

Abstract

Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels [†]

Hayba Badro *, Agnelo Furtado and Robert Henry

Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane QLD 4072, Australia; a.furtado@uq.edu.au (A.F.); robert.henry@uq.edu.au (R.H.)

* Correspondence: haybaq@yahoo.com

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Abstract: Due to the importance of the rice crop in Iraq, this study was conducted to determine the origin of the major varieties and understand the evolutionary relationships between Iraqi rice varieties and other Asian-rice accessions that could be significant in the improvement of this crop. Five varieties of *Oryza sativa* were obtained from Baghdad, Iraq; among these varieties, one, Amber33, is local and is one of the most highly valued varieties in Iraq because of its fragrance, and two varieties, Furat and Yasmin were introduced from Vietnam while the other two, Buhoot1 and Amber al-Baraka, were improved varieties; the whole genomic DNA was sequenced. Raw sequence reads of 33 domesticated Asian-rice accessions were obtained from the National Centre for Biotechnology Information (NCBI). The sequence of the whole chloroplast genome of 5 Iraqi varieties and 34 domesticated rice accessions was assembled while for nuclear genome analysis, only the sequences of 916 concatenated nuclear genes were assembled. The phylogenetic trees of both chloroplast and nuclear genomes were similar with insignificant differences at the end of the clades. Two main clusters, Indica and Japonica, and further five subclusters based upon their ecotype, *indica*, *aus*, *tropical-japonica*, *temperate-japonica* and *basmati* were created, where Amber33, Furat, Yasmin and Buhooth1 belonged to the *basmati*, *indica* and *japonica* ecotypes, respectively. The phylogenetic analysis of both chloroplast and nuclear genomes placed Amber33 in the *basmati* ecotype group as a sister of cultivars from Pakistan and India. This confirms the old traditional story that the Amber variety was transferred by a group of people who had migrated from India (the Southeast) and settled in southern Iraq a long time ago

Keywords: rice (*Oryza sativa*); evolutionary relationships; chloroplast genome; nuclear genome

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