

1 Introduction

2 *Lachancea Kluyveri* is the earliest diverging lineage of the known *Lachancea*
3 clade. *L. Kluyveri* experienced an introgression of 1Mb about XXX ago. The
4 introgression shows a difference in average GC-content of 13 % compared to
5 the rest of the *L. Kluyveri*.

6 Codon usage is assumed to be associated with the available tRNA pool
7 in a cell. Codons matching more abundant tRNA species are assumed to
8 minimize ribosome pausing due to reduced waiting time for a correct tRNA.
9 Differing codon usage bias in the introgressed region can either be caused by
10 differences in mutation bias, relating to XXXX, or differences in selection for
11 translation efficiency, indicate a shift in the available tRNA pool. Differences
12 in mutation bias should persist longer due to the absence of selection.

13 We asked if the difference in GC-content is reflected in differences in codon
14 usage bias. We analyzed the two genomic regions in the *L. Kluyveri* genome
15 together and separately. Our results indicate that the introgressed region
16 shows a different signature of codon usage bias. We employed a mechanis-
17 tical model that allowed us to distinguish between effects of mutation bias,
18 or bias in selection for translation efficiency. Further inspection showed that
19 mutation bias is dominating the observed difference, while differences in se-
20 lection bias between codons is mostly in agreement between the two genomic
21 regions.

22 • Introgression in Kluyveri, effects of introgressions, GC-content differ-

23 ence

- 24 • Codon Usage bias reflective of cellular environment, e.g. available
25 tRNA pool
- 26 • Mechanistic model allows to distinguish between effects of selection and
27 mutation on current observed state.

28 Results

- 29 • Question: GC-content variation causes difference in CUB, CUB differ-
30 ence driven by different selection or mutation environment of original
31 host
- 32 • C-left has lower % of high expression genes
- 33 • Observing variation in codon usage bias in kluyveri genome
- 34 • differences in mutation greater than in selection
- 35 • ignoring variation effects information extracted from the data
- 36 • no lachancia with similar cub known, most yeast have similar cub.

37 Discussion

- 38 • Faster decay of selection bias, versus mutation bias

- 39 • expected number of mutations, C-Left not at equilibrium
- 40 • low amount of high expression genes lead to longer persistence of GC-
- 41 difference?