

CODON USAGE IN *Citrus*

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In a citrus EST sequencing project carried at the Centro APTA Citros Sylvio Moreira - IAC, more than 280 thousands sequences were produced, constituting the largest citrus database of EST sequences in the world. The sequences were obtained from sweet orange (*Citrus sinensis* L. Osbeck), mandarin (*C. reticulata* Blanco), *Poncirus trifoliata* and other citrus species. Unigene sets were produced for each species individually. From these unigenes we extracted all the codons utilized in the coding frame. Evaluation of the codon usage for 73,223 putative genes of *Citrus* and *Poncirus* showed high similarity among the species. Analysis of the codon usage in the genus *Citrus* showed that C/G is favored in only 2 of 18 aminoacids. The XCG/XCC and XAT/XTT ratios are related to the avoidance of CG and AT doublets. Evaluation of these ratios showed that in *Citrus* they are 57 and 28, respectively, which is a little different from what is observed for dicots (61 and 47). The main difference was observed in XCG/XCC. Analysis of the absolute number of XCC and XCG in *Citrus* and *Arabidopsis* revealed that *Citrus* shows a little more XCC codons and, at the same time, much less XCG than *Arabidopsis*. This suggests that methylation in *Citrus* seems to be an important feature in regulating gene expression.