PlodAB

......aat[ttctgttattgagacggtcactgaaaactacaaattggcattggagttagataaa
tgagggttctatttgtgaacagagattaagacgaatcaaatta*cgcgatctaa*tt*ttagatcgcg*
aatttaacgttgggtct[ttcagagaaacagcctcccttgtcaagagggattaactgatactgaa
ctgatactgccgtacctgcattgctctgcttaactgaaaga**C**cattcgtataaaaacggtttatg
gat]tttagttatcaacaa**aggag**taagttatg

PppoA

..ttctatttcattgattgcttaattgtctcgccaaagcgactgcactcacagcgagacactagt
gtaatcccgtgtaattgatgactgagccgcttttgctagtctttaga**G**taccgacactctcacaa
a**agga**ctcatcaatg

PppoB

.........ttcaagccgcgttattcgcaggtgctctagcgttttaagagcaaagaactgtgtaa
ataaattggctagtgaacaggaattttctgattagacctaaaaagagggcatatggaaaacaaag
tgtaacaaggtgtaattgaataattgaagttactcttatattttgttaa**G**gctagagaaccagt
cttg*ttttaattaaaaa*tgtcatccgaaattacaattatattttgt*ttaaaaa*gg*tttttaa*ct
t**gaggg**aaaatcatg

Fig. S1. Comparison of promoters of different *M. mediterranea* genes enconding oxidases: *PlodAB* (this study), *PppoA* (1), *PppoB* (2). All sequences are shown up to the initial ATG codon. Putative rbs in bold. Transcriptional start site determined by 5’-RACE in bold upper case. Predicted -10 and -35 hexamers are underlined. Brackets in *PlodA* sequence indicate the two fragements cloned for generating *lacZ* fusions, *PlodAB* (252 bp) and *PlodAB* (115 bp). Double underlined italics indicate palindromic sequences of unknown function.

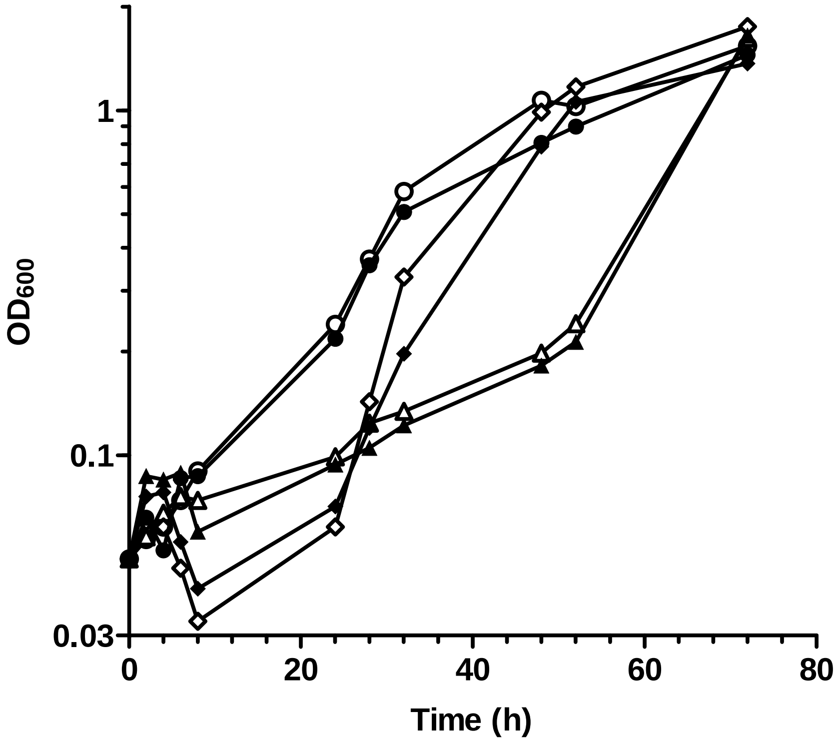

Fig. S2. Use of L-Lys, L-Arg and DAP by *M. mediterranea* MMB1-R (closed symbols) and LD (open symbols). Both strains were inoculated in MNL (glucose 30 mM and L-Lys 3 mM as nitrogen source) (diamonds) and media in which L-Lys is substituted by L-Arg (triangles) or DAP (circles).

References:

1. **Sanchez-Amat, A., P. Lucas-Elío, E. Fernández, J. C. Garcia-Borrón, and F. Solano**. 2001. Molecular cloning and functional characterization of a unique multipotent polyphenol oxidase from *Marinomonas mediterranea*. Biochim. Biophys. Acta **1547**:104-116.
2. **López-Serrano, D., F. Solano, and A. Sanchez-Amat**. 2004. Identification of an operon involved in tyrosinase activity and melanin synthesis in *Marinomonas mediterranea*. Gene **342**:179-187.