GrapeReSeq Consortium

Developing genomic tools to advance grapevine breeding programs.

What is the GrapeReSeq Consortium?

GrapeReSeq is a research project of the Transnational Plant Alliance for Novel Technologies consisting of members from France, Spain, Italy, and Germany. Its goal is to develop strategies and comprehensive tools for allele mining in the *Vitaceae* gene pool. Large scale re-sequencing in the *Vitis* genus will support identification of resistance genes, SNP discovery, high-throughput genotyping, and efficient marker-assisted breeding. Information about the project can be found at http://urgi.versailles.inra.fr/Projects/GrapeReSeq.

How many SNPs will be on the GrapeReSeq Vitis grapevine panel?

SNP content for the *Vitis*/grapevine panel is still being finalized. The panel will be designed using between 12,000 and 20,000 attempted bead types and the final SNP number will depend upon how many bead types are used per SNP (some require two, most require only one), and the number of SNPs that pass Illumina quality control for internal redundancy and representation. We expect final content to be between10,000 and 15,000 SNPs.

Which *Vitis*/grapevine lines are considered appropriate for these SNPs?

The SNPs include publicly available SNP data from the Vitis9kSNP set[1] that was validated using Infinium® technology, as well as new content generated from the collaboration. This SNP genotyping tool will be used for mapping and evaluating genetic diversity in the *Vitaceae* gene pool, to support the development of genetic resources and breeding programs that will reduce the use of chemical treatments in viticulture.

How were the SNPs discovered? How will they be selected?

One source of SNP data for this project has been generated from GrapeReSeq whole genome sequence data (performed on the Genome Analyzer IIx) from 46 *Vitis vinifera* [27 from the Associazione Istituto di Genomica Applicata (IGA), 19 from GrapeReSeq], four *V. sylvestris*, three *V. labrusca*, three *V. cinerea*, three *V. berlandieri*, three *V. aestivalis,* and three *Muscadinia rotundifolia* genotypes. SNP selection criteria include minimums in Q score quality, minimum design score threshold based upon the Infinium Assay Design Tool (ADT), and minimum coverage for each alternate allele. Additional content will be included from the Vitis9kSNP content. These data were derived from Hpa III Reduced Representation Libraries with Illumina sequencing using 17 grapevine samples. Final validated content in this available SNP pool includes SNPs segregating in *V. vinifera* (5,488 SNPs), segregating within wild *Vitis* species (208 SNPs), segregating within *Vitis* (1,069 SNPs), fixed within a single wild *Vitis* species (1,192 SNPs), content within candidate genes (735 SNPs), and various additional SNPs (296 SNPs). GrapeReSeq is working with research teams in Europe and at Illumina to finalize SNP content for a genotyping array that will be available to the Vitis/Grapevine breeding and genetics community.

How will the content be validated? How many of the SNPs can I expect to be segregating in my germplasm?

Candidate *Vitis*/grapevine SNPs will be validated and optimized for elite germplasm. Validation work is ongoing and details will be updated as more information becomes available. For the most up-to-date information, check http://urgi.versailles.inra.fr/Projects/GrapeReSeq.

What will I need (reagents, etc) to run the *Vitis*/grapevine genotyping panel?

Participants will receive all reagents necessary to run the chips included in their order at the consortium per sample price. For robust results, Illumina recommends a minimum of 200ng of DNA in a minimum concentration of 50 ng/µl (as measured by a fluorescent method of quantification). Access to an Illumina BeadArray™ Reader, iScan, HiScan®, or HiScanSQ™ system is required for processing the BeadChips. For customers with an instrument automation setup, a 24-sample tip guide is also required. Information on service providers and core facilities can be found at www.illumina.com/services.ilmn or by contacting your Illumina Account Manager.

What is the minimum order I can place? Can I order through Illumina FastTrack Services?

The minimum order (considered a reorder of an existing beadpool) is for 288 samples. A minimum of 1,152 samples is required for a split shipping schedule. Projects done through FastTrack Services require a minimum sample order of 564. FastTrack orders must be in multiples of 47 to allow for a control sample to be included for each 48-sample unit.

What is the consortium price?

Consortium pricing will depend upon the number of samples achieved worldwide by the deadline date determined by the content contributors ANR, GABI, Ministry of Research (Spain) and MiPAAF (Italy). To understand the tiers possible in pricing, please talk to your Illumina Agriculture Sales and Science Specialist or local Account Manager and refer to the iSelect Pomotional 2011 Pricing Calculator. Goals of the Consortium are to meet a minimum of 3,000 samples for 12,000 to 14,000 attempted beadtypes. Customers will be invoiced for the per sample price after the deadline for submission of Purchase Orders. These details will be updated as more information becomes available.

What are the benefits and responsibilities of accessing this pricing?

Members of the consortium will have reorder privileges for one year from the date of manufacture of the beadpool at the consortium price. The minimum sample number for a reorder is 288 samples. All consortium members must reference the GrapeReSeq content in any publications, public presentations, press releases, or public announcements resulting from the use of the consortium SNP content.

Is there a limit to how many samples I can order at the consortium price?

There is no upper limit to the number of samples that can be ordered for initial shipment. Requests for reorders (during the life of the bead pool) must be for at least 1,152 samples. If there is unanticipated demand for the bead pool, orders will be filled on a first-come, first-served basis until the bead pool is exhausted.

Can I reorder additional BeadChips?

The bead pool is manufactured in liquid phase and is available for one year from bead pool manufacture. When orders are filled, the liquid bead pool is stabilized onto BeadChips and processed through quality control, and those BeadChips are under warranty for a minimum of six months.This means that the effective time period during which experiments can be run is 18 months. Reorders can be submitted during the life of the bead pool.

I am in competition with other interested parties and do not want my interest in running samples widely publicized. Is it a consortia requirement that other members know about my experiments?

The intent of the consortium is to make all content publicly and openly available. Any information about your orders will be kept confidential. You can decide whether you are comfortable revealing the goals of your experiment to other GrapeReSeq participants. Illumina will only divulge the total samples numbers pooled by all participants that will secure the consortium price.

Will GrapeReSeq or Illumina be providing a cluster file for the genotyping positions?

The ability to provide a cluster file is still being evaluated. It is recommended that a minimum of 96 samples be used for clustering in any given project. If a cluster file is provided by the GrapeReSeq Consortium, Illumina will notify participants of its availability.

What are the benefits of participating in the GrapeReSeq consortium?

Illumina consortia spread the cost of creating genotyping tools over more samples, resulting in a lower per sample price than might be achieved by a single contributor. Email consortiamanager@illumina.com and we will have a representative contact you to answer any additional questions and help you place your order.

References

1. Myles s, Chia JM, Hurwitz B, Simon C, Zhong GY, et al. (2010) Rapid Genomic Characterization of the Genus *Vitis*, PLoS One 5:e8219.

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