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Design and Implementation of Internet-enabled High-throughput Phenotyping

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Genomic data from different plants, including crops, are now publicly available with novel genomes added every week. However, and despite this information, only 40% of the genes within plants have an assigned function. Automation and high-throughput phenotyping (HTP) have recently reduced many of the bottlenecks for conducting biological experiments that connect the genome with the phenome. However, automation and the ability to collect large amounts of data have brought new challenges including how to properly store, share, and manage it all, as well as how to keep researchers connected to their autonomous HTP experiments. To solve these issues, we designed and implemented an internet-enabled, high-throughput phenotyping architecture that solves both of these issues. To do so, we integrated *automatic management* of experiment data via CyVerse along with instant messenger-based communication between the HTP machines and researchers with the Slack API. We found that letting computers automatically manage the data on behalf of researchers as well as communicate various information about their status is extremely useful with respect to administering experiments as well as sharing and analyzing results. Moreover, the overhead to implement a system such as ours is relatively small and adaptable, lending itself to numerous other applications.