



# Journal of Basic & Applied Genetics

(Formerly MENDELIANA)

**JOURNAL OF THE ARGENTINE SOCIETY OF GENETICS**  
**REVISTA DE LA SOCIEDAD ARGENTINA DE GENÉTICA**

Proceedings

**XV Latin American Congress of Genetics**

**XLI Argentine Congress of Genetics**

**XLV Congress of the Chilean Society of Genetics**

**II Regional SAG-Litoral Meeting**

Actas

**XV Congreso Latinoamericano de Genética**

**XLI Congreso Argentino de Genética**

**XLV Congreso de la Sociedad de Genética de Chile**

**II Reunión Regional SAG-Litoral**

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# ACTAS

# ALAG

Argentina 2012

**XV CONGRESO LATINOAMERICANO DE GENÉTICA  
XLI CONGRESO ARGENTINO DE GENÉTICA  
XLV CONGRESO DE LA SOCIEDAD DE GENÉTICA DE CHILE  
II REUNIÓN REGIONAL SAG – LITORAL**

**ROSARIO, ARGENTINA, 28 AL 31 DE OCTUBRE DE 2012**

ORGANIZAN





Upland rice production in Brazil covers 50% of the area cropped with the species, which is a major staple food in the country. Weed infestation of cultivated rice fields is one of the main problems impacting the cost of production. There is a great demand for herbicide tolerant rice cultivars to make possible its use on low tillage production systems in rotation with soybean or other crops. The objective of this study was to develop near-isogenic inbred lines of upland rice tolerant to the imidazolinone class of herbicides. A backcross breeding program was established to transfer herbicide resistance to BRS Primavera using the cultivar Cypress CL as source of imidazolinone resistance. BRS Primavera is the standard upland cultivar for grain quality in Brazil. At each backcross generation the plants were submitted to a herbicide resistance bioassay and the resistant individuals were selected for backcrossing with BRS Primavera. Four-hundred herbicide resistant RC3 plants were genotyped with three multiplex panels of microsatellite composed of 16 markers in order to select the plants with the highest level of recovery of the recurrent parent genome. The selected plants were used to derive four herbicide resistant lines which were submitted to detailed agronomic evaluation for commercial release. The herbicide resistant line 07SEQCL441, which has an estimated genome recovery of 93.75%, high grain quality, average yield above 2.800 kg/ha and great potential for use in low tillage rotation systems will be released for commercial upland rice production.

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#### GENETIC DIVERSITY OF APIRENIC *Vitis* ACCESSIONS OF A GERMPLASM BANK

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The demand for seedless grape is increasing in different markets around the world. Grape breeding programs aim to combine the seedless trait with new aromas, flavors and colors to supply a growing market. Seedless control in *Vitis* is caused by stenopermy (normal pollination and fertilization, followed by embryonic degeneration). It is generally accepted that stable stenopermy

is limited to the varieties derived from White Kishmish. However, there is no reason to believe that the apirenic control is one and universal in grapes, since the “seedless” phenotype has been observed in different species of *Vitis*, which could probably be caused by different evolutionary processes. In this study we evaluated the genetic diversity of 185 seedless and normal accessions of *V. vinifera* and *V. labrusca* conserved by Embrapa’s Grape Germplasm Bank through the analysis of DNA polymorphism at 30 microsatellite loci. All markers presented PIC values above 0.63. The accessions were grouped in two main clusters, the first composed by *V. vinifera* accessions and the second by *V. labrusca* accessions. Most *V. vinifera* seedless accessions clustered with clones derived from Sultanin grapes. However, some seedless *V. vinifera* accessions were detected with predominant *V. labrusca* genetic background and clustered with the seedless *V. labrusca* variety Concord. A few *V. labrusca* clones clustered with *V. vinifera* accessions, and vice-versa, what indicates potential hybrids or labeling errors. Identity tests were performed for a number of accessions presenting the same genetic profile.

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#### SISTEMA DE CRUZAMENTO E DIVERSIDADE GENÉTICA EM UMA POPULAÇÃO DE *Eugenia dysenterica* DC

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O sistema de cruzamento molda o papel da endogamia na estrutura genética das populações. Apesar da alta diversidade de espécies, pouco se conhece sobre o sistema de cruzamento em árvores do Cerrado. Neste contexto, o objetivo deste trabalho foi estudar o sistema de cruzamento e a diversidade genética em uma população de *Eugenia dysenterica* (Myrtaceae), uma árvore polinizada por abelhas de grande porte e dispersa por mamíferos. Para tanto, sete marcadores microsatélites foram utilizados em seis famílias de polinização aberta (total de 94 sementes) oriundas de Mimoso-GO, com uma média de 17,666 indivíduos por família. O número de alelos variou entre 11 (Ed05) e 23 (EMBRA14). A população apresentou diversidade genética moderada ( $H_o=0,600$ ;  $H_e = 0,784$ ) e alto índice de endocruzamento ( $f=0,235$ ,