

TERMS OF REFERENCE TO CONTRACT A SERVICE PROVIDER FOR FULL GENOME SEQUENCING OF POTATO TISSUE SAMPLES

1. Main Objective:

- a) Full genome sequencing of diploid and tetraploid potato (*Solanum* sp.) genotypes by Hi-C, PacBio and Illumina short read as specified below. **The approximate haploid genome size of potato is 840Mb.**

	Diploid samples	Tetraploid samples	Total
Hi-C	6	4	10
Pac-Bio (HiFi)	5	4	9
Illumina short reads 50x	1		1

2. Scope of the project

Flash frozen potato tissue samples will be shipped from multiple labs (Canada, USA and Peru). The service provider will perform DNA extraction from the samples, construct libraries, and perform sequencing using the latest technology and release the raw sequencing data without extensive bioinformatics analysis.

3. Technical Specification:

- HMW DNA extraction for PacBio followed by integrity and concentration validation
- Library construction for HiFi reads for PacBio
- 2 PacBio SMRT cells for diploids, 3 for tetraploids
- Tissue sample preparation for Hi-C (Omni-C) Illumina library preparation
- Library construction and quality validation for Hi-C followed by Illumina sequencing
- DNA extraction for Illumina short reads followed by integrity and concentration validation
- Library construction for 50x Illumina paired-end followed by sequencing
- Sequence delivery via FTP transfer

4. Deliverables and dates for delivery:

- a. DNA quality and quantity report
- b. Quality check report of the sequencing libraries
- c. Quality check report of the sequencing runs
- d. Release the raw sequencing data without extensive bioinformatic analysis **within three months** after receiving the physical samples.