rv/Tn5-Fw	CTTCAGGAACATTTTATACACATCTACAAACAACCTTACAAGACGCCGCAACATAAAAAACGATTTTTTATGTTGTTCAAGCAA TGGAGGAGAACCAAAAAGGACGCCAAAAGAACCGCGCGAACATTACATATCGCTTTGTTTTAATTGAAATTAATCTCACGATACCTACAAT AACAACCTAAAATGTCATTTTACCCACCCTACAGAAGGCCGATATGAGTACATCTAAATCGACACCAATTGAACTTAAGATTAGTGAGAT GTTAAGCAACATCATGAATGAAAGGGGTATTTCAAAGAACAAACATACTACTCATATAGCTAATGTACTCGGTATAACCATCACCCACGCAAACCG TAAAATGAAAGGTTTTGCGTCATGGGAAAACTCACAGCTGGAAAAAGTCGCTAAGTCTTTAGGCTGACTCTTATACACAAGTGCG GCCGCGGCCTAGGCGGCCGAAGCTTGCAT
DNA fragment amplified with the oligonucleotides: Mut 6 stop-Fw/Tn5-Rv	GAATTCGGCCTAGGCGGCCAGATCTGATCAAGAGACAGGTCTTTAGGTGTAAGCCTCAGTGATTTATTTAAAAT GGTTGAGGACAGCTATGAGGAGAAACACGCCGGAAAATATATTTTCAACAAGGAAGAAATGGAGGGAGAGATAACCTTTTCCCCTG ATACAGAAAGAACATATTCAGCTGTTAAAATTAACGATCAATGGCATATTTTTAAAACAGATGATATTGAAGGCAATGACATTTATGA AGAATCGCGGCAAGGTGTTTTAAGATTTTCCGTTGAAAGTTCAGCAAGAGACAAGTCTAAGCCACGTATCGCTCTTCTGGATGACGATA AGGAGATTCTGACAACAACAGCTGAACTCCTGAAGAAAGGCCCATATAAAATTGACACCTTCACCAGTTGTGAAGATCTGATAGCAAG AATTCAATCAAGCCCATACGATGGATATATACTGGACTGGGTGGTGAATGATAAATCTGCATATGATGTTTGTAAGAAAATCCGCGA ATCCAAAAAACCACATGCAATGATTATCATCTTAACAGGACAAACAGGAGATTTTATAGATCAGGAAATTGCAGAAGCGTTTAA TGACTTCGACATTCTAGGC

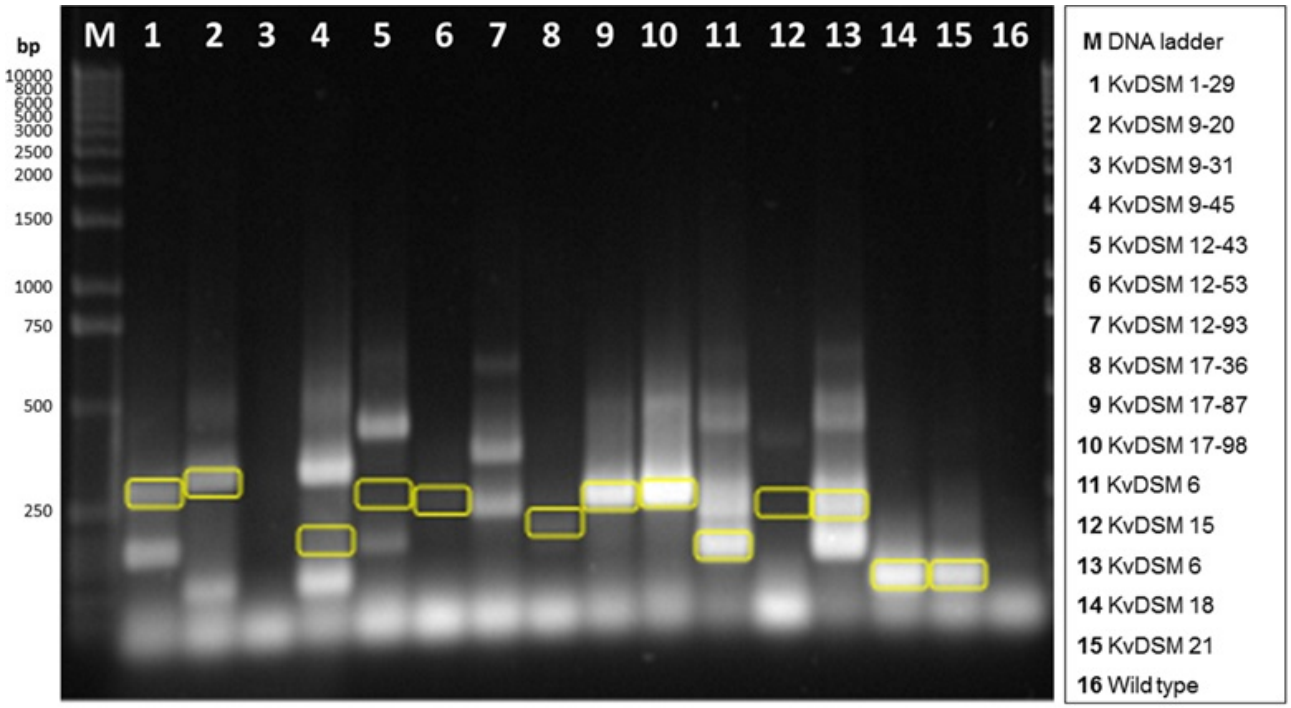
The blue letters correspond to the sequence of the *BetR* gene, the red ones to the mini-Tn5Km transposon and the green ones to a sequence upstream of the start of the gene. The underlined letters correspond to the repeated sequences given by the insertion of the transposon mini-Tn5Km.



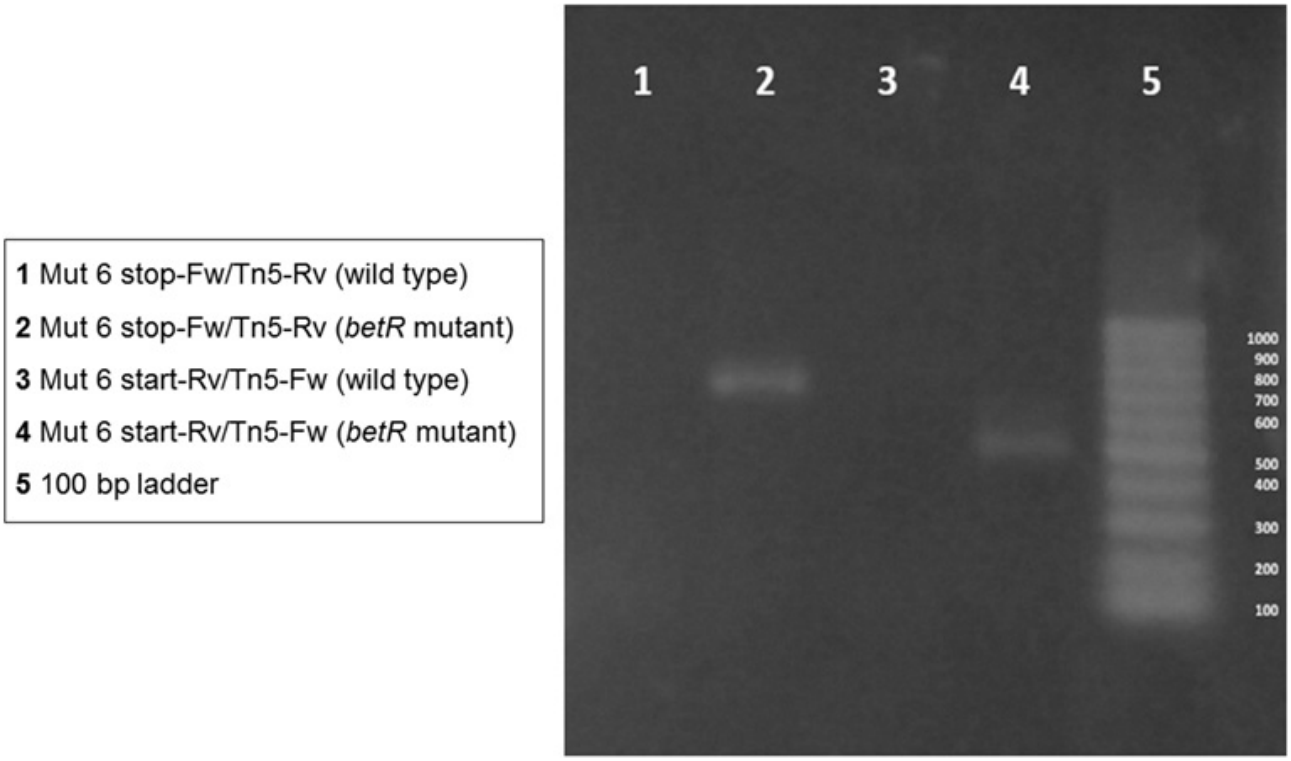
Supplementary Fig. (1). Construction of a plasmid vector for *trans* complementation of the *BetR* gene in *K. variicola* T29A::mini-Tn5Km. The *BetR* gene (blue) as well as a 223 bp sequence upstream of the gene start (green) and a 228 bp sequence downstream of the gene end (red) were amplified by PCR using primers with restriction sites KpnI and SacI. The amplification product was cloned into the vector pJET1.2/blunt. The brown arrow indicates the direction in which the insert was cloned.



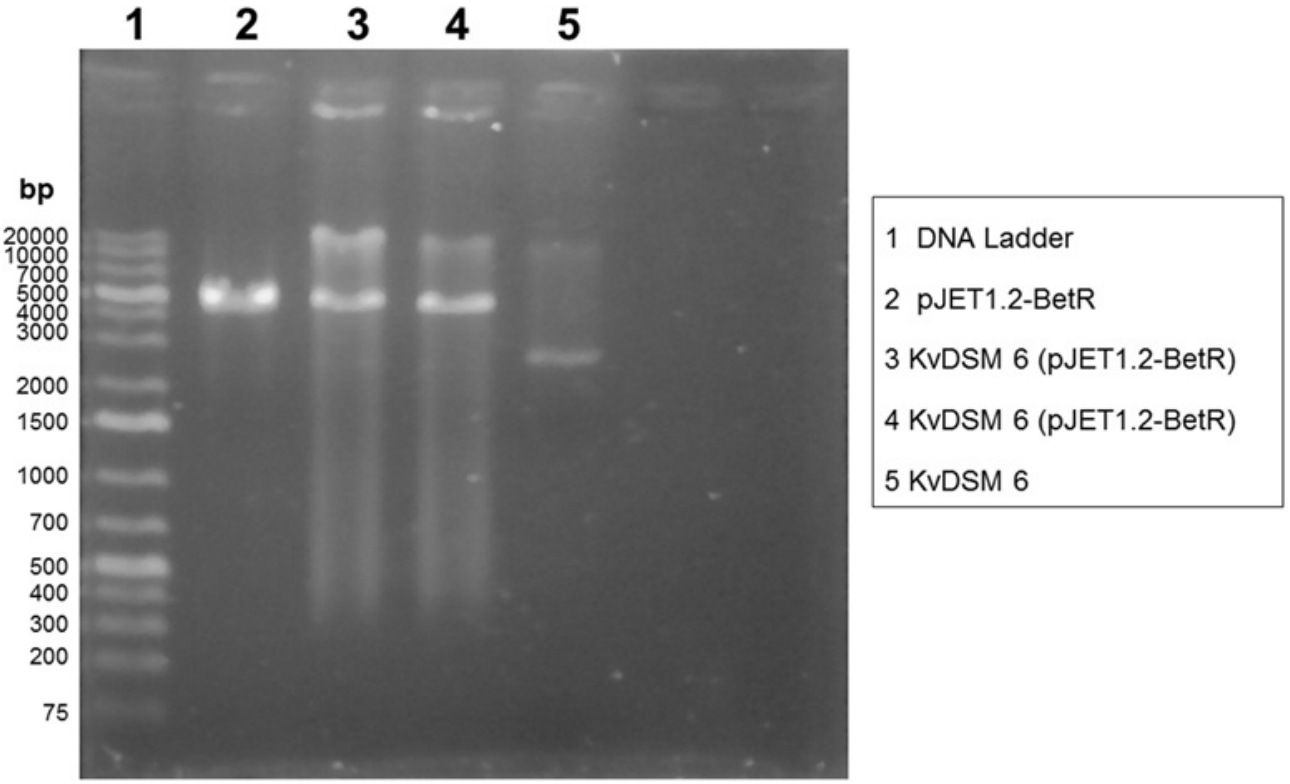
Supplementary Fig. (2). Plasmidic profile of some mutants of *K. variicola* T29A library (*K. variicola* T29A::mini-Tn5Km). The natural plasmid of this bacterium is observed, but the pUT mini-Tn5Km plasmid (7.05 Kb) is absent, which suggests that the mini-Tn5 transposon was integrated into the chromosome of the bacterium.



Supplementary Fig. (3). Band profile of the 14 mutants sensitive to desiccation-rehydration in a 2% agarose gel after amplification by an arbitrary PCR. . For the wild-type strain, there was no amplification. The DNA purified from the selected bands (denoted with a rectangle) was sequenced and compared with the databases to determine the insertion site of the mini-Tn5Km transposon.



Supplementary Fig. (4). The electrophoretic shift of the amplification products using oligonucleotides at the start and end of the *BetR* gene as well as oligonucleotides specific to the mini-Tn5 transposon. Mut 6 stop-Fw/Tn5-Rv and Mut 6 start-Rv/Tn5-Fw oligonucleotide pairs were used for the wild-type strain and the *BetR* mutant of K. variicola T29A, where the amplification products of 695 and 490 base pairs were observed, respectively.



Supplementary Fig. (5). Plasmid profile of the mutant interrupted in the *BetR* gene, with respect to some transformants of the mutant complemented *in trans* with the construction of pJET1.2-*BetR*.