## L12 Advanced DNA Assembly

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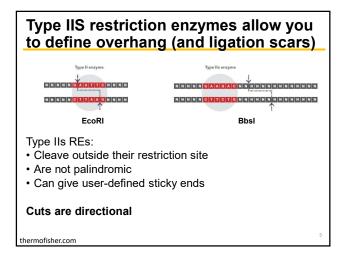


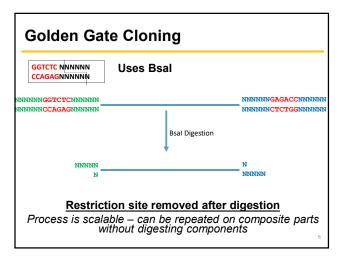
## Recall... Required components for DNA delivery 4 mechanisms to assemble DNA 1. Chemical addition 2. Homologous recombination 3. Annealing & Polymerization 4. Digestion & Ligation BioBrick™ Std Advantages - idempotent/scalable - Easily automatable - Easily automatable - Robust - Only 4 REs used Disadvantages - Need to remove internal Biobrick RE sites from all parts - Have a fixed scar (not good for protein fusions) - Can't add parts between parts

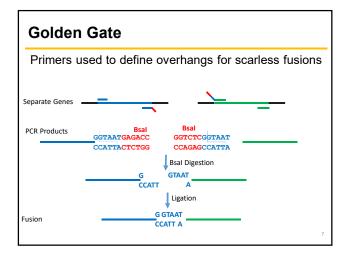
## This lecture....

- Scarless digestion + ligation
- Anneal + polymerization methods
- Recombination-based methods
- Summary

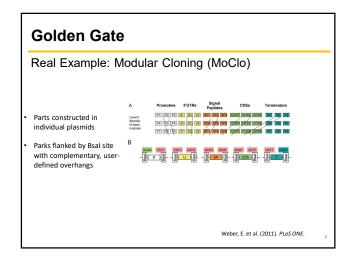
# Fusion proteins are common in biotech Scars between parts may cause frameshift mutations or disrupt folding (function) A PRODUCTION OF THE PROTECT OF THE PROPERTY OF THE P

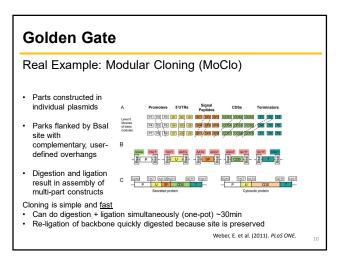


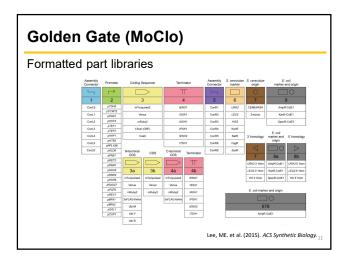


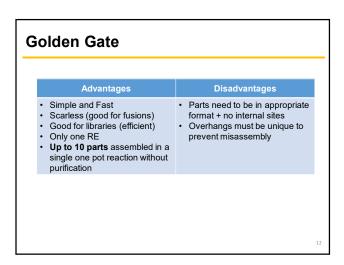


## Golden Gate GGTCTC NNNNNN CCAGAGNNNNNN Cleavage site is user-defined (specified by position relative to recognition site) • Can specify linker for fusion proteins • Can do multi-part assembly with 1 enzyme simultaneously • Assembly specified with unique complementary overhangs for each junction • Cloning is simple and fast • Can do digestion + ligation simultaneously (one-pot) ~30min • Re-ligation of backbone quickly digested because site is preserved









## Sequence-independent cloning methods

## RE-based assembly requires part formatting that may be difficult

Overhangs, no internal restriction sites

### **POLYMERIZATION + ANNEAL**

- 1. Gibson Chew Back Anneal (CBA)
- 2. Sequence + Ligase Independent Cloning (SLIC)
- 3. Splicing by Overlap Extension PCR (SOEing)

Gibson Assembly

Requires:

• Linear DNA with long regions of homology (~20 – 50 bp)

@ junctions

• 3 enzymes:

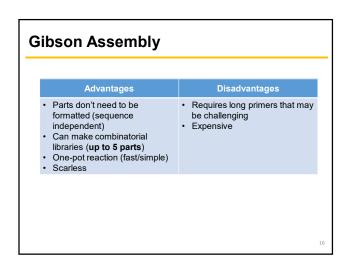
1. T5 Exonuclease
Chews back 5' end of DNA to make 3' overhang

2. Phusion/Proof-reading DNA polymerase
Repairs the gaps in overhangs via PCR

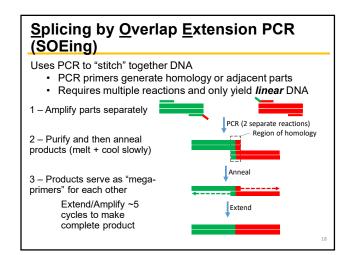
3. Taq DNA Ligase
Forms covalent bonds between parts

Enzymes chosen to work together in one pot at one temperature

## Gibson Assembly Workflow didNA hagments with overlapping ends. Add fragments to decord featuring to the following the followi



### Sequence + Ligation Independent Cloning (SLIC) · Like Gibson but no ligase or dNTPs to PCR product repair chew back T4 DNA polymerase T4 DNA polymerase 3' Exo activity (no dNTPs) has 3 exonuclease activity in absence of dNTPs T4 DNA polymerase (+ dCTP) Anneal (~25 bp overlaps) dCTPs added to control amount of chew back · Repair completed in ↓ Transformation https://j5.jbei.org/j5manual/pages/22.html host Disadvantages • Less efficient (bad for libraries) Cheaper



## SOEing → CPEC • Can do similar procedure with a vector + parts (no ligase needed) = Circular Polymerase Extension Cloning (CPEC) • Using just overlapping primers is how genes are synthesized JBELorg 19

## **SOEing Limitations**

- · Large stretches of ssDNA
  - Must avoid forming stable secondary structures and repeats
    - · Can lead to assembly failures or mutations at junctions

But potentially, cheaper → only need primers and polymerase

