

Gene Expression Profile Analysis for Circadian Promoter Activities of Cyanobacterial Bioluminescent Reporter Strains Using Non-Metric Multidimensional Scaling

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1 Introduction

Circadian rhythms in photosynthetic organisms are important features in their living forms, since the usage of solar energy in the day phase is an essential process for them. Approximately, during half of day, no solar energy is available, thus it is sometimes useful to alter cellular activities during this period. Recently, circadian rhythm of cyanobacteria turns out to be maintained by a small number of genes. Furthermore, oscillation of the circadian rhythm is reproduced in even *in vitro*[2] situation. However, it is uncertain how genetic network which makes use of the clock is regulated [1]. In this poster, we would like to clear out how the genetic network is regulated with and without circadian rhythms by using expression profiles of a bioluminescent reporter system. This system enables us to measure gene expression activities of each promoter of living cells with a high time resolution. The obtained time sequential gene expression profiles are analyzed by using non-metric multidimensional scaling method (nMDS)[3, 4].

2 Method

We have generated bioluminescent reporter strains carrying luciferase reporter genes under putative promoter regions of each ORF of *Synechococcus elongatus* PCC 7942. Bioluminescence of living cells is measured automatically under continuous light conditions. In this time, we have measured 127 ORFs sequentially aligned in the genome (c.a. 5 % of total genome) and found 68 clones exhibit reliable bioluminescence. Obtained gene expression profiles are analyzed by nMDS and the relationships between genes are shown as two dimensional alignment.

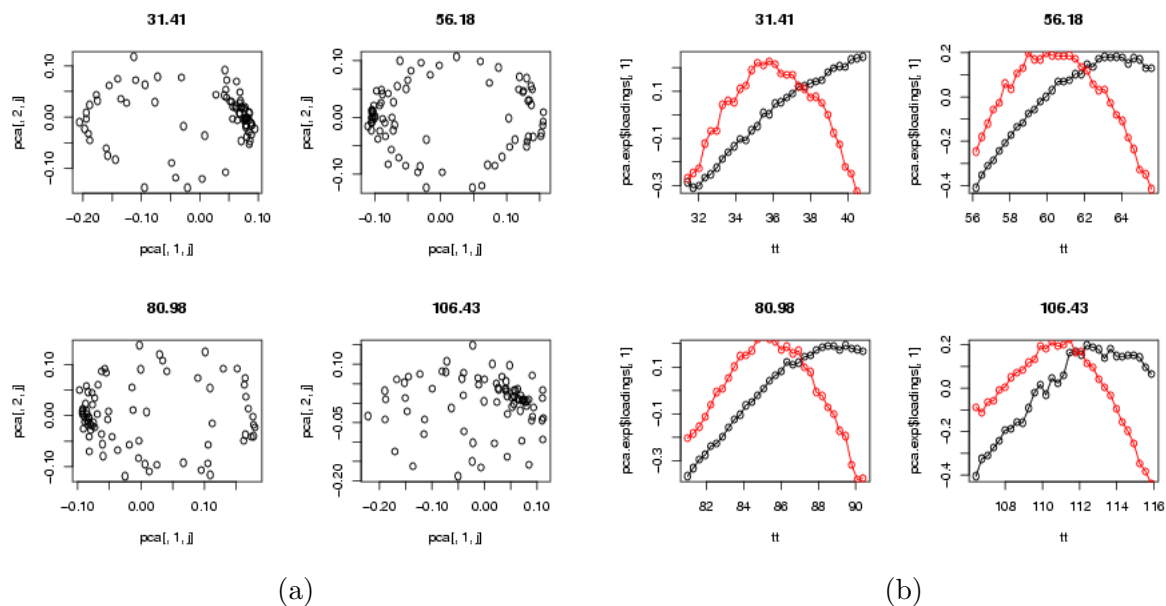


Figure 1: (a) 2D nMDS embeddings of promoters' bioluminescence. (b) The first and second principal components of standardized profiles.

3 Results

After analysing gene expression profiles by nMDS, we have found that circular gene alignment is obtained when we make use of partial gene expression profiles. In Figure 1(a), we have shown that two dimensional nMDS embedding of time interval from 31 hours to 41 hours, from 56 to 66, from 81 to 91, and from 106 to 116, by using sign-reversed correlation coefficients between gene expression profiles as dissimilarity. Circular arrangement of genes is obvious. In order to understand the meanings of circular arrangement, we have shown in Figure 1(b) the first and second principal components obtained by principal component analysis for gene standardized expression profiles. Clearly, these are parts of sinusoidal forms. This suggests that most of promoters exhibit sinusoidal oscillation although during some period these activities are inhibited.

References

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