P5 Stomatal response of *Camellia sinensis* (L.) O. Kuntze to elevated carbon dioxide

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Camellia sinensis leaves are used to produce tea. Limited research has been conducted on the stomatal response of *C. sinensis* to elevated CO₂. This study determined the stomatal and related physiological responses of C. sinensis to elevated CO₂. Plants were grown under elevated (800ppm) and ambient (400ppm) CO2 concentrations in controlled environment chambers for nine months. Stomatal density and stomatal index did not respond to elevated CO₂ and fieldbased studies confirmed the relative insensitivity of C. sinensis stomatal frequency to environmental change. However, stomatal conductance (g.) decreased by 25%, suggesting an aperture level response. Guard cell length (GCL) showed a significant 3% decrease, implying that stomatal dimensions were more responsive to CO_2 than stomatal numbers in *C. sinensis*. There was no significant relationship between stomatal density and GCL. Net photosynthetic rate increased by 57% showing that CO₂ supply was not a limiting factor despite the lower g_s. A 15% reduction in leaf N at elevated CO₂ indicated photosynthetic down-regulation. Decreased gs led to an increase in instantaneous water use efficiency (WUE). Palisade and spongy parenchyma thickness increased thereby facilitating higher photosynthesis. Thus, C. sinensis responds to predicted future increases in CO2 by adaptations in stomatal size and leaf anatomy leading to increased photosynthesis and WUE.

P6 Deep evolutionary origins of stomatal development

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Stomata in angiosperms are formed by asymmetric and symmetric divisions controlled by a suite of positive and negative regulators of cell development. Stoma-like complexes are found on ancient plant cuticle fossils and on the sporophytes of extant mosses and hornworts. It is not known, however, whether these are orthologous structures to tracheophyte stomata. Recent evidence suggests angiosperm-like molecular signalling and physiological responses in the stomata of the model moss *Physcomitrella*. To determine whether stomata are monophyletic, we investigated the role of several moss gene homologues to those involved in *Arabidopsis* stomatal development. Expression of moss genes homologous to SPEECHLESS, MUTE, and FAMA complement mutant Arabidopsis plants defective in those genes (McAlister & Bergmann, 2011). Here we investigate whether knocking out these genes in the moss will affect stomatal development. Furthermore, we explore the roles of moss genes similar to epidermal patterning factors 1 (EPF1 & 2) and the TOO MANY MOUTHS (TMM) receptor-like protein. Our data suggest that the mechanism of stomatal development has been broadly conserved across land plant evolution.