

# Prospects of genomic resources available at the global databases for the flora of United Arab Emirates

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[Rahul A. Jamdade](#) , [Tamer Mahmoud](#) & [Sanjay Gairola](#)

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## Abstract

This article emphasizes available genomic resources at the global databases National Center for Biotechnology Information (NCBI) GenBank, Gramene and Phytozome for the selected 378 plant taxa of the United Arab Emirates (UAE). Germplasm of these species was collected and banked at the Sharjah Seed Bank and Herbarium (SSBH) along with their related information on habit, habitat and occurrence. The occurrence statistics exhibits almost 19.84% species under rare-to-very rare category, the GenBank search statistics for this category indicates 17.72% species as studied and 2.11% as not studied. Overall, from the global search statistics for 378 plant species, it seems that about 40 (10.58%) species remained unstudied. Most of the unstudied species were herbaceous plants belonging to the mountainous habitat. Moreover, full genomes were recorded for 7 species at NCBI GenBank, 2 species at Phytozome and 1 species at Gramene database. The local search statistics (for UAE) exhibits about 10.58% of the flora that still remained unstudied and only 11 (2.90%) of the recorded species were having genomic information at NCBI GenBank. It is necessary to prioritize studies on such species that could provide valuable insight on their genetic composition in order to understand their adaptation to the natural environment. At present, the SSBH is cataloguing UAE's flora using core barcode and assisted markers that could provide a robust DNA barcode library for native plants of UAE. Our study appeals researchers to recognize and prioritize the species that need attention to enrich their genomic resources at the global databases by supporting nucleotide libraries with their conspecifics. At present, genomic resources for UAE plant taxa are limited, but with the advent of low-cost sequencing technologies these resources would flourish in the near future. Nevertheless, the information generated through genomic studies could be utilized for conservation and management of threatened and endangered plant species, Crop Wild Relatives and medicinal plants. We hope this article will promote interest in conducting additional studies in genomics of desert plants by encouraging researchers to participate in this emerging field.