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Deciphering and prediction of plant dynamics under field conditions

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Elucidation of plant dynamics under fluctuating natural environments is a challenging goal in plant physiology. Recently, using a computer statistics integrating a series of transcriptome data of field-grown rice leaves during an entire crop season and several corresponding environmental data such as solar radiation and ambient temperature, most parts of transcriptome have been modeled. This reveals the detailed contributions of developmental timing, circadian clocks and each environmental factor to transcriptome dynamics in the field and can predict transcriptome dynamics under given environments. Furthermore, some traits such as flowering time in natural environments have been shown to be predicted by mathematical models based on gene-networks parameterized with data obtained in the laboratory, and phenology models refined by knowledge of molecular genetics. New molecular physiology is beginning in plant science.

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Introduction

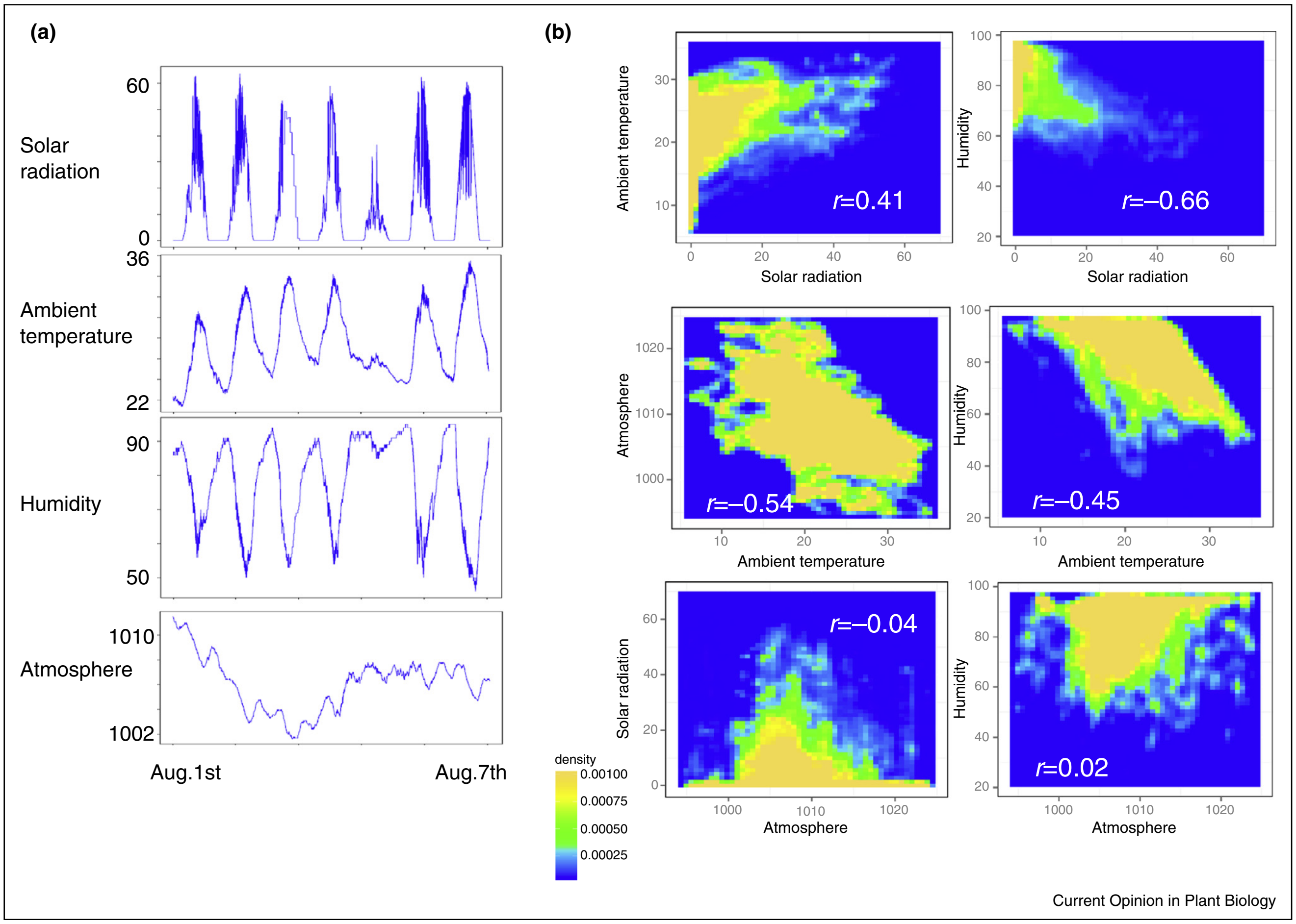
Plants have evolved under natural conditions and propagated in their growth areas according to ecological and agricultural niches. The interactions between daily and seasonal fluctuations of surrounding environments and natural genetic variation in a plant species are major determinants of successful propagation of plants. For example, there are many quantitative trait loci (QTLs) to control flowering time (or heading date) reported in rice [1]. Among such QTLs, the utilization of non-functional alleles of *Ghd7* has resulted in the early flowering trait with no photoperiodic responses and has contributed to the spread of rice cultivation into northern parts at higher latitudes beyond the temperate climate area [2]. It is noteworthy that summer climates in northern areas delimit the boundary of appropriate dates of flowering time for local rice cultivars. Thus, viewing plants *in natura* is essential to elucidate the nature of plant life.

However, many plant molecular biologists often hesitate to examine plants under natural conditions because the daily and seasonal fluctuations of ambient environments often result in low reproducibility of experimental results compared with artificially well-controlled conditions. Recently, our group demonstrated that statistical modeling, combining field transcriptome data and corresponding environmental data, provides a powerful method to overcome the problem of explaining dynamics of each gene and extracting valuable biological information from transcriptome data of field-grown samples [3••]. Here, I review some related analyses using statistical or mathematical models and introduce some perspectives on physiological analysis of plants using such modeling in the future.

The importance of research under natural environments

Researchers usually try to keep experimental conditions constant for reproducible scientific results and prefer to perform experiments under artificially controlled conditions, although natural ambient environments of plants can rapidly fluctuate in a complex manner. Here, each environmental factor under natural conditions can be considered to be an almost independent stimulus of biological events (Figure 1) although there may be some causal relationships among environmental factors (Figure 1a). For example, strong sunlight (solar radiation) may locally increase ambient temperature and humidity, which can lead to cloudy weather and result in shade. Accordingly, environmental factors are not always independent and can be affected by each other as seen in Figure 1a. Various local factors such as geography, however, affect environmental factors. Thus, compared with clear daily correlation among them, the global correlation between environments during long terms (or, several seasons) becomes weak (Figure 1b) although some time-lag effects between one factor and another may increase such correlation. It is of note that some unexpected correlations between such external environment factors and biological stimuli can result in novel production of genetic regulatory networks during evolution. It has been reported that *Escherichia coli* can use high temperature as a sign of low oxygen concentration, because it evolved according to a negative correlation between

Figure 1



Correlation among environmental factors. **(a)** An example of temporal changes of each environmental factor for a week during the crop season. Data was used from Aug. 1st to Aug. 7th in 2008 at Tsukuba (Japan). Units are kJ/min/m^2 for radiation, °C for ambient temperature, % for humidity, hPa for atmosphere. **(b)** Correlation among environmental factors. Scatter plots based on 2-demenstional probability density. Data was used from Jun. 25th to Oct. 31th in 2008 at Tsukuba (Japan). Pearson's co-relation coefficient (*r*) was simply calculated without any time-lags. Note that some density saturation occurred at 100% for humidity and 0 kJ/min/m^2 for solar radiation.

temperature and oxygen resulting from its migration between mammal intestines and the outside world [4•]. Thus, viewing under natural conditions is required for a comprehensive understanding of biological materials.

Another example that led us to consider the importance of scientific study under natural environments is a trend in the study of plant circadian clocks. In many studies, researchers in this field tried to measure free-running periods of their target events (or gene expressions) under constant light or dark conditions because of scientific interest in self-oscillation mechanisms [5]. However, it is well known that genes configuring the plant circadian clocks often exhibit rhythmic expression, but show severe decreases in expression within a few days of such constant conditions [6,7]. This result may reflect the fact that the plant circadian clock has evolved under diurnal conditions with daily fluctuations. Since it is unrealistic to artificially construct experimental conditions mimicking natural environments, we must consider how to utilize the natural environments for scientific research [8–11].

Dealing with plant perception of environmental factors under field conditions

Within the last two decades, many genes have been genetically identified among various plant species. Although we have learned much concerning molecular mechanisms of biological phenomena related to plants, we still do not generally know how plants perceive the natural environmental changes that modulate gene expression. The major reason for this lack of knowledge is because most plant molecular biologists performed biological experiments with binary experimental conditions of their interest – the two conditions being with and without the stimuli in laboratory controlled environments. This might