Screening *S. cerevisiae* with high RNA content using global Transcriptome Machinery Engineering and its characterization

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The current trend for food is using natural flavor source instead of artificial sweeteners for health. Yeast extracts are perfectly natural sweeteners globally used for a variety of foods, but yeast with high RNA (flavorous nucleotide) content is depended on overseas now. To produce yeast with high flavorous nucleotide, the priority is selection or improvement of high RNA containing yeast. Using global Transcriptome Machinery Engineering (gTME), screening high RNA containing yeast mutant is expected. Mutant library of *STP15* encoding the TATA-binding protein of *Saccharomyces cerevisiae* was generated using gTME. The total number of mutant yeast colonies were approximately $5 \times 10^5$ on YSCD-Ura plate. To detect acidic-RNase restricted strain (lethal mutant), as RNase activity is inhibited by K+ ion, colonies growing well on YPD plate and non-growing on containing KCl (1.5M) plate were selected, approximately 2.4% of $5 \times 10^5$ colonies. These selected mutants have the possibility to accumulate high RNA at general yeast culture (acid condition, pH<7). To screen mutants containing higher RNA, quantitative analyses of RNA contents of selected mutant yeasts were measured by PCA and orcinol methods. The highest RNA contained mutant yeast stain was selected and characterized.