Supporting Materials

Large-scale survey of the intraspecific fitness and cell morphology variation in a protoploid yeast species

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Supporting Figures

Figure S1. Cumulative proportion of variance of the principal component analysis for the phenotypes. Grey bars indicate the proportion of variance (left axis) explained by the PCs. Red circles indicate the cumulative proportion of variance (right axis) explained by the PCs. The horizontal dashed red line indicates 60% and 90% of the cumulative proportion of variance.

Figure S2. Relationships between specific growth rate, lag phase and yield of biomass. The fitness parameters were extracted from high-density growth curves. A high correlation is found when comparing growth rates and yield of biomass (A) whereas the lag phase feature do not correlate with neither yield of biomass (B) nor growth rates (C).

Figure S3. Trait variation with *L. kluyveri* according to the environmental condition classes. Hierarchical clustering of trait profiles was performed using a centered Pearson correlation metric and average linkage mapping for carbon sources, toxins and environment and metabolites classes. The color scale represents results where high growth rates are depicted in red and slow growth rates in blue.

Figure S4. Pair plots of PC scores for the 27 *L. kluyveri* species. Principal component analysis of *L. kluyveri* morphological variation. Strains are represented by their coordinates along the first five principal components. Box colors represent geographical origins as red with America, purple with Europe, and orange with Asia, using the same colors as in Figure 2B.

Supporting Tables

Table S1. List of strains used in this study.

Table S2. List of tested conditions.

Table S3. Principal component loadings used for the characterization of each PC.

Figure S1

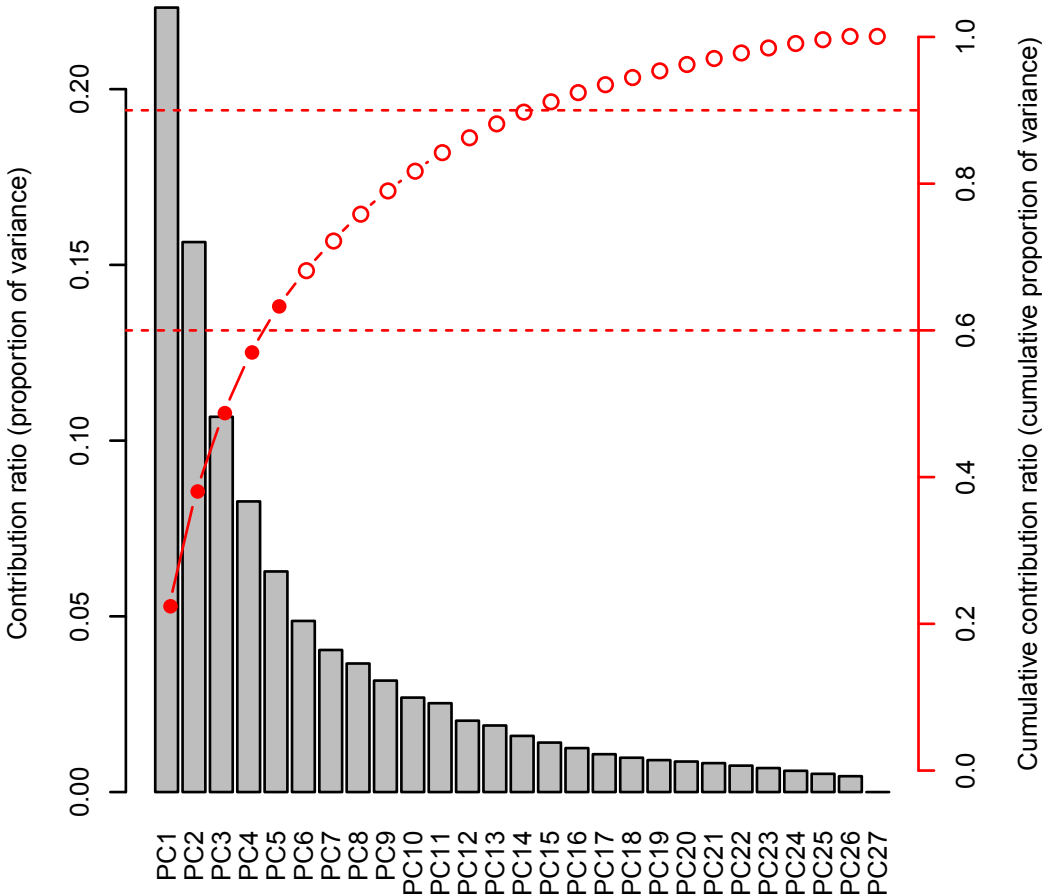
Contribution ratio (proportion of variance)
0.00
0.05
0.10
0.15
0.20
PC1
PC2
PC3
PC4
PC5
PC6
PC7
PC8
PC9
PC10
PC11
PC12
PC13
PC14
PC15
PC16
PC17
PC18
PC19
PC20
PC21
PC22
PC23
PC24
PC25
PC26
PC27
0.0
0.2
0.4
0.6
0.8
1.0
Cumulative contribution ratio (cumulative proportion of variance)

Figure S2

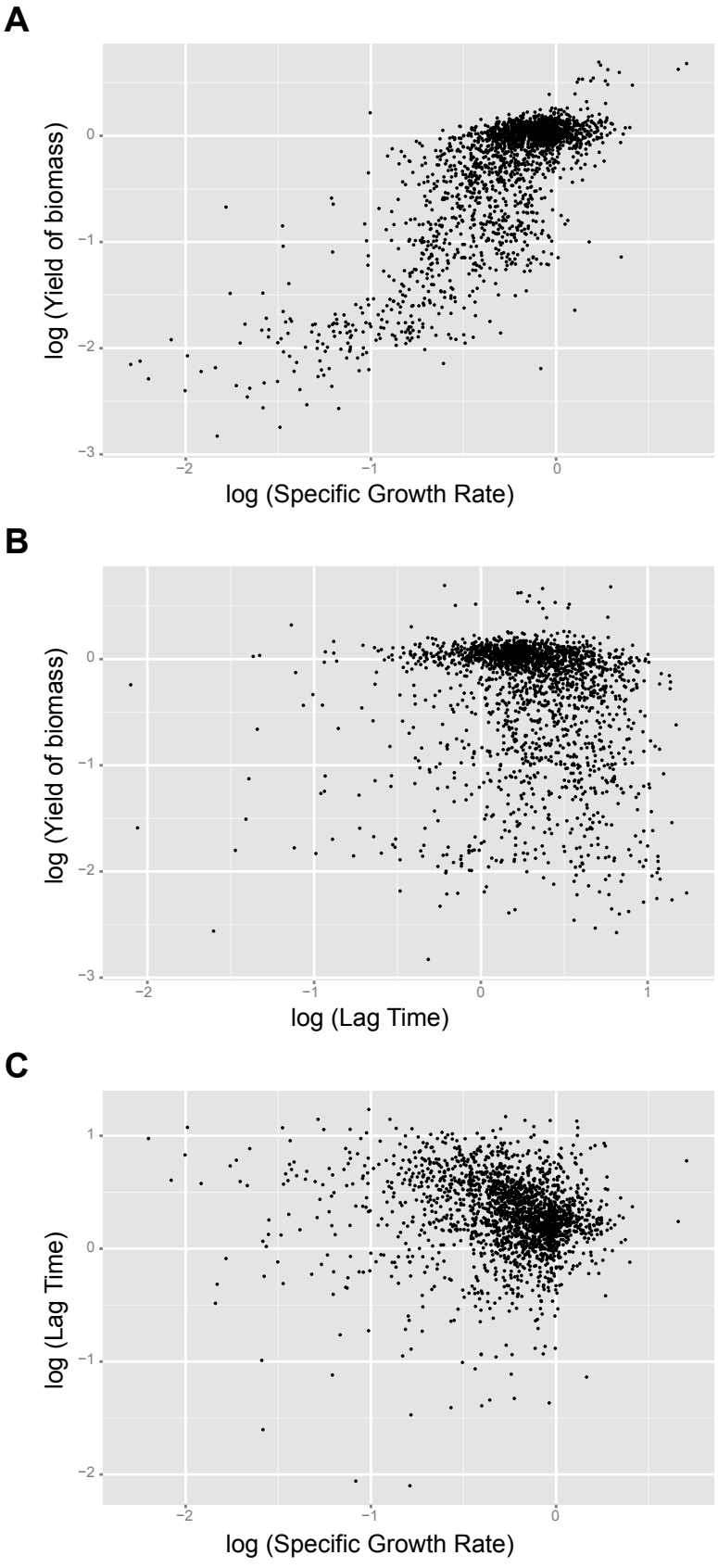
A
log (Yield of biomass)
log (Specific Growth Rate)
B
log (Yield of biomass)
log (Lag Time)
C
log (Lag Time)
log (Specific Growth Rate)

Figure S3

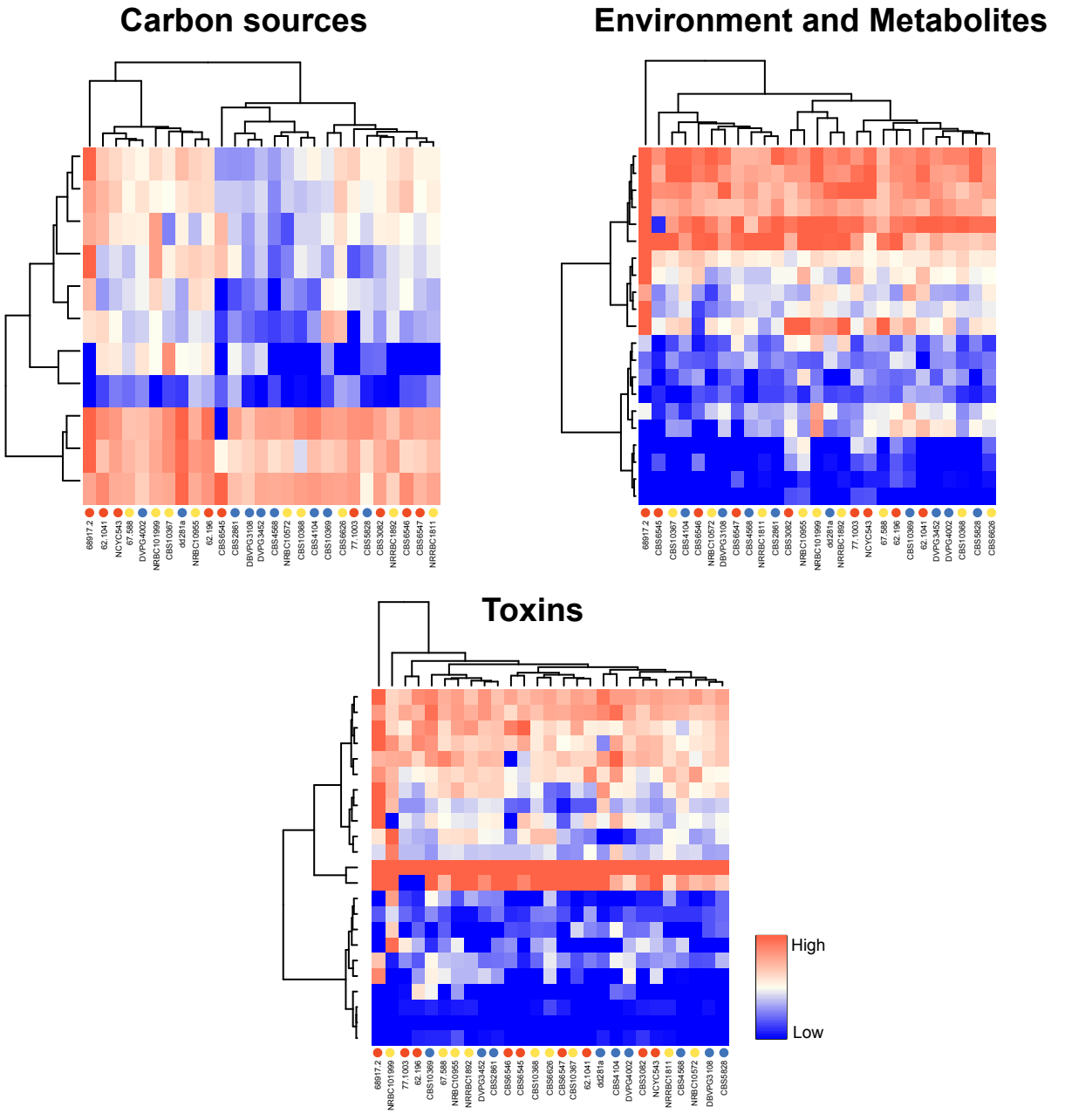
Carbon sources
Environment and Metabolites
Toxins
High
Low

Figure S4

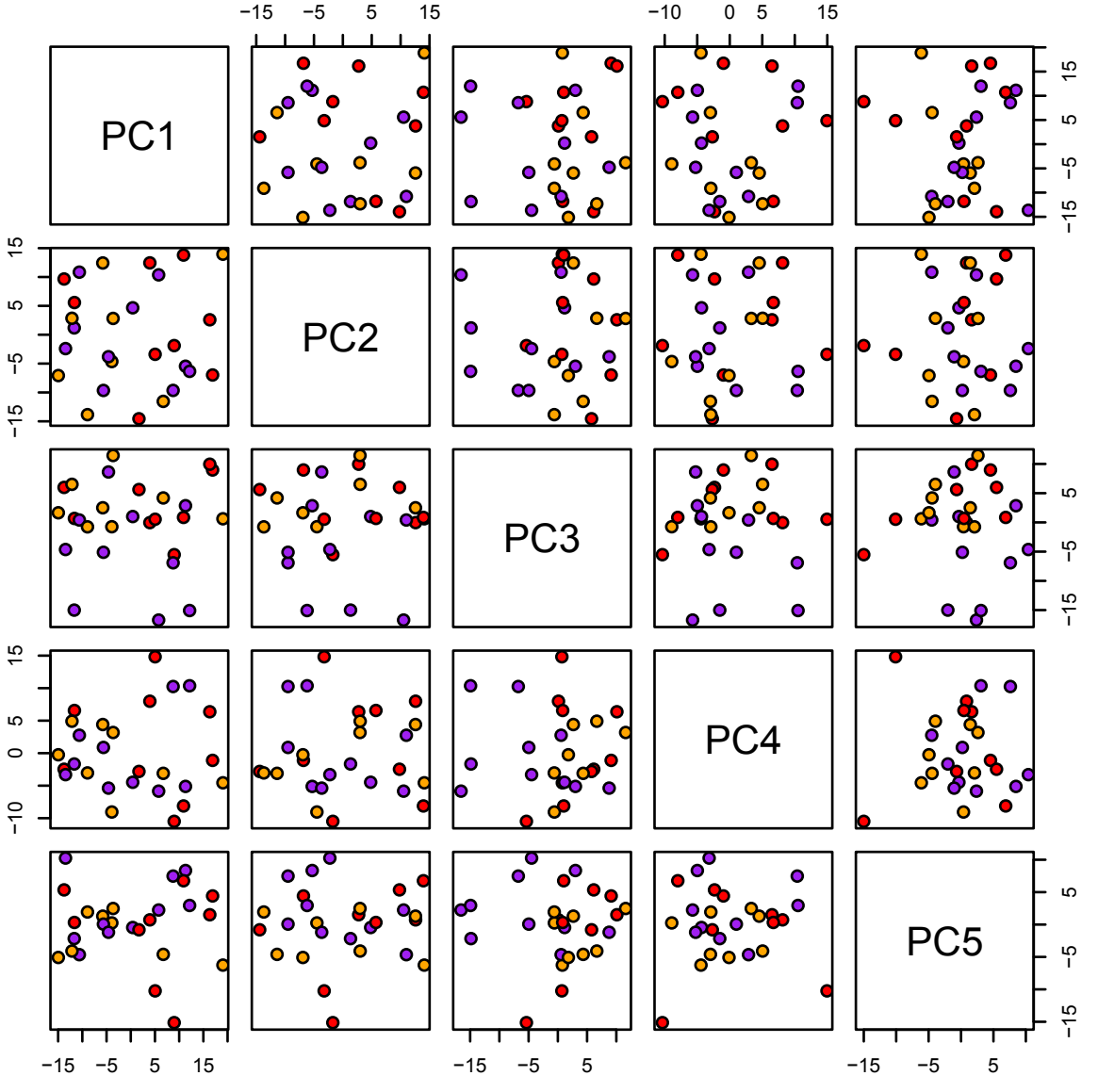

Table S1. Strains used in this study

Strain	Ecological niches	Geographical origins
62-1041	Willow exudate	USA, California, Davis
CBS 3082	*Drosophila pinicola*	USA, California
77-1003	Unknown	USA, California
NCYC 543	*Drosophila pinicola*	USA, California
62-196	*Taraxacum* officinale	Canada, Saskatoon
CBS 6545	Salix exudate	USA, California
CBS 6546	Exudate of Populus sp.	USA, California
CBS 6547	*Drosophila pseudobscura*	USA, California, Gualala Creek
CBS 6626	Exudate of tree	Japan, Mt. Takamatsu
NRBC 1892	Tree exudate	Japan
CBS 10367	*Quercus Mongolica* exudate	Russia, Kedrova pas natural reserve
CBS 10368	*Quercus Mongolica* exudate	Russia, Sikhote-Alinsky nature reserve
CBS 4104	Soil	Netherlands, Wageningen
68.917-2	Exudate of Populus trichocarpa	Canada
DBVPG 4002	Cavern	Italy
67-588	*Ulmus japonica* exudate	Japan, Yamabe
NRBC 1811	Partially decaying leaf	Japan
NRBC 10572	Moss	Thailland
NRBC 10955	Decaying leaf of Rhizophora mucronata	Japan
CBS 10369	Unknown	Spain
NRBC 101999	Decaying leaf of Rhizophora mucronata	Japan
CBS 5828	Soil	Denmark
dd281a	Forest	Germany, Heidelberg
CBS 2861	Soil	Sweden
CBS 4568	Soil	Sweden
DBVPG 3452	Soil	Sweden, Ultana
DBVPG 3108	Soil	Netherlands

Table S2. Conditions used in this study. The classification "Carbon utilization" indicates that the 2% of dextrose was substituted by other carbon sources.

Condition	Concentration	Class
Acetate	2 %	Carbon source
Ethanol	2 %	Carbon source
Ethanol	5 %	Carbon source
Galactose	2 %	Carbon source
Glucose	2 %	Carbon source
Glycerol	2 %	Carbon source
Mannitol	2 %	Carbon source
Raffinose	2 %	Carbon source
Sorbitol	2 %	Carbon source
Succinate	2 %	Carbon source
Sucrose	2 %	Carbon source
Xylose	2 %	Carbon source
$CaCl_2$	600 mM	Environment
$CaCl_2$	100 mM	Environment
Cold	23 °C	Environment
$CoSO_4$	0.1 mM	Environment
$CoSO_4$	0.05 mM	Environment
$CuSO_4$	7.5 mM	Environment
$CuSO_4$	5 mM	Environment
Ethanol	10 %	Environment
Ethanol	5 %	Environment
Heat	40 °C	Environment
Heat	37 °C	Environment
Heat	38 °C	Environment
LiCl	5 mM	Environment
LiCl	1 mM	Environment
Methanol	8 %	Environment
Methanol	5 %	Environment
NaCl	1 M	Environment
NaCl	0.5 M	Environment
NaCl	0.75 M	Environment
NiSO4	10 mM	Environment
YNB		Environment
5-FU	10^{-4} M	Toxins
5-FU	10^{-6} M	Toxins
6-azauracil	1250 mg/ml	Toxins
6-azauracil	500 mg/ml	Toxins
Arsenic	0.5 mM	Toxins
Arsenic	0.05 mM	Toxins
B-	10 mM	Toxins

mercaptoethanol		
Caffein	2.25 mg/ml	Toxins
Caffein	1.5 mg/ml	Toxins
Cycloheximide	10^{-5} M	Toxins
Cycloheximide	10^{-6} M	Toxins
DMSO	8 %	Toxins
DMSO	6 %	Toxins
DMSO	4 %	Toxins
DTT	1.4 mM	Toxins
Nystatin	10^{-6} M	Toxins
Nystatin	5.10^{-7} M	Toxins
Rapamycin	10^{-7} M	Toxins
Rapamycin	10^{-8} M	Toxins
SDS	0.03 %	Toxins
SDS	0.01 %	Toxins
SDS	0.003 %	Toxins