

A discussion document to identify research priorities for quinoa

Target traits – what needs to be delivered (along with a few research questions)

A crop whose cost needs to fall significantly, to be grown on marginal lands to alleviate malnutrition for people in poor regions

Larger grains

- Seed longevity, high germination
- Pre-harvest sprouting resistance

Early vigour

(Herbicide resistance

- For a range of herbicides, stacked – e.g. imidazole (Pursuit, Beyond)

Disease resistance

- **Downy mildew**, leaf curl virus

Day length insensitivity – manipulate short-day trait

An *ideotype* more akin to conventional cereals, for high density, low lodging, high input, mechanised agriculture

- Dwarfing
- Reduced branching, one or a few compact inflorescences
- Optimisation for mechanical harvesting
- Low variability / heterogeneity (residual heterozygosity, transposons?)

Pest resistance

- Aphids, lepidopteran larvae

Yield in target environments – which will select for various types of drought tolerance in water-limited environments

- **Heat tolerance** (reproductive tolerance)
- Root development
- **Cold tolerance**
- Salinity tolerance
- The role of the bladders
- Nutrient use efficiency
 - o To reduce inputs, and/or to increase efficiency of recovery of inputs

Grain quality

- Low saponins
- Colour (white, red, black)

Use of biomass

- Leaves for human/animal consumption
- Storage roots?
- Biofuels

Key platforms – what is needed to deliver

Genotyping database

- Modelled on those already developed for other species
- Re-sequencing and genotyping service

Phenotyping database

Open Breeding API developed at Cornell with support from B & M Gates Foundation. For registering traits.

Social science programs to present “**the whole package**”, extension programs, integration with existing agricultural systems, developing markets

A core global germplasm collection

- genotyped and phenotyped
- diversity and population structure of quinoa defined and covered
- establish a DOI system, in line with that being developed for all plants (DivSeek)

Genome re-sequencing

- SNPs and indels defined

Mapping populations for open use

- Association mapping, based on the core global germplasm collection
- Nested association mapping population
- Bi-parental mapping populations
- Mechanisms to facilitate sharing of data and comparisons of results, meta-analyses etc
- Doubled haploids

Mutant populations

- EMS, neutron

Genomic selection protocols

Collection of wild relatives

- For future injection of natural genetic diversity
- Re-sequence genomes
- Phenotype for basic description of the lines

Hybridisation protocols

- Chemical gametocides, heat-based male sterilisation
- CMS systems
- For generation of commercial F1 hybrid seed

Advanced genetics

- Allohexaploids and other enhanced ploidy lines
- Genetic transformation
 - o Stable transformation
 - o Transient transformation, virus-based systems
 - o Genome editing, Crispr-Cas9

- **28 December 16**