Additional question from the October 15, 2020 webinar: "PanOat: Why Does The World Need 30 Oat Genomes?"

Q: What level of functional understanding of oat genes we will get by using pangenomics?

A: This is a good question. In the actual "PanOat plan" we will get an approximate atlas of gene expression (what genes are expressed, in what tissue, at what stage, and in what lines) but only at a high level and with a certain degree of statistical noise. But compared to what is available now, that will be like having a whole bible vs. just 10 commandments. It will provide the groundwork for people who know a lot about a particular pathway to develop and test hypotheses. A lot of this depends on progress that is being made in model species. As an example, if you know of candidate genes or pathways that affect tissue culture success in model species like Arabidopsis or Brachypodium, you would be able to test whether some of these vary between the PanOat line 'Park' vs. other lines that do not culture well. –Nick Tinker.