



Nuclear DNA content affects the productivity of conifer forests by altering hydraulic architecture

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Predictions of future global climate rely on feedbacks between terrestrial vegetation and the global carbon cycle, but the exact mechanisms underlying this relationship are still being discussed. One of the key knowledge gaps lies on the scaling of cellular processes to the ecosystem level. Here we examine whether an under-explored plant trait, inter-specific variation in the bulk amount of DNA in unreplicated somatic cells (2C DNA content), can explain inter-specific variation in the maximum productivity of conifer forests. We expected 2C DNA content to be negatively related to conifer productivity because: 1) it is positively correlated with cell volume (which, in turn, potentially affects structural features such as leaf mass area, a strong predictor of photosynthetic capacity); 2) it is positively correlated with stomatal size (with larger stomata leading to lower overall stomatal conductance and, by extension, lower CO₂ uptake); and 3) larger genome sizes may reduce P availability in RNA (which has been hypothesized to slow growth).

We present the results of regression and independent contrasts in different monospecific forests encompassing a 52° latitudinal gradient, each being dominated by 1 of 35 different conifer species. Contrary to expectations, we observed a positive correlation between genome size and maximum Gross Primary Productivity ($R^2 = 0.47$) and also between genome size maximum tree height ($R^2 = 0.27$). This correlation was apparently driven by the effects of genome size on stem hydraulics, since 2C DNA was positively correlated with wood density ($R^2 = 0.40$) and also with resistance to cavitation (P50, $R^2 = 0.28$). That is, increased genome sizes have a positive effect on the productivity of conifer forests by affecting the vascular tissues to increase their capacity for water transport. Our results shed a new light on the evolution of the vascular system of conifer forests and how they affect ecosystem productivity, and indicate the potential to further explore the trait of genome size for understanding global patterns of forest productivity.