

## Editorial: Sustainable production of renewable energy from non-food crops

Since the world faced the petroleum crisis in the 1970s and people started to realize the limitation of fossil energy resources coupled with concerns over the effects of increasing carbon dioxide in the atmosphere, major efforts were devoted to the search for alternative energy sources. In this context, the huge potential of plant biomass, which could replace fossil oil, has generated a significant interest towards the sustainable production of renewable energy.

Initially, biofuels were produced from food crops with high content of carbohydrates such as sugar from sugarcane or sugar beet, starch from corn for ethanol fermentation, and vegetable oil from edible oilseed crops for biodiesel production, although controversial opinions on the matter existed. In the meantime, biofuel production has developed forward to a second and third generation of biofuels produced from non-food biomass, which does not compete with classical food production crops. In the latter case, research is focusing on the use of bulk plant biomass such as cellulose from the cell walls (e.g. switch grass, poplar and *Miscanthus*), or triacylglycerols from new and non-food oil crops, e.g. *Jatropha*, but also oil palm, *Camelina* and algae, to produce more positive outcomes for our future need of sustainable energy.

Given the growing importance and increasing attention of biofuel plants with their environmental advantages of reducing greenhouse gas emissions as compared to fossil fuel consumption, we considered time to be right for a dedicated Special issue of the science and biotechnology behind renewable biofuel crops. Therefore, this Special issue of several invited articles discusses both annual and perennial biofuel

crops, and highlights the approaches by which they are genetically improved using a range of different technologies and applications and the economic production of biofuels.

There are numerous strategies and powerful advanced plant biotechnology tools to improve crops or fuel feedstock to produce or process high quality biofuel (bioethanol and biodiesel). Some attempts to produce lignocellulosic biofuels still need to be developed into economically feasible strategies, as in the case of sucrose conversion through biomass oriented breeding or by manipulating the cell wall composition of bioenergy feedstocks to decrease lignin content and increase biomass.

Given the high genetic variability and the favorable proportions of cell wall components in *Populus*, a valuable bioenergy feedstock, Porth and El-Kassby [1] describe the huge opportunities of the family *Salicaceae* with a specific focus on poplars. They review economically important traits relevant for intensively managed biofuel crop plantations, genomic and phenotypic resources of poplars available, breeding strategies, bioprocesses and downstream applications related to the efficient exploitation of this bioethanol crop.

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One attractive strategy to generate biofuel plants with altered cell wall properties involves genetic engineering (recombination DNA)



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strategies. With this aim, Poovaiah et al. [2] overexpressed PvSUS1, one of four identified isoforms of sucrose synthase (SUS) in *Panicum virgatum*, which converts sucrose and uridine di-phosphate (UDP) into UDP-glucose and fructose, leading to increased biomass in transgenic switch grass. These results have significant implications in improving biofuel yield in bioenergy crops, especially in transgene stacks for increasing saccharification and biomass. To achieve this, it is necessary to understand complex-signaling networks closely linked to the metabolism and the molecular mechanisms underlying plant biomass production. In addition, understanding how plants can adjust their metabolic pathways in response to environment stimuli to convert biomass into biofuel.

Considering that some of the most promising feedstocks for biodiesel production, such as oil palm (*Elaeis guineensis*), jatropha (*Jatropha curcas*), macaw palm (*Acrocomia aculeata*), and pongamia (*Pongamia pinnata*) are perennial crops, genomic breeding is therefore one of the most promising ways to foster the development of perennial crops dedicated to biodiesel production [3]. Since traditional selective breeding of perennial crops relies on scor-

ing plants over several years (10 to 14 years in the case of *Jatropha* and 18 to 20 years in the case of oil palm), using molecular markers for the selection of the best genotypes in breeding populations under field evaluation has recently emerged as the foundation of “genomic breeding”. This allows breeders to obtain higher selective accuracy, and to reduce the time needed to select elite individuals in breeding programs of perennial crops, especially in comparison to traditional selection based on phenotypic data only.

...however, major efforts need to be devoted to the genetic improvement of renewable energy crops to meet the high expectations of alternative energy sources...

To develop effective breeding programs in perennial crops, e.g. *Jatropha*, it is necessary to increase our understanding of intraspecific variability and interspecific relationships, providing insights into population structure or adaptation. Moreover, to accelerate the process of genetic improvement of oil seed crops, the identification of natural variation in genes of interest is important. Since most of the functional variation resides in the coding regions of the genome, the identification of SNP markers in these regions allows to discover alleles that are under selection and affect gene expression. For this purpose, high-throughput and cost effective technologies such as Eco TILLING, allow to investigate the function of candidate genes by discovering new SNPs [4].

Finally, camelina is introduced as an underutilized oilseed with a considerable potential for sustainable oil production [5]. Camelina is the crop

plant most closely related to the genetic model plant *Arabidopsis*, it has been proposed as a most suitable biotechnology platform for translating *Arabidopsis* results into a field crop. Therefore, this example illustrates the biorefinery potential of camelina improvement, which allows for the fine-tuning of fatty acid composition depending on utilization needs: For biofuel production, RNAi suppression of desaturase genes can help to produce high-oleic acid oils, whereas fatty acid elongase and desaturase gene cassettes can make camelina to synthesize long-chain polyunsaturated oils with unique health properties, which are only found in marine fish oils at present.

Although the list of crops and platforms is far from being complete, the applications presented are serving as examples of state-of-the-art developments, which could also be transferred to other biofuel production platforms.

We wish to thank all contributors to this Special issue and hope that its appearance will raise the interest and understanding of biofuels.



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## References

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- [2] Poovaiyah, C. R., Mazarei, M., Decker, S. R., Turner, G. B. et al., Transgenic switchgrass (*Panicum virgatum* L.) biomass is increased by overexpression of switchgrass sucrose synthase (*PvSUS1*). *Biotechnol. J.* 2015, 10, 552–563.
- [3] Alonso Alves, A., Laviola, B. G., Formighieri, E. F., Carels, N., Perennial plants for biofuel production: Bridging genomics and field research. *Biotechnol. J.* 2015, 10, 505–507.
- [4] Maghuly, F., Jankowicz-Cieslak, J., Pabinger, S., Till, B. J., Laimer, M., Geographic origin is not supported by the genetic variability found in a large living collection of *Jatropha curcas* with accessions from three continents. *Biotechnol. J.* 2015, 10, 536–551.
- [5] Vollmann, J., Eynck, C., Camelina as a sustainable oilseed crop: Contributions of plant breeding and genetic engineering. *Biotechnol. J.* 2015, 10, 525–535.



#### Cover illustration

**Special issue: Renewable Energy Crops**, edited by Margit Laimer, Fatemeh Maghuly, Johann Vollmann and Nicolas Carels. Given the growing importance of environmental advantages of biofuel plants reducing greenhouse gas emissions as compared to fossil fuel consumption, second and third generation biofuels today are produced from both annual and perennial non-food biofuel crops, e.g. switchgrass, poplar and *Miscanthus*, or from new and non-food oil crops, like *Jatropha*, *Camelina* and oil palm. To achieve an economic production of biofuels for our future need of sustainable energy, genetic improvement of the plant material must be obtained by a range of different biotechnologies.

## Biotechnology Journal – list of articles published in the April 2015 issue.

### Editorial: Sustainable production of renewable energy from non-food crops

Margit Laimer, Fatemeh Maghuly, Johann Vollmann and Nicolas Carels

<http://dx.doi.org/10.1002/biot.201500100>

#### Forum

### Perennial plants for biofuel production: Bridging genomics and field research

Alexandre Alonso Alves, Bruno G. Laviola, Eduardo F. Formighieri, Nicolas Carels

<http://dx.doi.org/10.1002/biot.201400201>

#### Commentary

### More than one way to skin a cat: in-situ engineering of an antibody through photo-conjugated C2 domain

Andrew Kroetsch and Sheldon Park

<http://dx.doi.org/10.1002/biot.201500051>

#### Review

### Using *Populus* as a lignocellulosic feedstock for bioethanol

Ilga Porth and Yousry A. El-Kassaby

<http://dx.doi.org/10.1002/biot.201400194>

#### Review

### Camelina as a sustainable oilseed crop:

### Contributions of plant breeding and genetic engineering

Johann Vollmann and Christina Eynck

<http://dx.doi.org/10.1002/biot.201400200>

#### Research Article

### Geographic origin is not supported by the genetic variability found in a large living collection of *Jatropha curcas* with accessions from three continents

Fatemeh Maghuly, Joanna Jankowicz-Cieslak, Stephan Pabinger, Bradley J. Till and Margit Laimer

<http://dx.doi.org/10.1002/biot.201400196>

#### Research Article

### Transgenic switchgrass (*Panicum virgatum* L.) biomass is increased by overexpression of switchgrass sucrose synthase (*PvSUS1*)

Charleson R. Poovaiah, Mitra Mazarei, Stephen R. Decker, Geoffrey B. Turner, Robert W. Sykes, Mark F. Davis and C. Neal Stewart, Jr.

<http://dx.doi.org/10.1002/biot.201400499>

#### Research Article

### In vivo biotinylation and incorporation of a photo-inducible unnatural amino acid to an antibody-binding domain improve site-specific labeling of antibodies

Sara Kanje and Sophia Hober

<http://dx.doi.org/10.1002/biot.201400808>

#### Research Article

### Xylan catabolism is improved by blending bioprospecting and metabolic pathway engineering in *Saccharomyces cerevisiae*

Sun-Mi Lee, Taylor Jellison, and Hal S. Alper

<http://dx.doi.org/10.1002/biot.201400622>

#### Biotech Methods

### Cellulose-based filter aids increase the capacity of depth filters during the downstream processing of plant-derived biopharmaceutical proteins

Johannes F. Buyel, Patrick Opdensteinen, Rainer Fischer

<http://dx.doi.org/10.1002/biot.201400611>

#### Research Article

### Ca<sup>2+</sup> and Mg<sup>2+</sup> binding site engineering increases the degradation of polyethylene terephthalate films by polyester hydrolases from *Thermobifida fusca*

Johannes Then, Ren Wei, Thorsten Oeser, Markus Barth, Matheus R. Belisário-Ferrari, Juliane Schmidt and Wolfgang Zimmermann

<http://dx.doi.org/10.1002/biot.201400620>

Research Article

**Production of curcuminoids from tyrosine by a metabolically engineered *Escherichia coli* using caffeic acid as an intermediate**

*Joana L. Rodrigues, Rafael G. Araújo, Kristala L. J. Prather, Leon D. Kluskens, and Ligia R. Rodrigues*

<http://dx.doi.org/10.1002/biot.201400637>

Research Article

**Buffer-free therapeutic antibody preparations provide a viable alternative to conventionally buffered solutions: From protein buffer capacity prediction to bioprocess applications**

*Sven Bahrenburg, Anne R. Karow, Patrick Garidel*

<http://dx.doi.org/10.1002/biot.201400531>

Research Article

**Over-expression of ICE2 stabilizes cytochrome P450 reductase in *Saccharomyces cerevisiae* and *Pichia pastoris***

*Anita Emmerstorfer, Miriam Wimmer-Teubenbacher, Tamara Wriessnegger, Erich Leitner, Monika Müller, Iwona Kaluzna, Martin Schürmann, Daniel Mink, Günther Zellnig, Helmut Schwab and Harald Pichler*

<http://dx.doi.org/10.1002/biot.201400780>

Research Article

**Indole generates quiescent and metabolically active *Escherichia coli* cultures**

*Chih-Chin Chen, Rupali Walia, Krishna J. Mukherjee, Subhashree Mahalik and David K. Summers*

<http://dx.doi.org/10.1002/biot.201400381>

Biotech Method

**Optimized Sleeping Beauty transposons rapidly generate stable transgenic cell lines**

*Eric Kowarz, Denise Löscher, Rolf Marschalek*

<http://dx.doi.org/10.1002/biot.201400821>