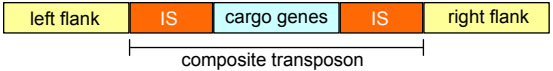
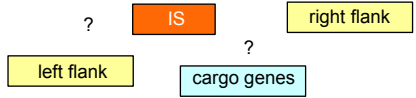


**A** It is easy to identify composite transposons from complete genomes



**B** It is impossible to identify composite transposons from partial genomes



**C** It is possible to identify composite transposons from assembly graphs:

