Vitigene: A database for grape genomics and genetic resources delivery that benefits grape growers and scientific communities

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Objectives

Diseases are the limiting factor to grow non-native grapes in many areas of the United States. For example, Pierce's disease limits European grape (Vitis vinifera) production in most part of the southeastern United States. Disease resistance of the non-native grape could be improved by incorporating the resistance from the Native American grape species such as Vitis shuttleworthii, Vitis aestivalis, Vitis riparia and Vitis rotundiforlia by cross pollination. Alternatively, a 'molecular breeding approach' could be used to assist and accelerate the conventional breeding process. The recent development and availability of large number of gene sequence (EST) data makes the molecular approach more realistic than ever before. This project is to collect and host the EST /gene sequences of the native American grape species in a database supported by a IBM DB2 Content Manager Software.

System Architecture

IBM DB2 Content Manager software architecture is open, portable, and extensible. Content Manager uses triangular architecture, with Library Server and Resource Manager as the foundation, and client applications on top. There are various client options (client for windows, e-client, and customized client) available. Content Manager system architecture can be build with two-tier or three-tier configuration using different client options, on one or mixed platforms.





CM Interface Development

Data Model



Major Interface



Heterogeneous Integration

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NCBI Web Site





Content Manager eClient

Phenotype information



Viticultural practice



Functional Annotation and Ontology Search

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Current situation and benefits

current database. pictures

Work in Progress

American Grapes remote access





Host 13000 grape ESTs sequences and 1000 grape EST-SSR marker sequences in the

Multiple format files integration, sharing and retrieval: including sequence files,

Halved the time needed to add new data, hastening discoveries

Garnered worldwide recognition for the university through improved collaboration while strengthening local grape-breeding programs

- Continuing to hosting new EST sequences, chromatogram, and putative function of

- A list of putative SSR and SNP markers, identification of markers for genotyping, disease resistance /stress tolerance

- Expression profiling (microarray data, proteomic profiles)

- Storage of phenotypic images correlated to viticulturally important genes

- Outreach and training: The database is linked and indexed with heterogeneous data sets that provide a convenient platform to train scholars and students on site or via