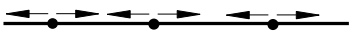
Replichores and gene orientation

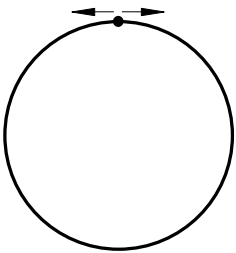
Replichores: origin and terminus of replication

Eukaryota



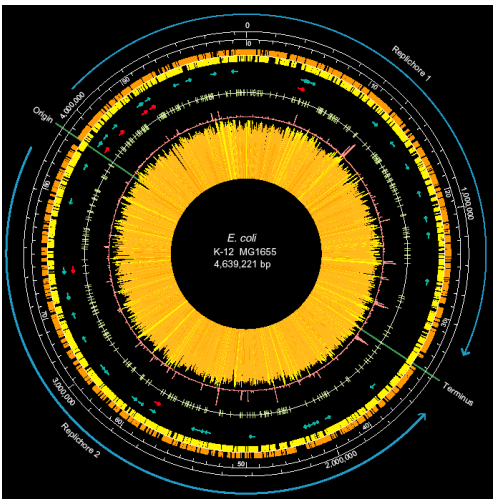
Many origins

Bacteria

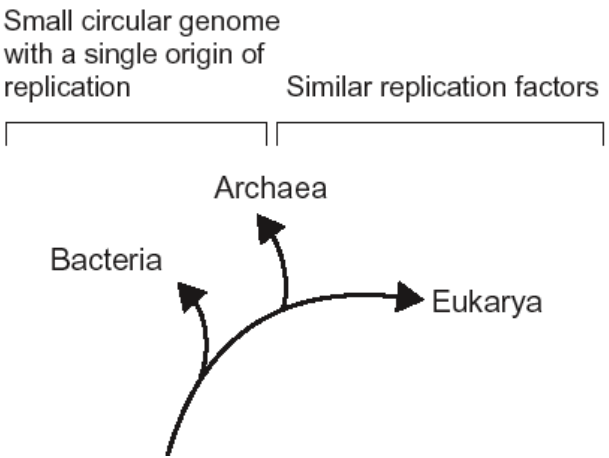


A single origin

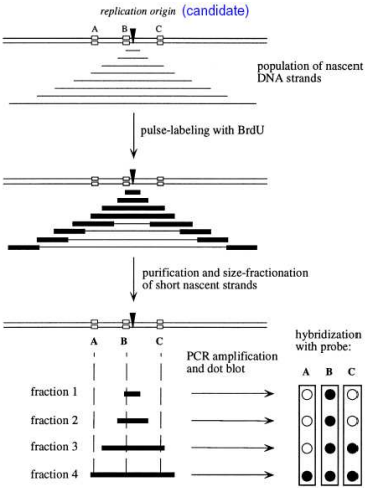
There are two replichores per chromosome



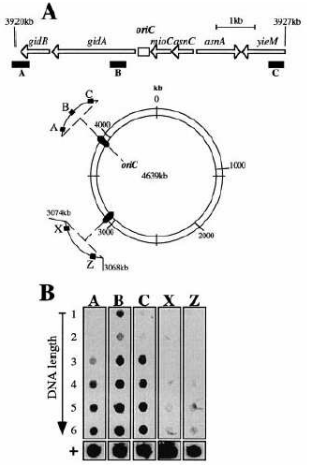
Archae & Bacteria



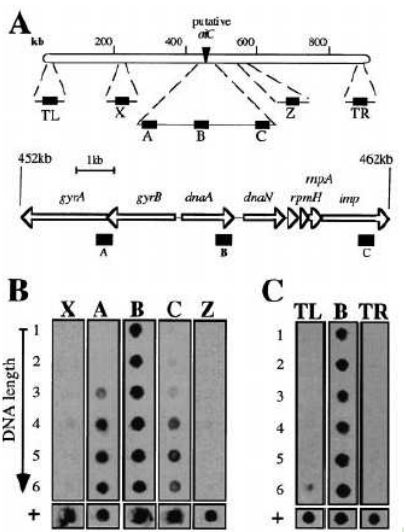
Looking for the origin



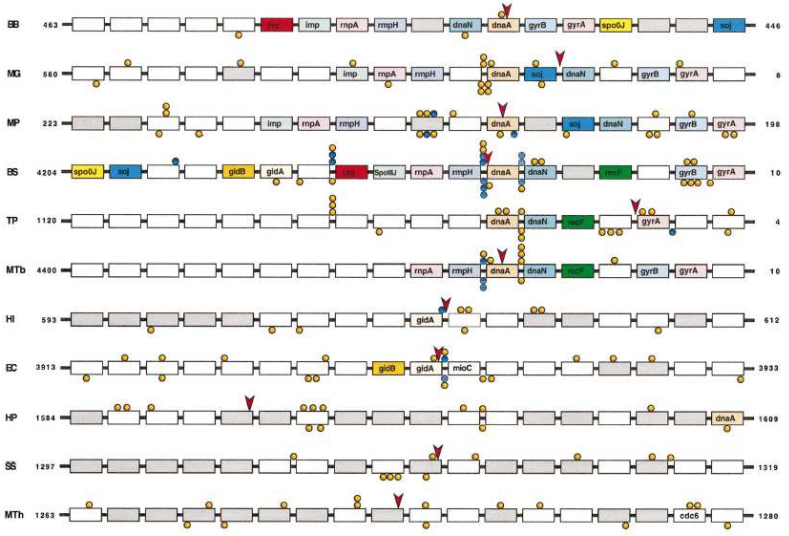
Looking for the origin in *E. coli*



Looking for the origin in *B. burgdorferi*

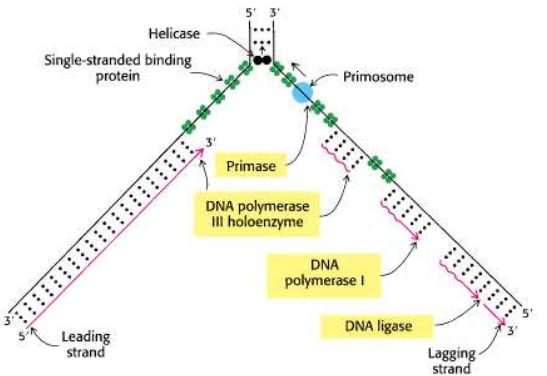


Zoom at the origin

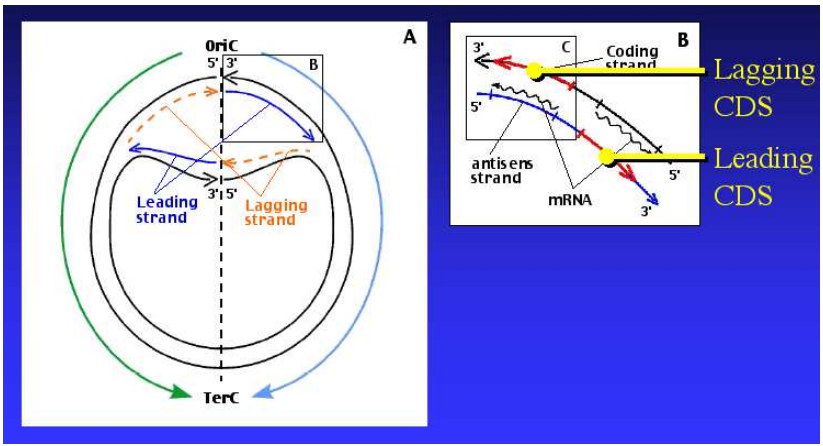


How replication works?

http://highered.mcgraw-hill.com/olcweb/cgi/pluginpop.cgi?it=swf::535::535::/sites/dl/free/0072437316/120076/micro04.swf



Leading and lagging CDS



Are genes equally reparted on both strands?

Study this yourself:
Download the `bsubt_2011.zip` file for *B. subtilis* on the class webpage, and study the repartition of genes on the genome, relatively to the origin and terminus of replication and the strand.

You will need to know the position of the origin and terminus of replication. As a good approximation, use:

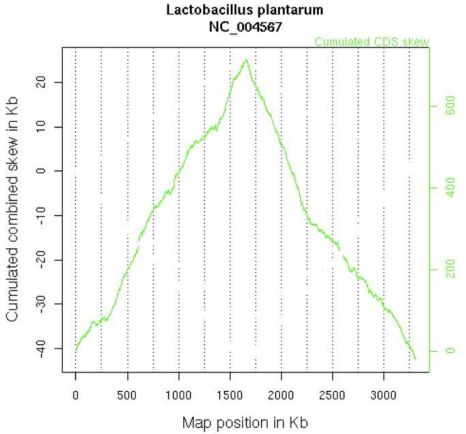
- Origin : 0 bp
- Terminus : 2.1 Mb

Bonus: How to define the two first colonnes of the `.ptt` file from the third one? In R? In another language?

More leading CDS than lagging CDS

For those about to rock. . .

Another way to see it: CDS skew *Lactobacillus plantarum*



CDS skew is proportionnal to the number of CDS on the "+" strand minus the number of CDS on the "-" strand, while going along the genome.

Can you do the same graph for *B. subtilis*?

CDS skew in B. subtilis

Collisions between polymerases

1: Science 1992 Nov 20;258(5086):1362-5 Related Articles, Books

Consequences of replication fork movement through transcription units in vivo.

French S.

Department of Biology, University of Virginia, Charlottesville 22903.

To examine the basis for the evolutionary selection for codirectionality of replication and transcription in Escherichia coli, electron microscopy was used to visualize replication from an inducible ColE1 replication origin inserted into the Escherichia coli chromosome upstream (5') or downstream (3') of rrnB, a ribosomal RNA operon. Active rrnB operons were replicated either in the same direction in which they were transcribed or in the opposite direction. In either direction, RNA polymerases were dislodged during replication. When replication and transcription were codirectional, the rate of replication fork movement was similar to that observed in nontranscribed regions. When replication and transcription occurred in opposite directions, replication fork movement was reduced.

Connection with essentiality

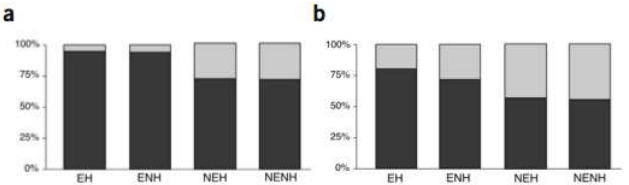


Figure 1 Distribution of genes between the leading (dark gray) and the lagging (light gray) strands of the genome of *B. subtilis* (**a**) and *E. coli* (**b**). H, highly expressed; NH, non-highly expressed; E, essential; NE, non-essential.

Rocha, E.P.C. & Danchin, A. (2003) *Nature Genetics*, **34**:377-378.

Essentiality and the quest for the smallest autonomous genome

2 main approaches:

- By deletion : define all essential genes by single deletion, coupled deletion, bioinformatics prediction, and try to delete all the non-essential genes.
- By addition : synthetize an entirely new genome doing only what you want it to do : this is called *synthetic biology*.
- The minimal genome should contain 250-300 genes (estimation from Koonin E., *Nature Rev. Micobiol.* (2003) **1**)