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اسم الباحث:

تاريخ اعتماد تسجيل البحث: 2012/11/21

نوع البحث: أكاديمي

عنوان البحث:

التحليل الكمي لمواقع الصفات الوراثية التي تتحكم في نقل نواتج البناء الضوئي عبر اللحاء في نبات أذن الفار

طريقة البحث:

In order to identify genetic loci involved in the regulation of assimilate transport in plants, QTL analysis using *Arabidopsis thaliana* recombinant inbred lines derived from the cross between Landsberg erecta (Ler) and Shakhara (Sha) was conducted. Phloem exudates of 20 or 35 day old plants were collected with the EDTA-exudation method. The main component of carbohydrates in phloem exudates was sucrose, whereas glucose and fructose were also detected. Ten and nine QTLs in total for sucrose and glucose export from leaves were found, respectively. Some of the detected QTLs were found to be age-dependent while others were not. Some of these QTLs co-locate with previously detected QTLs affecting sugar content in different plant organs or with growth-related traits in the same population. Near isogenic lines, carrying short Sha introgressions in Ler background have been used to confirm some of the detected QTLs. The possible roles of these QTLs for carbohydrate transport in plants and for sugar accumulation were discussed, and also the suggested candidate genes.



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د ارسلة العلاقة بين نمو النبات و محتوى الكربوهيدارت و وقت التزهير في عشيرة و ا رثية إريكتا كوندا ار (لنبات أذن الفأر ×) لانداسبر

طريقة البحث:

Arabidopsis thaliana natural variation was used to study plant performance viewed as the accumulation of photoassimilates, their allocation and storage, in relation to other growth-related features and flowering-related traits. Quantitative trait locus (QTL) analysis using recombinant inbred lines derived from the cross between Landsberg erecta (originating from Poland) and Kondara (originating from Tajikistan) grown on hydroponics, revealed QTLs for the different aspects of plant growth-related traits, sugar and starch contents and flowering-related traits. Co-locations of QTLs for these different aspects were detected at different regions, mainly at the ER locus; the top of chromosomes 3, 4 and 5; and the bottom of chromosome 5. Increased plant growth was associated with early flowering and leaf transitory starch, and correlated negatively with the levels of soluble sugar at early phases of development. From the significant correlations and the co-locations of the QTLs for these aspects, we conclude that there is a complex relationship between plant growth-related traits, carbohydrate content and flowering-related traits.



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عنوان البحث:

التباين الطبيعي لكمون البذرة في نبات أذن الفأر ينظم من خلال مسارات وراثية تاركمية وجزينية

طريقة البحث:

Timing of germination is presumably under strong natural selection as it determines the environmental conditions in which a plant germinates and initiates its postembryonic life cycle. To investigate how seed dormancy is controlled, quantitative trait loci (QTL) analyses has been performed in six *Arabidopsis thaliana* recombinant inbred line populations by analyzing them simultaneously using a mixed model QTL approach. The recombinant inbred line populations were derived from crosses between the reference accession *Landsberg erecta* (Ler) and accessions from different world regions. In total, 11 delay of germination (DOG) QTL have been identified, and nine of them have been confirmed by near isogenic lines (NILs). The absence of strong epistatic interactions between the different DOG loci suggests that they affect dormancy mainly by distinct genetic pathways. This was confirmed by analyzing the transcriptome of freshly harvested dry seeds of five different DOG NILs. All five DOG NILs showed discernible and different expression patterns compared with the expression of their genetic background Ler. The genes identified in the different DOG NILs represent largely different gene ontology profiles. It is proposed that natural variation for seed dormancy in *Arabidopsis* is mainly controlled by different additive genetic and molecular pathways rather than epistatic interactions, indicating the involvement of several independent pathways.



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عنوان البحث:

التأثير القوي لوسط النمو و أجزء النبات المختلفة علي تدييي الموائل الجينية لمرليي الفيتيات و العناصر المختلفة ف ثلاثة عشائر لنبات أ ا ربيوبسيس ثاليانا (أذن الفار).

طريقة البحث:

The regulation of mineral accumulation in plants is genetically complex, with several genetic loci involved in the control of one mineral and loci affecting the accumulation of different minerals. To investigate the role of growth medium and organ type on the genetics of mineral accumulation, two existing (Ler x Kond, Ler x An-1) and one new (Ler x Eri-1) *Arabidopsis thaliana* Recombinant Inbred Line populations were raised on soil and hydroponics as substrates. Seeds, roots, and/or rosettes were sampled for the determination of their Ca, Fe, K, Mg, Mn, P or Zn concentrations. For seeds only, the concentration of phytate (IP6), a strong chelator of seed minerals, was determined. Correlations between minerals/IP6, populations, growth conditions, and organs were determined and mineral/IP6 concentration data were used to identify quantitative trait loci (QTLs) for these traits. A striking difference was found between QTLs identified for soil-grown versus hydroponics-grown populations and between QTLs identified for different plant organs. Three common QTLs were identified for several populations, growth conditions, and organs, one of which corresponded to the ERECTA locus, variation of which has a strong effect on plant morphology