

表 2 细菌基因组三核苷酸转移概率矩阵间的欧几里德距离

Table 2 The Euclidian distance of trinucleotide transition probability matrices of bacterial genomes

	<i>L. lac</i> _MG	<i>L. lac</i> _SK	<i>L. lac</i> _I1	<i>S. pyo</i> _M1	<i>P. pen</i> _AT	<i>S. aur</i> _US	<i>A. met</i> _QY
<i>L. lac</i> _MG	0						
<i>L. lac</i> _SK	0.044	0					
<i>L. lac</i> _I1	0.062	0.073	0				
<i>S. pyo</i> _M1	0.291	0.295	0.308	0			
<i>P. pen</i> _AT	0.321	0.324	0.324	0.305	0		
<i>S. aur</i> _US	0.392	0.396	0.390	0.392	0.334	0	
<i>A. met</i> _QY	0.382	0.388	0.397	0.320	0.349	0.372	0