

Overexpression of a chaperonin protein decreases biomass recalcitrance in poplar

Background

- Prefoldins, a type of protein chaperones, are typically involved in protein folding and trafficking.

Approach

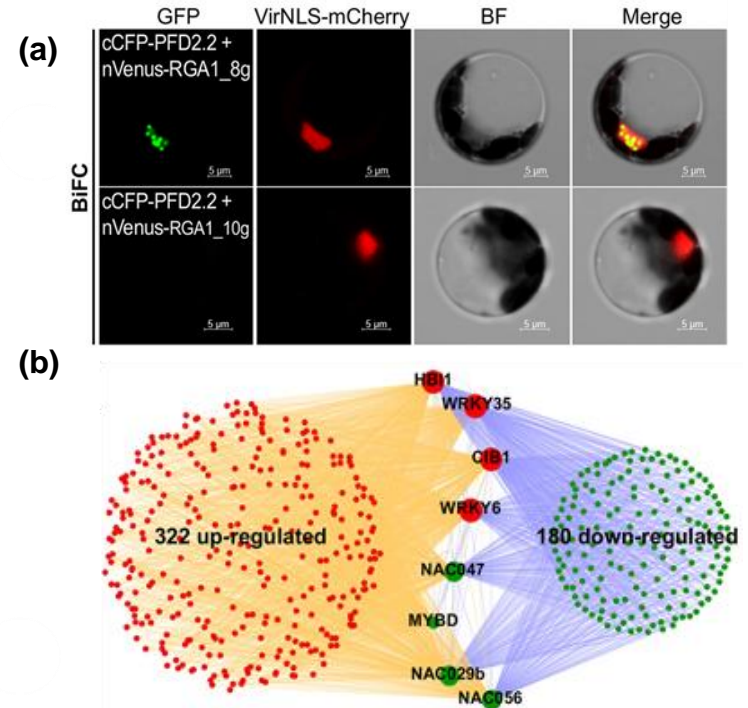
- A multi-omics strategy was used to uncover a previously unknown role of a Prefoldin subunit in regulating cell wall chemical composition in *Populus*.
- Identify genetic factors regulating cell wall chemistry to facilitate genetic engineering for improved feedstocks.

Highlights

- The lignin syringyl/guaiacyl ratio was increased, but cellulose content and crystallinity index were unchanged in transgenic plants overexpressing a Prefoldin subunit gene PdPFD2.2.
- Biomass production and sugar release were simultaneously improved in the *Populus* transgenic plants overexpressing PdPFD2.2.
- Transcriptomic and metabolomic analyses revealed that secondary metabolic pathways and transcription factors were affected by overexpressing PdPFD2.2.
- PdPFD2.2 acts by physically interacting with the DELLA protein RGA1_8g.

Significance

- This study provides a promising target for genetic engineering to improve multiple feedstock characteristics to enhance biofuel conversion and reduce the cost of lignocellulosic biofuel production in multiple species.
- It also illustrates new phenotypes and functions from a widespread eukaryotic protein, prefoldin.



Transcriptomic and metabolomic analyses revealed that secondary metabolic pathways were affected by overexpressing PdPFD2.2. (a) PdPFD2.2 (green) can physically interact with DELLA protein RGA1_8g, and its subcellular localization in the nucleus (red) is affected by the interaction – shown here in the poplar protoplast. (b) Eight hub transcription factors were identified based on the transcriptomic analysis between control and *Populus* transgenic plants overexpressing PdPFD2.2.