

Machine learning may enable bioengineering of the most abundant enzyme on the planet

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A Newcastle University study has for the first time shown that machine

learning can predict the biological properties of the most abundant enzyme on Earth—Rubisco.

Rubisco (Ribulose-1,5-bisphosphate carboxylase/oxygenase) is responsible for providing carbon for almost all life on Earth. Rubisco functions by converting atmospheric CO₂ from the Earth's atmosphere to organic carbon matter, which is essential to sustain most life on Earth.

For some time now, [natural variation](#) has been observed among Rubisco proteins of [land plants](#) and modeling studies have shown that transplanting Rubisco proteins with certain functional properties can increase the amount of atmospheric CO₂ [crop plants](#) can uptake and store.

Study lead author, Wasim Iqbal, a Ph.D. researcher at Newcastle University's School of Natural and Environmental Sciences, part of Dr. Maxim Kapralov's group, developed a machine learning tool which can predict the performance properties of numerous land plant Rubisco proteins with surprisingly good accuracy. The hope is that this tool will enable the hunt for a 'supercharged' Rubisco protein that can be bioengineered into major crops such as wheat.

Published in the *Journal Of Experimental Botany*, the study presents a useful tool for screening and predicting plant Rubisco kinetics for engineering efforts as well as for fundamental studies on Rubisco evolution and adaptation. Screening the natural diversity of Rubisco kinetics is the main strategy used to find better Rubiscos for crop engineering efforts.

Wasim says that their "study will have huge implications for [climate models](#) and bioengineering crops."

"This study provides plant biologists with a pre-screening tool for

highlighting Rubisco species exhibiting better kinetics for crop engineering efforts."

"The machine learning tool can be used to improve the accuracy of global photosynthesis estimates. The Rubisco performance properties our model predicts are compatible with Earth system models (ESM) used by climate scientists. Currently, ESMs use a single set of Rubisco properties from the same species (or sometimes a handful) for estimating photosynthesis at the ecosystem scale. Our [machine learning](#) tool could provide predictions for most land plants improving the accuracy of ESMs."

Next steps of this work include isolating the best Rubisco proteins identified from predictions in the lab and attempting to bioengineer a [plant species](#) with a foreign Rubisco protein.

More information: Wasim A Iqbal et al, Predicting plant Rubisco kinetics from RbcL sequence data using machine learning, *Journal of Experimental Botany* (2022). [DOI: 10.1093/jxb/erac368](https://doi.org/10.1093/jxb/erac368)

Provided by Newcastle University

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