332(F433)

DIFFERENTIAL RESPONSE OF THE H^+-ATPase ACTIVITY AND PM SURFACE POTENTIALS IN ES8 AND ET8 ROOTS OF WHEAT AFFECTED BY ALUMINUM

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Here we report the H^+-ATPase activity and surface potentials (zeta potentials) of plasma membrane (PM) vesicles isolated from tip (1cm) and tip-less roots in Al-sensitive (ES8) and Al-tolerant (ET8) of wheat by Al. Al (2.6 μM) inhibited the H^+-ATPase activity of PM vesicles of ES8 prepared from only tip roots after 4h treatment. Congruent with H^+-ATPase activity, the zeta potential depolarized only in the PM vesicles isolated from Al-treated tip roots of ES8 and different resting potentials were observed between ES8 and ET8. Interestingly, H^+-ATPase activity increased and zeta potentials hyperpolarized slightly after Al treatment in only tip-less roots of ES8 and in both root portions of ET8. H^+-transport rate of inside-out PM vesicles was monitored by acridine orange and a similar result of activity as H^+-ATPase was obtained. The H^+-ATPase activity of tip root vesicles of ES8 was sensitive to Al (0 to 10 μM) in vitro but tip-less root vesicles sustained the activity. However, H^+-ATPase activity of ET8 PM vesicles of tip root increased, though tip-less root sustained the activity. The zeta potential measured under in vitro Al treatment showed a similar result. Immunolocalization of H^+-ATPase revealed a dcreases in the intensity of apical cells as well as matured cells in ES8 but not in ET8 after 4h Al treatment in vivo.

333(F434)

ROLE OF ROOT HAIRS AND LATERAL ROOTS IN SILICON UPTAKE BY RICE PLANTS

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Rice (*Oryza sativa* L.) is known as a Si accumulator plant. However, the mechanism responsible for the effective uptake of Si by the roots of rice is not understood. We investigated the role of root hairs and lateral roots in Si uptake using rice mutants which are defective in formation of root hairs (RH2) and lateral roots (RM109). Short-term (up to 12h) uptake experiments showed that there was no significant difference in Si uptake between the RH2 mutant and wild type (WT) rice (cv. Ochikara) from either low (0.15 mM) or high (1.5 mM) Si solution. However, the Si uptake of RM109 was much lower than that of WT. The Si uptake as well as the shoot Si concentration of WT was more than double that for RM109, but similar to RH2, when plants were grown for 1 month either in a nutrient solution containing 1.5 mM Si or in soil amended with sodium silicate. The number of silica bodies of third leaf of RM109 was only 1/3 of that of WT and RH2. Using a compartmentation technique, Si uptake for different zones of the roots was compared. Si uptake at the root tip (0-1 cm, without lateral roots or root hairs) was similar between WT and the two mutant lines. However, the Si uptake by root sections of RM109 behind 1 cm was significantly lower than WT, while no differences were observed between WT and RH2. Together, these results clearly indicate that lateral roots but not root hairs contribute to Si uptake by rice. Analysis of F2 plants between RM109 and WT showed that Si uptake effectiveness and lateral root formation are inherited together, and that formation of lateral roots and subsequent Si uptake is controlled by a single dominant gene.

334(F435)

The structure of a regulatory gene *CCM1* and screening of its target genes by using *Chlamydomonas* cDNA macroarray.

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Chlamydomonas reinhardtii induces a set of genes for carbon concentrating mechanism (CCM) to acclimate to CO_2-limiting conditions. It is not known, however, how CO_2 signals are sensed and transduced. We have isolated a *CCM1* gene, which complements pleiotropic deficiency of low-CO_2 characteristics in high-CO_2 requiring mutant C16 (2000 annual meeting). *CCM1* transcript and protein were expressed constitutively, suggesting that CCM1 is posttranslationally modified to transduce CO_2-signal. Amino acid sequence deduced from cDNA contains a region which has significant similarity to Zn-finger domain, suggesting that this region should play an important role for its function.

It is indicated that *CCM1* is essential to regulate a set of genes for CCM. So we screened its target genes by using cDNA macroarray spotted with 960 genes. Comparison of gene expression profile of C16 with that of wild-type revealed that 16 genes showed two times higher intensities of wild-type than that of C16 defective in *CCM1*. Of these genes, low-CO_2 inducible genes reported previously such as *CAH1* and *Mca*, encoding carbonic anhydrase were contained. Furthermore, a putative ABC-type transporter was also regulated by *CCM1*. It is possible that this protein transports CO_2 or HCO_3^-. Moreover there are several novel CO_2-responsible genes, indicating that this cDNA macroarray is useful for screening.

335(F436)

REPRESSION OF LOW-CO_2 INDUCIBLE GENES BY ACETATE IN *CHLAMYDOMONAS REINHARDTII*

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Acetate represses the expression of low-CO_2 inducible genes in *Chlamydomonas reinhardtii*. Two possible triggers of the acetate-dependent repression of low-CO_2 inducible genes have been proposed; (i) elevation of intracellular CO_2 concentration caused by increase in respiration and (ii) down-regulation of PSII activity. In this study, we used a respiratory deficient mutant *dum-1* to elucidate the repression mechanism. The *dum-1* did not show the acetate-dependent repression of low-CO_2 inducible genes. In the mutant, respiratory rate was not increased by addition of acetate while PSII activity was down-regulated as observed in wild type strain. These results indicate that not the down-regulation of PSII, but stimulation of respiration is a main reason for the acetate-dependent repression of low-CO_2 inducible genes.