Genetic loci controlling intraspecific variation of stomatal response to CO2 in *Arabidopsis thaliana*

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Stomata regulate exchange of water and carbon between plants and atmosphere. Guard cells which form stoma sense and respond to CO_2; however, the mechanisms and the protein that binds to CO_2 are still unknown. Such a response is particularly important due to constantly rising atmospheric CO_2. This study aimed to find the quantitative trait loci (QTL) related to stomatal CO_2 responsiveness in *Arabidopsis thaliana* after finding a right candidate pair for QTL mapping. Seeds of 10 different ecotypes were sown and then grown in a controlled growth chamber at 400 µmol mol^{-1} of CO_2 concentration. Then *in situ* leaf stomatal conductance (g_s) was measured at 200, 400 and 800 µmol mol^{-1} of CO_2 concentrations with gas exchange instrument for one mature rosette leaf of each five-week-old plant. The g_s value that changed less than 2% over five minutes was recorded as the steady-state for each level of CO_2. Leaf mass per unit area (LMA), stomatal density, stomatal length and maximum stomatal conductance of CO_2 (g_{smax}) were also estimated for each plant. We finally found that stomatal apertures decline and increase at CO_2 levels above and below the growth concentration of 400 µmol mol^{-1}, respectively. Also ANOVA single factor revealed that some clones were different in g_s at 400 µmol mol^{-1} and in relative response to increased CO_2 level; they also differed in stomatal density and length and g_{smax}. The finding was confirmed by a second experimental set. Thus, a few selected clones were selected as the candidate pair for QTL analysis. Experimental population for QTL mapping was 42 samples of F2 generation from a cross between these clones grown in the same condition as before. g_s was measured for

five-week-old plants at 400 and 800 µmol mol^{-1} of CO_2 concentration. However, genetic analysis was only performed for 12 samples consisting six samples that showed the highest and six samples that showed the lowest g_s due to time constraints, using 20 simple sequence length polymorphism markers. The locus of the trait stomatal CO_2 response could not be detected in this study although initial comparison of phenotypes and genotypes by QTLNetwork-2.0 indicated that the QTL is positioned on chromosome IV. However, plants with weak responses showed genotype of strong responses and vice versa, opposite to what expected. Department of Plant and Environmental sciences, University of Gothenburg

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