



**Préavis d'adjudication de contrat (PAC)
Advanced Contract Award Notice (ACAN)**

SEL: 01B46-16-164

An Advance Contract Award Notice (ACAN) is a notification through the open bidding methodology of the intent to award a directed contract.

An Advance Contract Award Notice (ACAN) allows departments and agencies to post a notice, for no less than fifteen calendar days, indicating to the supplier community that it intends to award a good, service or construction contract to a pre-identified contractor. If no other supplier submits, on or before the closing date, a statement of capabilities that meets the requirements set out in the ACAN, the competitive requirements of the government's contracting policy have been met. Following notification to suppliers not successful in demonstrating that their statements of capabilities meets the requirements set out in the ACAN, the contract may then be awarded using the Treasury Board's electronic bidding authorities.

If other potential suppliers submit Statements of Capabilities during the fifteen calendar day posting period, and meet the requirements set out in the ACAN, the department or agency must proceed to a full tendering process on either the government's electronic tendering service or through traditional means, in order to award the contract.

Applicability of trade agreements and other obligations

Agreement on Internal Trade, World Trade Organization – Agreement on Government Procurement, North American Free Trade Agreement, Canada-Chile Free Trade Agreement, Canada-Columbia Free Trade Agreement, Canada-Honduras Free Trade Agreement, Canada-Korea Free Trade Agreement, Canada-Panama Free Trade Agreement and Canada-Peru Free Trade Agreement.

Objective of the ACAN

The objective of this ACAN is to establish a standing offer that will enable research scientists to issue subsequent call-ups for high throughput sequencing services for their work in soil microbial ecology and genetic improvement of agricultural plants, at any time in a year, for three years. This standing Offer will be necessary in order for research scientists to obtain data within a reasonable timeframe and ensure that ongoing research projects run smoothly.

Statement of Work

We will require the following services: (1) preparation of microorganism DNA amplicons and sequencing of these barcoded amplicons; (2) DNA sample preparation and sequencing for plant genotyping; (3) cDNA library preparation for transcriptome analysis of plant samples; and (4) Sanger sequencing of PCR products.

2016–2017

Preparation of barcoded fungal ITS amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using 544 DNA samples and produced by PCR amplification (sometime in a nested protocol), normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of barcoded bacterial 16S amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using 272 DNA samples and produced by PCR amplification, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.



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Preparation of pSSU-ITS-pLSU (1.5 kb) *Glomeromycota* amplicon libraries for PacBio SMRT sequencing using 368 DNA samples. The amplicons will be barcoded and placed in 41 sequencing pools (runs). These amplicons will be produced by PCR amplification, sometimes in a nested protocol, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of four DNA sample libraries to perform genotyping-by-sequencing using a Illumina HiSeq 4000 PE 150-bp sequencer. Each library will consists of 96 DNA samples (three libraries each containing 96 alfalfa samples and one library containing 96 red clover samples). Our laboratory will provide the DNA samples. Each sample will have to be digested with one or more restriction enzymes according to a protocol that will be established for each library. A specific barcode will be added to each sample before the 96 samples from each library are multiplexed. Each library will be amplified by PCR before being purified to preserve suitably sized DNA fragments. Each library will be quality-controlled and sequenced on a lane of the Illumina HiSeq 4000 PE 150-bp sequencer.

2017–2018

Preparation of barcoded fungal ITS amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using series of 72 and 200 DNA samples and produced by PCR amplification, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of barcoded bacterial 16S amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using 72 DNA samples and produced by PCR amplification (sometimes by nested PCR), normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of pSSU-ITS-pLSU (1.5 kb) *Glomeromycota* amplicon libraries for PacBio SMRT sequencing using 368 DNA samples. The amplicons will be barcoded and placed in 41 sequencing pools (runs). These amplicons will be produced by PCR amplification, sometimes in a nested protocol, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of eight DNA sample libraries to perform genotyping-by-sequencing (GBS) using a Illumina HiSeq 4000 PE 150-bp sequencer, as described for 2016–2017. Each library will consists of 96 DNA samples. Each library will be quality-controlled and will have to be sequenced on a lane of the Illumina HiSeq 4000 PE 150-bp sequencer or equivalent device, depending on the state of advancement of the available technologies.

Preparation of eight libraries, each containing four cDNA samples, for transcriptome analysis of alfalfa samples. Each library will be **quality-controlled**. Each library will be sequenced on a lane of the Illumina HiSeq 4000 PE 150-bp sequencer or equivalent device. The supplier will analyze the sequences obtained according to the established procedures and deliver an analysis report (containing a description of the methods and analysis, statistics, software version, results and link to download each results file individually).

2018–2019

Preparation of barcoded fungal ITS amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using series of 72 and 200 DNA samples and produced by



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PCR amplification, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Preparation of barcoded bacterial 16S amplicons for paired-end sequencing using MiSeq PE300 in two pools (runs). These amplicons will be prepared using 72 DNA samples and produced by PCR amplification, normalized and quality-controlled. The preparation of these amplicons could require primer design and synthesis.

Note that the QRDC laboratories will provide the DNA samples for services (1) through (3), as well as the PCR products for the Sanger sequencing in service (4).

Estimated Value

The total value of the sequencing budget for fiscal years 2016–2017, 2017–2018 and 2018–2019 are \$114,000, \$145,000 and \$80,000 respectively which brings us to a grand total of 339 000.00 plus tax.

Time Frame

The required activities will run from January 2017 to March 31st, 2019.

The sequencing results will normally have to be delivered within two months of the receipt of quality samples.

The contract should be executed in phases corresponding to the need of the researchers. In particular, the work for:

2016-17, which is described under point 5 will be sent to Genome Quebec on 10 January 2016 and should be completed on 29 March 2017 at the latest.

2017-2018, which are described under point 5 will be sent to Genome Quebec in 5-8 call-ups distributed along the year. All works will need to be completed on 29 March 2018 at the latest.

2018-2019, which are described under point 5 will be sent to Genome Quebec in 2-3 call-ups distributed along the year. All works will need to be completed on 29 March 2019 at the latest.

Proposed Supplier

Génome Québec

630 Boulevard René-Lévesque West, Office 2660
Montréal (Québec)
H3B 1S6

SOLE SOURCE JUSTIFICATION

- There is not enough time left before our research funding disappears at the end of the current fiscal year for us to wait for another supplier to develop a protocol for this application. A service request technically could not be drafted instead because it was impossible to know whether a new protocol for the long fungal amplicon sequencing technology by SMRT could be used and, if so, for what applications. We needed to collect our soil and root samples in the field and develop and debug the method with GQ. We received the



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sequencing data from GQ on September 29, 2016. We then had to quickly install new software on our server and adjust the bioinformatics pipeline to accommodate the new data format before we could find these results meaningful on October 21, 2016. It is now impossible to complete a competitive bidding process and perform the work before our non-renewable research budgets disappear on March 31, 2017.

- If we are unable to use GQ as the supplier, the following major losses would occur: cancellation of five three-year research projects with a value of \$402,112; waste of the 2015–2016 and 2016–2017 salaries of research scientists (6), technicians (8), labourers (5) and students (2) at an estimated cost of \$375,000; and breach of two memoranda of understanding with the university.
- GQ has solid expertise and competitive prices.
- Coherence in data among years in projects. We have used the services of GQ for a number of the projects currently under way, and it is necessary to use the same supplier (instruments, products and environment) for the continuation of these projects so that results from different years can be compared. The use of a sole provider of sequencing services ensures that the data files produced will be in a format with which we are familiar and that we can process using software already installed on our computers. The installation of specialized software on Crown networks is not recommended by the IT Centre because it poses a security risk and requires verification, a process that takes several months and is incompatible with the need to quickly verify (at the latest by the end of the fiscal year) whether the service supplier's work is acceptable.

SUPPLIERS' RIGHT TO SUBMIT A STATEMENT OF CAPABILITIES

Suppliers who consider themselves fully qualified and available to provide the services described herein, may submit a statement of capabilities in writing to the contact person identified in this Notice on or before the closing date of this Notice. The statement of capabilities must clearly demonstrate how the supplier meets the stated requirements.

Closing date for the submission of the Statement of Capabilities:

December 19, 2016 at 2:00PM (Eastern Standard Time)

Inquiries and Submission of Statements of Capabilities: requests for information shall be submitted **IN WRITING** to the contracting authority:

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