Identification of *Klebsiella Varicola* 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.

<table>
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<tr>
<th>PCR Product</th>
<th>Sequence</th>
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| DNA fragment amplified with the oligonucleotides: Mut 6 start-Rv/Tn5-Fw | UTTCAGGGACATTTTATACATCTACAAACAACCTTACAAGACGCCGCAACATAAAAAACGATTTTTTATGTTGTTCAAGCAA TGGAGGAGAACCAAAAAGGACGCCAAAAGAACCGCGCGAACATTACATATCGCTTTGTTTTAATTGAAATTAATCTCACGATACCTACAAT AACAACCTTTAAATGTCAATTITTCACACCCACGAGACCGGGAATAGCAGCAGTGAACACATGATGAATGCTAGGTAATACCTCATTACCATGG
| DNA fragment amplified with the oligonucleotides: Mut 6 stop-Fw/Tn5-Rv | GAATTCGGCCTAGGCGGCCAGATCTGATCAAGAGACAGGTCTTTAGGTGTAAGCCTCAGTGATTTATTTAAAAT GGTTGAGGACAGCTATGGAGAAGAAACGCCCCGAAAATATATTITCAACAACAGGAAGAAATGGAAGGAGATATTTTCTTTTCCTTG ATACAGGAAAGACATATCTGACTGAAAATATAACATCGGAAACGACGAGAAGGAATGATGGAAAGGACATTATGGAGAAATGACGAGATTA GAGATCGCCAGAACGGGTTTAAATGTTTGGCTTTGAGAAAGATCTCGCCTTCTCTCGTAGAGCTAGTA AGGAGATTTTGACAAACAGCGGCTGAACTCGTCGGAAGAAAGCCCATTATAAAATGGAACCTACACCATGAGTTGGAATGTCGAATCGAAAG AATTCACATCAAGGCGCATCGATATATATATCTGCAGCTGGAGAAATGAAATATTTGATACCTCATTACCATGG

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.
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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.