



TALLER

SELECCIÓN GENÓMICA: NUEVAS ESTRATEGIAS EN EL ESTUDIO Y APLICACIÓN DE GENÓMICA EN VIDES



CENTRO REGIONAL INIA LA PLATINA

El taller será dictado por la **Dra. Paola Barba** – Cornell, Geneva Grapevine Breeding and Genetics Program – USA, y el **Dr. Timothée Flutre** – UMR AGAP, INRA Montpellier – France

Lugar: Salón Auditorio, INIA La Platina

Fecha y hora: Martes 25 y Miércoles 26 de marzo 2014 de 9 am a 17 hrs.

Invitación a Taller:

SELECCIÓN GENÓMICA: NUEVAS ESTRATEGIAS EN EL ESTUDIO Y APLICACIÓN DE GENÓMICA EN VIDES

Dr. Julio Kalazich Barassi, Director Nacional de INIA, y Juan Carolus Brown Bauzá, Presidente del Consorcio **BIOFRUTALES**, invitan a participar del taller “Selección Genómica: Nuevas estrategias en el estudio y aplicación de genómica en vides”, los días martes 25 y miércoles 26 de marzo del 2014 en INIA La Platina.

El taller será dictado por los destacados investigadores internacionales:

- **Dra. Paola Barba – Cornell**, Geneva Grapevine Breeding and Genetics Program - USA.
- **Dr. Timothée Flutre – UMR AGAP, INRA Montpellier – France**

Estas actividades se enmarcan dentro de los proyectos “Desarrollo y aplicación de herramientas de genómica e ingeniería genética para potenciar el fitomejoramiento de vides de mesa” (Código FONDEF-G09-1007) y “Desarrollo y aplicación de técnicas de ingeniería genética para potenciar el fitomejoramiento del cerezo” (Código FONDEF-G09-1008), que cuentan con el apoyo del programa FONDEF de CONICYT, y el proyecto “Programa de Mejoramiento Genético para el desarrollo de nuevas variedades de uvas de mesa en función del mercado nacional e internacional” (Código 09PMG-7229) que es apoyado por el Comité Innova Chile de CORFO. Estos proyectos son ejecutados por INIA y co-financiados por el Consorcio Biofrutales.

Se expondrá la experiencia científica y práctica de dos de los más importantes grupos mundiales de investigación de genómica aplicada en vides.

El Taller tendrá duración de dos días y las invitaciones son personalizadas.

Agradeceremos confirmar su participación a Viviana Sandoval al teléfono 02 – 25779102 o al correo vsandova@inia.cl

Lugar: Salón Auditorio, Centro Regional INIA La Platina

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Programa del Taller:

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Martes 25 de Marzo

BLOQUE 1 Grape Breeding Work in INRA and CORNELL

9:00 - 10:30 Presentation of the "Diversity, Adaptation and Breeding of Grapevine" research team, INRA Montpellier, Francia. Dr. Timothée Flutre.

The UMR AGAP, joint unit between CIRAD, INRA and SupAgro, is gathering several research teams and technical platforms working on tropical and Mediterranean crops. Timothee Flutre, newly recruited at the INRA to develop genomic selection in grapevine, will briefly present this unit and then present the "Diversity, Adaptation and Breeding of Grapevine" team.

10:45 - 12:15 Grapevine breeding at Cornell: Integrating technologies for the development of cold climate varieties with disease resistance. Dra. Paola Barba

Aiming to satisfy New York grapevine industry requirements, the breeding program at Cornell develops hybrid wine and table grape varieties with tolerance to cold climate and strong disease pressure. With the support of VitisGen –a \$9 million collaborative project– next generation tools have been incorporated to the program, allowing the identification of valuable traits and speeding up the generation of commercial varieties.

12:30 - 14:00 Horario de Almuerzo (Taller no incluye almuerzo)

BLOQUE 2 Strategies for Genetic Applications

14:00 - 17:00 Combining Genomic Selection and Genetic Determinism Studies of Complex Traits for Grape Selection. Dr. Timothée Flutre.

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Miércoles 26 de Marzo

BLOQUE 3 Introduction to Genomic Selection: a journey to quantitative/statistical genetics

Agriculture started with the domestication of wild species to sustain human needs. In practice it consisted in selecting the best individuals for particular traits. Biologists in general and geneticists in particular naturally got interested in understanding this process. They soon realized that any phenotype is the result of interactions between genotype and environment. The genotype being unknown but inherited, they had to develop new mathematical tools to estimate and predict it, thereby heavily participating in the foundations of statistics. With the discovery of DNA, genotypes slowly became measurable. First at a small scale, researchers invented QTL mapping by using correlation between neutral markers and causal loci. Thanks to the improvement in genotyping technologies and in modeling of high-dimensional data sets, it is now possible to predict phenotypes in a test population from genotypes only, thanks to estimates obtained on a trained population using genome-wide data. This procedure known as "genomic selection" is especially promising for perennial plants, and most future efforts will likely attempt to comprehensively consider genotype x environment interactions in more sustainable breeding programs. In order to provide a strong basis to anyone for understanding genomic selection, this talk will follow a historical path, introducing in turn fundamental concepts in genetics and statistics, illustrated by the work of giants in these fields.

8:30 - 9:20 Transition to agriculture and domestication (history, examples, major questions).
Dr. Timothée Flutre

9:20 - 10:10 Intertwined history of genetics and statistics (basic concepts in chronological order, linear regression, least-squares, heritability, infinitesimal model). Dr. Timothée Flutre

10:30 - 11:15 On mixed models and QTL mapping (linear mixed model, REML, BLUP, linkage disequilibrium, QTL mapping, marker-assisted selection). Dr. Timothée Flutre

11:15 - 11:45 On mixed models and QTL mapping (linear mixed model, REML, BLUP, linkage disequilibrium, QTL mapping, marker-assisted selection). Dr. Timothée Flutre

11:45 - 12:30 Cheap genotyping and sparse models leading to genomic selection (high-throughput technologies, genomic selection as a mix of BLUP and QTL mapping, sparsity and shrinkage priors, determinants of accuracy). Dr. Timothée Flutre

12:30 - 14:00 Horario de Almuerzo (Taller no incluye almuerzo)

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Miércoles 26 de Marzo – continuación tarde

BLOQUE 4 Genotyping-by-Sequencing (GBS)

14:45 – 15:30 Concepts, principles and methodology of Genotyping-by-Sequencing (GBS)

Including reviews of laboratory protocol and data analysis pipeline. Summary of free tools for analysis. filtering strategies, sources of error, cost. Dra. Paola Barba

15:45 – 16:30 How can we use thousands of GBS markers to improve cultivars? Dra. Paola Barba.

GBS applied to crosses and diversity panels. A review of uses in marker discovery, phylogeny, linkage mapping of QTL in biparental crosses, fine-mapping QTL, genomic selection, Genome Wide Association Studies (GWAS), NAM-GWAS and improving reference genome assembly.

16:30 – 17:15 What have we learn from grapes through GBS? Dra. Paola Barba

Focused on genetics and biology, this session will show results from research in biparental populations for quantitative and qualitative traits, and their application in marker assisted selection, generation of genetic maps and improvement of reference genome. Diversity analysis of the USDA germplasm and other wild collections will also be presented.