

Table S4. Experimental data on quinone biosynthesis for the genera containing studied genomes.

Genus	Synthesized quinones (this research)	Number of the studied genomes	Reference(s)
<i>Acinetobacter</i>	UQ	1	(1)
<i>Actinomyces</i>	MK+DMK	1	(1, 2)
<i>Alistipes</i>	MK+DMK	1	(3)
<i>Bacillus</i>	MK+DMK	1	(1)
<i>Bacteroides</i>	MK+DMK	44	(2, 4)
<i>Bifidobacterium</i>	-	15	(2, 4)
<i>Butyrivibrio</i>	-	2	(2)
<i>Campylobacter</i>	MK+DMK	2	(1)
<i>Citrobacter</i>	UQ+MK+DMK	2	(5)
<i>Clostridium</i>	-	21	(1, 2)
<i>Corynebacterium</i>	MK+DMK	1	(1)
<i>Desulfovibrio</i>	MK+DMK	2	(1)
<i>Enterobacter</i>	UQ+MK+DMK	1	(1)
<i>Enterococcus</i>	DMK	5	(6)
<i>Escherichia</i>	UQ+MK+DMK	7	(1)
<i>Eubacterium</i>	-	8	(4)
<i>Fusobacterium</i>	MK+DMK	14	(2)
<i>Gordonibacter</i>	MK+DMK	1	(7)
<i>Helicobacter</i>	MK+DMK	5	(8)
<i>Klebsiella</i>	UQ+MK+DMK	1	(1)
<i>Lactobacillus</i>	MK / -	36	(1)
<i>Leuconostoc</i>	MK+DMK	1	(1)
<i>Listeria</i>	MK+DMK	1	(1)
<i>Parabacteroides</i>	MK+DMK	4	(9)
<i>Pediococcus</i>	-	2	(1)
<i>Prevotella</i>	MK+DMK	2	(10)
<i>Proteus</i>	UQ+MK+DMK	1	(1)
<i>Providencia</i>	UQ+MK+DMK	4	(11)
<i>Ralstonia</i>	UQ	1	(12)
<i>Ruminococcus</i>	-	9	(2)
<i>Salmonella</i>	UQ+MK+DMK	1	(1)
<i>Streptococcus</i>	-	4	(1)
<i>Veillonella</i>	MK+DMK	2	(2, 4)

REFERENCES

1. **Meganathan R.** 2001. Biosynthesis of menaquinone (vitamin K₂) and ubiquinone (coenzyme Q): a perspective on enzymatic mechanisms. *Vitam Horm* **61**:173-218.
2. **Fernandez F, Collins MD.** 1987. Vitamin K composition of anaerobic gut bacteria. *FEMS Microbiol Lett* **41**:175-180.
3. **Nagai F, Morotomi M, Watanabe Y, Sakon H, Tanaka R.** 2010. *Alistipes indistinctus* sp. nov. and *Odoribacter laneus* sp. nov., common members of the human intestinal microbiota isolated from faeces. *Int J Syst Evol Microbiol* **60**:1296-1302.
4. **Ramotar K, Conly JM, Chubb H, Louie TJ.** 1984. Production of menaquinones by intestinal anaerobes. *J Infect Dis* **150**:213-218.
5. **Novotny C, Kapralek F.** 1979. Participation of quinone and cytochrome b in tetrathionate reductase respiratory chain of *Citrobacter freundii*. *Biochem J* **178**:237-240.
6. **Portela CA, Smart KF, Tumanov S, Cook GM, Villas-Boas SG.** 2014. Global metabolic response of *Enterococcus faecalis* to oxygen. *J Bacteriol* **196**:2012-2022.
7. **Selma MV, Tomas-Barberan FA, Beltran D, Garcia-Villalba R, Espin JC.** 2014. *Gordonibacter urolithinfaciens* sp. nov., a urolithin-producing bacterium isolated from the human gut. *Int J Syst Evol Microbiol* **64**:2346-2352.
8. **Arakawa C, Kuratsu M, Furihata K, Hiratsuka T, Itoh N, Seto H, Dairi T.** 2011. Diversity of the early step of the futasoline pathway. *Antimicrob Agents Chemother* **55**:913-916.
9. **Sakamoto M, Benno Y.** 2006. Reclassification of *Bacteroides distasonis*, *Bacteroides goldsteinii* and *Bacteroides merdae* as *Parabacteroides distasonis* gen. nov., comb. nov., *Parabacteroides goldsteinii* comb. nov. and *Parabacteroides merdae* comb. nov. *Int J Syst Evol Microbiol* **56**:1599-1605.
10. **Sakamoto M, Umeda M, Ishikawa I, Benno Y.** 2005. *Prevotella multisaccharivorax* sp. nov., isolated from human subgingival plaque. *Int J Syst Evol Microbiol* **55**:1839-1843.
11. **Macinga DR, Cook GM, Poole RK, Rather PN.** 1998. Identification and characterization of aarF, a locus required for production of ubiquinone in *Providencia stuartii* and *Escherichia coli* and for expression of 2'-N-acetyltransferase in *P. stuartii*. *J Bacteriol* **180**:128-135.
12. **Radu V, Frielingsdorf S, Evans SD, Lenz O, Jeuken LJ.** 2014. Enhanced oxygen-tolerance of the full heterotrimeric membrane-bound [NiFe]-hydrogenase of *Ralstonia eutropha*. *J Am Chem Soc* **136**:8512-8515.