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DEVELOPING A WORKFLOW FOR MANAGEMENT OF INFORMATION FROM A PLANT TRANSFORMATION FACILITY

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Good Laboratory Practices, or GLP, are a set of management principles of research laboratories activities that provide a framework within which studies are planned and performed in order to ensure results consistency and reliability. In order to enforce the GLP adoption, it is important to demonstrate that the information produced and processes applied to obtain it are correct and traceable. Therefore, the use of automated systems to follow each step of the research in a laboratory can be of significant assistance. These systems are called Laboratory Information Management Systems (LIMS) and are now often used in research laboratories. In this work we describe the use of a LIMS based on workflows to manage the data from the Plant Genetic Transformation Laboratory at EMBRAPA Milho e Sorgo, that works on the analysis and production of transgenic maize and sorghum plants. Transgenics are organisms whose DNA is modified using genetic engineering aiming to introduce a new characteristic which does not occur naturally in that species. We have developed a workflow to manage the information from the processes to obtain genetically modified plants to be used in the LIMS Flux (Satya Sistemas). A workflow in XPDL format was constructed using the Together Workflow Editor tool and imported into the system where data are stored in a MySQL database. This workflow models the data and the activities of maize transformation mediated by *Agrobacterium tumefaciens,* in which the user defines the genetic construction specifications, the plant genotypes and conditions for the transformation, transgenic callus selection and plant regeneration. Finally, from workbench to glasshouses, the system stores experimental protocols and data from the whole processes up to obtaining and storing modified seeds, thus ensuring that GLP are followed. This work presents a solution for the management of information produced by a laboratory working with transgenic plants and our hope is to contribute with a quality improvement of the produced data. Supported by: FAPEMIG, CNPq.