

**Random chromosome partitioning in the polyploid bacterium**

*Thermus thermophilus* HB27

Haijuan Li

College of Biological and Environmental Engineering, Xi'an University, Xi'an 710065, Shaanxi, China

Corresponding author:

Haijuan Li

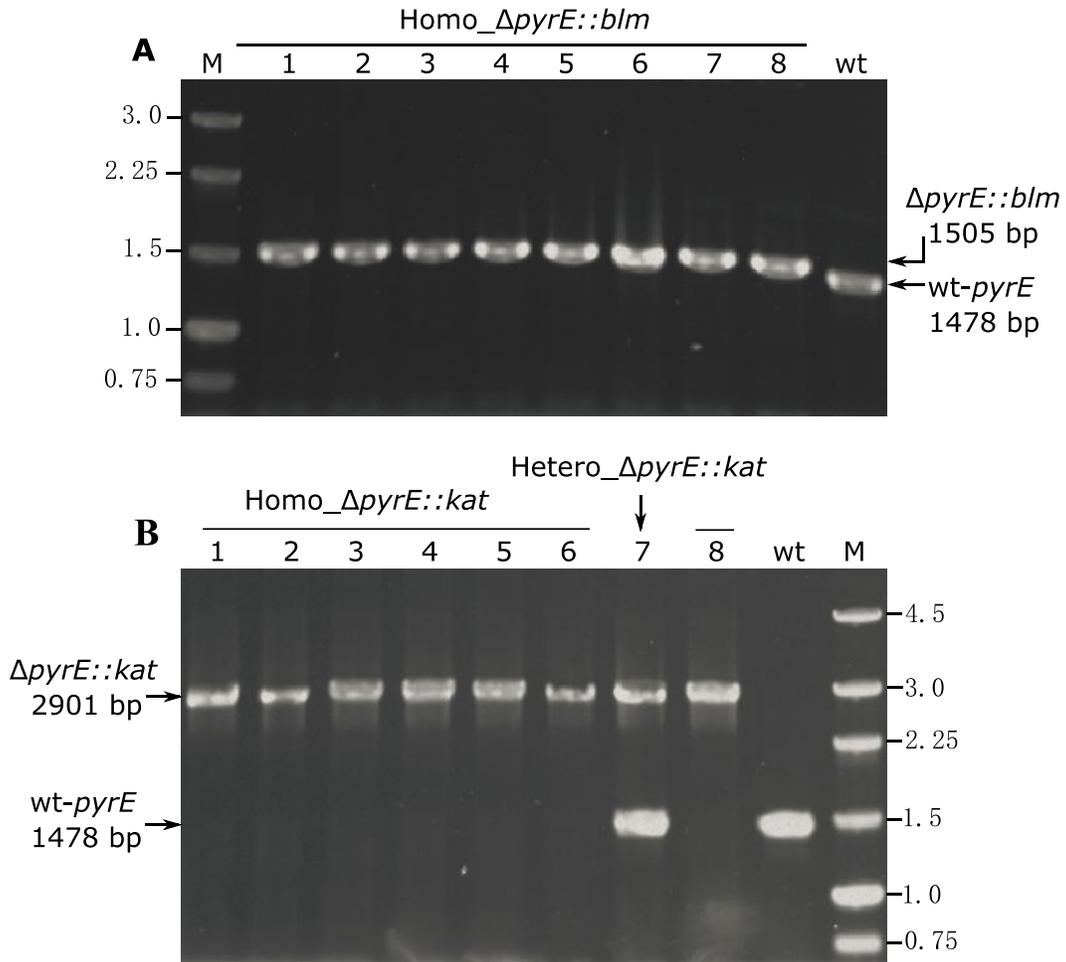
College of Biological and Environmental Engineering, Xi'an University, No. 168 South Taibai Road,

Xi'an, 710065, China

Email: haijuanli@xawl.edu.cn

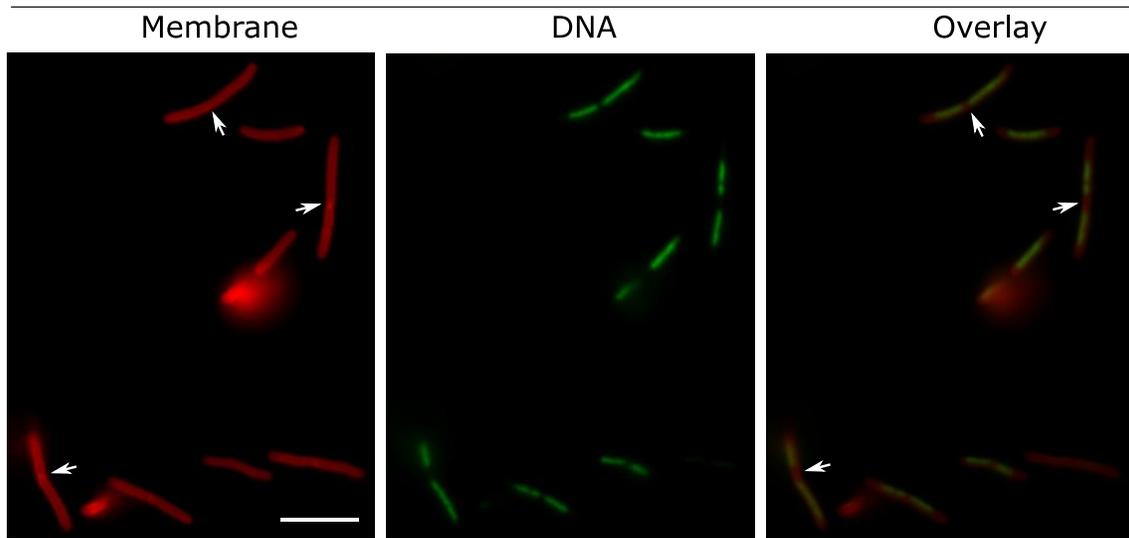
Tel.: +86-29-88241902

**Supplementary data**

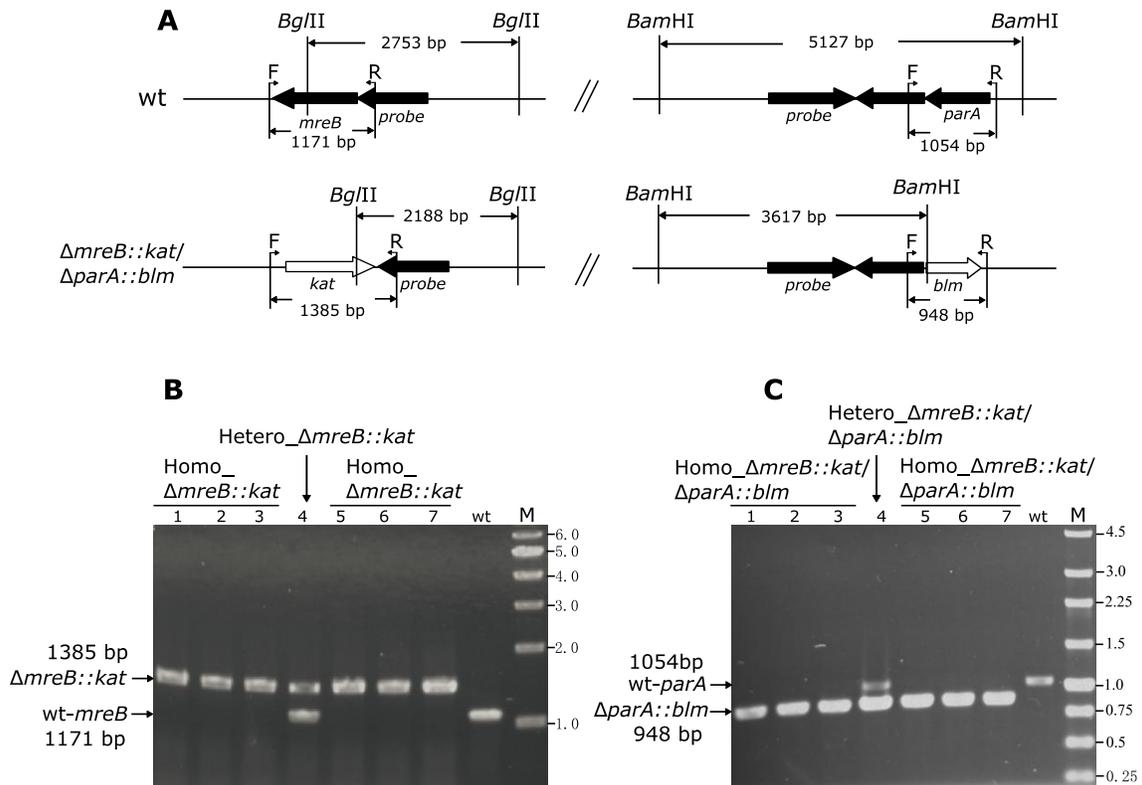


**Figure S1** Generation of homozygous  $\Delta pyrE::blm$  (A) and  $\Delta pyrE::kat$  (B) mutants. The allele exchange vectors pJ- $\Delta pyrE::blm$  and pCT3FK-2 were linearized, and transformed into *T. thermophilus* HB27 respectively. For each transformation, eight colonies were randomly selected, and PCR was used to determine the homozygous mutant in which the wild-type *pyrE* gene was completely replaced by *blm* or *kat* allele.

*T. thermophilus*  
HB27

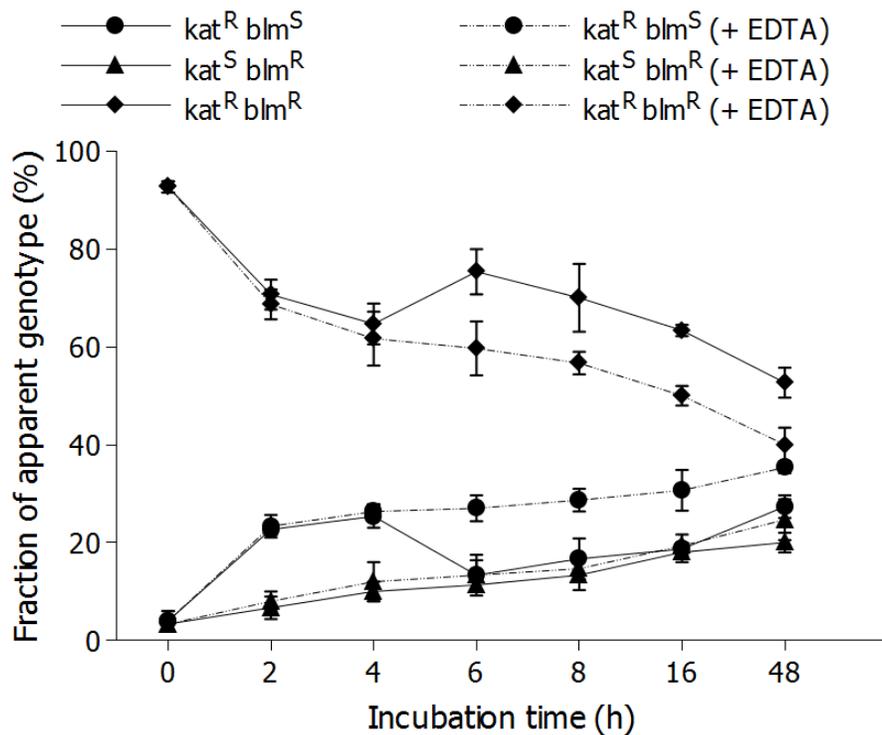


**Figure S2** Representative image of dividing *T. thermophilus* HB27 cells in which septa are not formed at mid-cell positions. Septa are pointed with white arrows, bar, 5  $\mu$ m.



**Figure S3** Generation of homozygous single gene deletion mutant  $\Delta$ *mreB*::*kat* (B) and double gene deletion

mutant  $\Delta mreB::kat/\Delta parA::blm$  (C). (A) Schematic drawings of the genotypes of the wild-type and mutant *mreB* and *parA* gene loci, respectively. Primers used for PCR detection of the mutant are shown with F and R. (B) The allele exchange vector pUC- $\Delta mreB::kat$  was linearized, and transformed into *T. thermophilus* HB27 followed by selection on agar plates supplemented with kanamycin. Seven transformants were randomly selected and PCR was used to determine the homozygous  $\Delta mreB::kat$  deletion mutants (primers flanking *mreB*). (C) pUC- $\Delta parA::blm$  was sequentially transformed into the correct  $\Delta mreB::kat$  strain, and the homozygous double gene deletion mutant  $\Delta mreB::kat/\Delta parA::blm$  was determined by PCR using primers flanking the *parA* gene.



**Figure S4** The allele segregation kinetics of the heterozygous strain HL01 grown in selection-free liquid medium with and without addition of EDTA. The preculture was grown with both antibiotics, upon washing away the antibiotics, the culture was re-inoculated into two batches of growth parallelly, and EDTA was added to one of the growth (final concentration 1mM/L). The fraction of apparent genotype was scored by spreading the culture on antibiotic-free agar plates and streaking 50 colonies from each time point on plates containing kanamycin and bleomycin, respectively. Solid lines: the apparent genotype changes in the culture without adding EDTA; dashed lines: the apparent genotype changes in the culture with addition of EDTA. Shown are mean and standard deviation from three independent repeats.