



## Regarding the future of the 6K Oat Illumina Array

As some of you are already aware, Illumina has run out of the current 6K beadpool.

Obviously, this abrupt loss of an important genotyping platform is not ideal and messes with many of our plans moving forward. Our sales representative, Adam Hauge had no idea that the beadpool reserve was so close to gone. He assures me that he will make sure to alert us of low levels in the future. (He is checking the levels of the other Ag arrays)

So now the question is what do we want to do? We have a couple options:

- 1) Resynthesize the existing beadpool. To maintain the same price per sample (\$16.50), Illumina would be looking for ~20,000 sample commitment. We can adjust the design.
- 2) Synthesize a new higher density chip. Cost would be dependent on # SNPs and # of samples.
- 3) Subset the 6K (and/or GBS) SNPs that work well and add them to a multi -species XT array focused on genomic section. I have just started working on this and I am targeting 2-3K SNPs in each of the small grain crops, plus any other crop that wants to join. The main goal is get enough capacity to obtain \$10 per sample. Illumina needs 100,000 samples over 2 years to obtain this, so it will take some time to build consensus.
- 4) Targeted sequencing: I just submitted a design for 2,500 SNPs to a platform called [Allegro](#), which is a targeted amplicon/capture sequencing approach. Cost is ~ \$15/sample for this (including sequencing). There are several other technologies out there as well, but they have not worked particularly well in polyploids. Hopefully this one is better.
- 5) Non-targeted sequencing: GBS is still a viable option for allele discovery, and the [Rapture](#) addition that our friends at AAFC have developed works well. Unfortunately, I can't officially support this at the Genotyping Lab.
- 6) Imputation Sequencing: We are close to the point where we can think about this with all of the genomes coming onboard. This would entail deep sequencing founder lines (10X would cost about ~\$900), skim sequencing the rest and imputing everything. The cheapest WGS library kit I have found is [Riptide](#) for ~\$10 per sample, plus ~\$5-\$10 for sequencing.

I would like everyone's feedback on what they would like to do. In a way, all of the above options will be pursued, but I would like to know your priority list and capacity moving forward.



Please see this link to a quick survey to relay your responses. Even those of you who don't think about the genotyping all day long, I would still appreciate your response to the first 4 questions.

[Oat Community Genotyping Survey](#)

The deadline for replies is March 19, 2021. A meeting will then be set up to discuss the results.

Thank you for your participation,

-Jason.

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