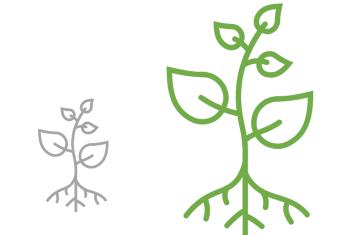
The perils and promise of single-gene solutions to crop yield: extraordinary claims require extraordinary evidence

Merritt Khaipho-Burch¹, Mark Cooper^{2,3}, José Crossa⁴, Natalia de Leon⁵, James Holland⁶, Ramsey Lewis⁶, Susan McCouch¹, Seth Murray⁷, Ismail Rabbi⁸, Pamela Ronald⁹, Jeffrey Ross-Ibarra¹⁰, Detlef Weigel¹¹, Jianbing Yan¹², Edward S. Buckler^{1,13}

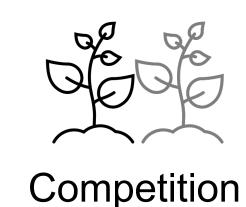
Peer review is failing within high-impact journals that publish 8-68% increases in intrinsic plant yield. These publications are often flawed in how they measure field performance by:

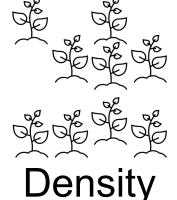
Not utilizing elite germplasm

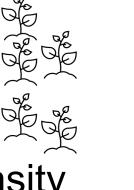


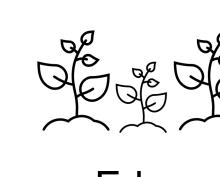
Backcross changes into ex-PVP lines or similar commercially competitive germplasm.

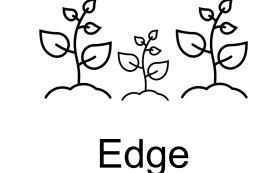
Not testing G x E x M x T effects











Irrigation



Fertilizer



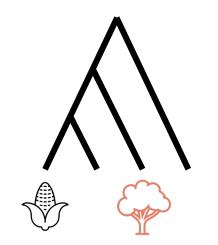
transplanting

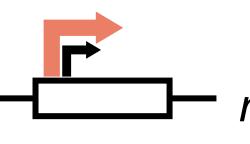
Not following standard management

Measuring single plant vs plot yield



Forgetting evolution





Investigate 'missed' or novel genetic variation.

Not developing collaborations







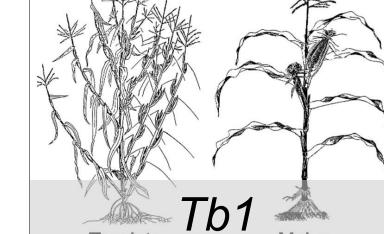
Yield data from single

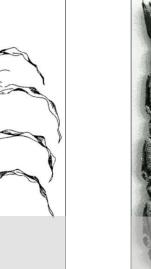
plants is not scalable to

plot-wide effects.

Some single genes have worked well in domestication and to stabilize yield; however, robust yield increases are delivered using genomic selection. Our field needs to communicate yield testing standards better.







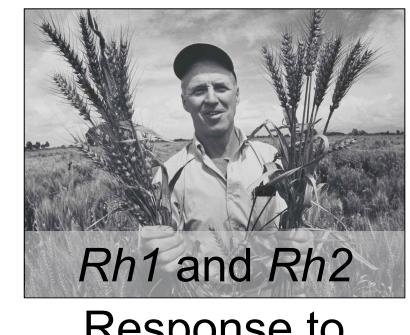
Limited env. adaptation

Improving harvestability

Processing & consumption



Global warming induced pests



Response to synthetic fertilizers



Figure adapted from Jesse Poland

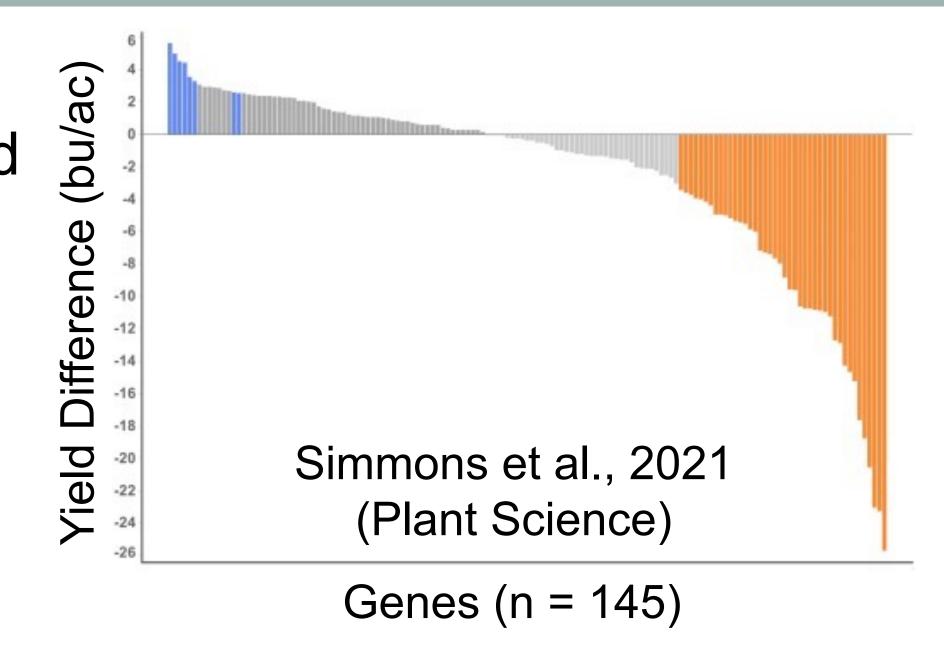
Molecular biologists don't seem to know this one simple trick to increase intrinsic plant yield.

(It's genomic selection)

Most of yield "breakthroughs" have never translated into significant gains once tested at scale.

1600+ gene constructs were field tested at scale, only 8 significantly increased yield and had small effects (1-4%).

Most gene constructs significantly decrease or have no effect on yield.



Take a flyer!

From Molecular Gene Discovery to Field Performanc

Measure plot yield
Yield data from single plants is not scalable to plot wide effects.

We suggest approaches to communicate to molecular researchers and reviewers when evaluating the impact of single genes on crop yield:



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