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## Green production of biodiesel from microalgae lipids

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**B**iodiesel production from lipids-rich feedstock is potentially an acceptable and suitable substitute to petroleum diesel. The re-shaping of the available technologies to greener alternatives is needed for fuel production. To produce a sustainable fuel that reduces dependency on fossil fuels and utilize a feedstock that does not compete with food stock and at same time contributes to the reduction of CO<sub>2</sub> emissions, microalgae lipids were suggested. Utilization of microalgae as a feedstock for biodiesel production is well known worldwide but the production process is not yet economical where the biodiesel cost from microalgae is still high compared to petroleum diesel which is associated from the down-streaming cost. The green extraction and reaction processes could be viable and utilization of the proteins in the leftover biomass pharmaceutical and food applications could justify such high costly processes. Extraction of microalgae lipids using green solvents such as supercritical CO<sub>2</sub> and ionic liquids eliminates the need for using toxic organic chemicals. Moreover, integrating microalgae lipids extraction with enzymatic trans-esterification in one unit renders the use of such expensive process. However, these still needs extensive studies and developments before being commercialized. Such researches could lead to a major development in sustainable biodiesel production especially if the leftover biomass can be used for pharmaceutical applications.

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## Genome-scale identification of cell-wall related genes in switchgrass through comparative genomics and computational analyses of transcriptomic data

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**S**ubstantial efforts have been invested in the past two decades into identification of plant cell-wall (PCW) related genes in several genomes such as *Arabidopsis thaliana*, *Oryza sativa* (rice) and *Zea mays* (maize) having led to large pools of predicted PCW genes in these organisms. However, no such gene list has been identified in the bioenergy crop switchgrass (*Panicum virgatum*). Here we present a computational study for prediction of PCW genes in switchgrass using a two-step procedure: Homology mapping of all annotated PCW genes in these three organisms to switchgrass, giving rise to the initial list of 991 genes and candidate selection from the 991 mapped genes based on co-expression analyses of transcriptomic which leads to the identification of 104 large groups of co-expressed genes each under a sufficiently large number of conditions referred to as co-expression modules (CEMs) which cover 830 genes and represent our initial PCW genes in switchgrass. We then extended this co-expression analysis to include all the switchgrass genes and found additional 847 genes that are strongly co-expressed with some of the 104 CEMs, hence also predicted as PCW genes, 123 of the predicted genes are homologous to predicted PCW genes in *Arabidopsis*.

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