# Memorias VII Simposio Internacional de Biotecnología Vegetal (17-21 de abril de 2006). Memories of the VII International Symposium on Plant Biotechnology ( April 17-21, 2006)

## CONFERENCIAS

### RIESGOS DE FLUJO GENETICO DEL MAIZ TRANSGENICO EN CRIOLLOS DE MEXICO: ESTUDIOS EN SISTEMAS TRADICIONALES

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**RESUMEN**

La biotecnología y los productos transgénicos recientemente han revolucionado la agricultura en los países desarrollados; sin embargo, representan riesgos biológicos importantes en las zonas de diversidad genética de especies vegetales debido a que pueden provocar efectos desconocidos. En el caso del maíz, las empresas transnacionales están tratando de introducir maíz a México y argumentan no riesgo para los maíces criollos. El presente estudio tuvo como fundamento conocer algunos factores importantes que influyen en el flujo genético entre maíces criollos en sistemas tradicionales. Se condujeron en Jalisco, México tres estudios: 1. Flujo genético entre parcelas de maíz usando marcadores moleculares; 2. Uso de mezclas de polen para determinar fecundación preferencial; y 3. Análisis de patrones isoenzimáticos para identificar flujo genético acumulado a través del tiempo. De ello se derivó que el flujo genético entre parcelas adyacentes de maíz ocurre en forma exponencial disminuyendo a 1.0% a los 30 m en condiciones normales, y a 2.7% en dirección del viento. Las polinizaciones con mezcla de polen indica que los maíces criollos prefieren al polen propio, aunque en algunos casos el polen extraño o de maíz mejorado logra también fecundar; según el estudio isoenzimático, el flujo genético se acumula lentamente a través del tiempo en las poblaciones cambiando su estructura genética a pesar de fuerzas ambientales y selección por el hombre. En conjunto, tales estudios indican que el flujo genético en maíz está presente a gran distancia y a través del tiempo en proporciones considerables, y no es posible por ahora determinar con exactitud los límites para evitarla; por tanto, la intención de introducir los maíces transgénicos a México para producción comercial debe posponerse hasta no disponer de información suficiente acerca de cómo evitar el flujo genético y determinar los efectos en los maíces criollos.

Palabras clave: criollos, flujo genético, maíz, transgénicos, sistemas tradicionales

### GENEFLOW RISKS FROM TRANSGENIC CORN TOWARD MEXICAN LANDRACES: STUDIES IN TRADITIONAL SYSTEMS

**ABSTRACT**

Recently, biotechnology and transgenic products have been an important role of agriculture successful in developed countries; however, such as products are representing biological risks in regions where genetic diversity is important, because unknown genetic effects could be introduced to crop species. International companies want introduce transgenic corn into Mexico, and they ignore risk about gene flow toward landraces. This study had as object to know some important factors of gene flow among landraces in traditional systems. In Jalisco, Mexico were carried out three different studies: 1. Gene flow estimation among adjacent corn fields measured by molecular markers; 2. Pollen mixtures to determinate preferential pollination; 3. Isozyme analysis to identify gene flow accumulated across time. Studies suggest gene flow among adjacent corn fields occurs in exponential way decreasing until reach 1.0% at 30 m far from the source in normal conditions, and 2.7% on wind direction. Pollination by pollen mixtures showed that corn landraces prefer their own pollen, although in some cases they are pollinated by foreign pollen from modern bred corn; according to isozyme study, gene flow is accumulated slowly across the time changing genetic structure of corn landraces. Global results show that gene flow in corn occurs at long distance at higher level, and it is not possible by now determinate factors to avoid it. That is why, suggests given by companies to use transgenic corn are not appropriate to do it. So, is suggested that introduction of transgenic corn to Mexico must be postponed until enough information is available about gene flow and their risks toward land races.

Key words: landraces, gene flow, transgenic, traditional systems

## ROLE OF ABSCISIC ACID IN THE SUSCEPTIBLE INTERACTION OF TOMATO WITH NECROTROPHIC PATHOGENS

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### ABSTRACT

The plant hormone abscisic acid (ABA) emerges as an important factor affecting disease tolerance in tomato. The ABA deficient sitiens mutant of tomato, blocked in aldehyde oxidase, the last step in the ABA biosynthetic pathway, is resistant to necrotrophic fungi such as *Botrytis cinerea* and *Sclerotinia sclerotiorum* and to the necrotrophic bacterium *Erwinia chrysanthemi*. Application of exogenous ABA during the development of the sitiens mutant restores the disease susceptibility to wild type levels, while a pulse ABA application shortly before infection only leads to partial susceptibility. Sitiens plants show an early oxidative burst with the production of hydrogen peroxide (after staining microscopically detectable after 8h, macroscopically detectable after 12h) after *B. cinerea* infection, while this burst is not present in the wild type. Application of ascorbate and catalase blocks this early oxidative burst and leads again to disease susceptibility. Tom1 tomato arrays were used to compare wild type and sitiens plants at 0 and 8h after leaf infection with *B. cinerea*. After extensive statistical analysis 240 genes remained significant differentially induced as a result of *B. cinerea* infection. Our microarray data indicate that lysine metabolism and photorespiration in the peroxisomes are important in the early resistance response of tomato to *B. cinerea*. This mechanism is already activated 8 hours after infection, the time point at which *B. cinerea* attempts to penetrate the cell. We are currently testing the hypothesis that resistance in sitiens to *B. cinerea* can be explained by a very early induced pre-invasive defense mechanism in which peroxisomes and active oxygen species (AOS) play an important role. These AOS induce cell wall changes at the point of penetration. Basal ABA levels in wild type tomato appear to repress these defence mechanisms.

Key words: ABA biosynthetic pathway, *Botrytis cinerea*, *Erwinia chrysanthemi, Sclerotinia sclerotiorum*

## SOME MOLECULAR TRAITS IN INCOMPATIBLE AND COMPATIBLE INTERACTIONS IN *PHASEOLUS VULGARIS* / *COLLETOTRICHUM LINDEMUTHIANUM* PATHOSYSTEMS

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### ABSTRACT

Even the importance of common bean as worldwide crop legume and protein source in the nourishment for people in poor regions, and the great harvest losses because of diseases where the anthracnose is one of the more serious, scarce studies in molecular biology have been done in relation to plant defense response to pathogen. Genes as Phenylalanine amonialyase, Chalcone synthase and others, as well as combinations of cultivars/races of plant and pathogen respectively has been perhaps the more extensive studied. Our focus has been the molecular interaction between *Phaseolus vulgaris* and *Colletotrichum lindemuthianum* fungus, the causal agent of anthracnose, to identify plant defense genes of early response and susceptibility factors. We have searched the plant defense response by means of subtractive hybridization and other standard microscopy and molecular protocols (northern, Southern and reverse Southern blots). In results, five plant genes over-expressed in resistant plant reaction, moreover four genes induced in compatible pathosystem. Sequence characteristics of genes with high induction in resistant plant reaction align with calcium-binding proteins, SUMO, SINA and _-glucosidase genes; that is, molecular processes of calcium signaling cascades, protein-tagging for subcellular localization/preservation of substrates, and enzymatic activities for salicylic acid biosynthesis or toward fungal wall components. Cultivar beans of Mesoamerican and Andean pools exhibit differential pattern expression for SUMO gene. The calcium-binding protein is also co-regulated by light/dark (day/night) normal transition, and together with SUMO differentially induced by several abiotic stresses. The genes induced in susceptible interaction align partially with genes of hypothetical or unknown proteins of plant or fungal origin. In conclusion, five genes early over-expressed in resistant reaction, one co-regulated by day/night transition, two induced also in abiotic stress, three possible biological functions, with some differences between Mesoamerican and Andean beans, and four genes of unknown function in susceptible interaction.

Key words: abiotic stress, anthracnose, *Phaseolus vulgaris*, plant defense response, susceptibility factors

## ALGUNOS RASGOS MOLECULARES DE INTERACCIONES COMPATIBLE E INCOMPATIBLE EN PATOSISTEMAS DE *PHASEOLUS VULGARIS* / *COLLETOTRICHUM LINDEMUTHIANUM*

### RESUMEN

Aún dada la importancia del cultivo de frijol a nivel mundial y como fuente de proteína en la dieta para pueblos de regiones pobres, además las grandes pérdidas a causa de enfermedades como la antracnosis, pocos estudios en biología molecular se han realizado en la respuesta de defensa en planta ante el patógeno. Genes que codifican para Fenilalanina amonialiasa, Chalcona sintasa entre otros, así como combinaciones de variedades/razas de planta y patógeno respectivamente ha sido los más estudiados. El objetivo fue el estudio de la interacción molecular entre *Phaseolus vulgaris* y el hongo *Colletotrichum lindemuthianum* causante de la antracnosis, para identificar genes de defensa de respuesta temprana en planta y genes de susceptibilidad. Se procedió mediante hibridación substractiva y protocolos estándares de microscopía y biología molecular (northern, Southern y Southern en reverso). En resultados, cinco genes de origen vegetal sobre-expresados en reacción de resistencia y cuatro en planta susceptible. Características de las secuencias de estos genes alinean con proteínas de unión a calcio, SUMO, SINA y â-glucosidasa; esto es, procesos moleculares como cascadas de señalización vía calcio, marcaje de proteínas para localización subcelular o preservación, y actividad enzimática para biosíntesis de ácido salicílico o degradación de pared celular del hongo. La proteína de unión a calcio con expresión co-regulada por transición normal de luz/oscuridad (día/noche), y junto con SUMO, ambos inducidos diferencialmente por estrés abiótico. Frijoles Mesoamericanos y Andinos exhiben patrón de expresión diferencial del gen SUMO. Los genes inducidos en interacción de susceptibilidad alinean parcialmente con genes de proteínas desconocidas de origen vegetal o fúngico. En conclusión, cinco genes de sobre-expresión temprana en reacción de resistencia, uno co-regulado por transición día/noche, dos inducidos también en estrés abiótico, tres posibles funciones biológicas, con algunas diferencias entre frijoles Mesoamericanos y Andinos, y cuatro genes de función desconocida en interacción susceptible.

Palabras clave: antracnosis, estrés abiótico, genes de susceptibilidad, *Phaseolus vulgaris*, respuesta de defensa

## AMINO ACID METABOLISM AND NUTRITIONAL QUALITY IMPROVEMENT IN PLANTS

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### ABSTRACT

Plant derived food and feed is a major source of protein for humans and domestic animals; however the level of essential amino acids in plant-derived protein is usually inadequate with respect to dietary needs. The most limiting essential amino acids in crop plants are typically lysine, methionine and threonine, which are synthesized from aspartate through a branched pathway. We aim to understand the regulation of the aspartate pathway, using *Arabidopsis thaliana* as model plant, to study the differences in lysine and methionine biosynthesis in different plant species and to enhance the level of essential amino acids in crops. To better understand aspartate derived amino acid metabolism in *A.thaliana*, insertion mutants for genes encoding enzymes of the aspartate pathway are being analyzed. Preliminary evidence suggests the existence of novel regulatory mechanisms, which influence the interaction between the different branches of the aspartate pathway. A major difference between leguminous plants and non-legumes appears in the lysine branch of the aspartate pathway. The critical enzyme in lysine biosynthesis is dihydrodipicolinate synthase (DHDPS) that, according to all studies up to now, is strongly feedback inhibited by lysine in plants. In the model legume *Medicago truncatula* however, we found evidence for the presence of two differentially expressed *dhdps* genes, one encoding a lysine sensitive and one encoding a lysine insensitive DHDPS. This may explain the rather high lysine content in seeds of leguminous plants. Finally we aim to enhance the accumulation of essential amino acids in edible parts of various crop plants including sorghum, potato, rice, and beans. This involves overexpression in these plants of genes encoding feedback insensitive forms of the key enzymes of the aspartate pathway and/or genes encoding lysine and methionine rich proteins.

Key words: *Arabidopsis thaliana,* aspartate pathway, lysine, methionine