

# As Green as a Leaf: Carbon Dioxide Recovery in Design

By SONG Jianlan (Staff Reporter)

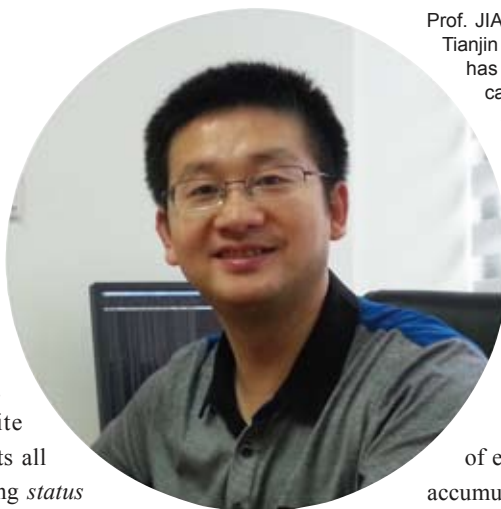
The ability of plants to efficiently turn carbon dioxide into hydrocarbons has long fascinated biologists. Its underlying mechanism has, however, remained unclear despite long-term efforts made by scientists all over the world. Given this frustrating *status quo*, not many people would dare to dream about creating some mechanisms equivalent to photosynthesis, let alone something even more versatile than that.

It might not be that hard, nevertheless, for Prof. JIANG Huifeng, a computational biologist at the CAS Tianjin Institute of Industrial Biotechnology (TIB), to bypass this dihard barrier to meet the goal.

“What we are doing now is to create some novel reactions or pathways that have never existed in the natural evolution of the host organism,” says JIANG when introducing to the author his work.

“For example, yeasts can never use carbon dioxide as the sole carbon source in their metabolism. We can design a new pathway of metabolism, however, to render them the ability to breathe in carbon dioxide, utilize it, and secrete something beyond your expectation, say propyl alcohol and others, like clothes and even foods,” he continues.

Through this artificial pathway in design, JIANG’s team aims to seize the molecules of carbon dioxide in the air and turn them into basic hydrocarbons containing one, two or three carbon atoms in their chains. Using these small molecules of hydrocarbons as “building blocks”, they will be able to synthesize more complicated hydrocarbons, such as those containing four, five, six, or more carbon atoms.



Prof. JIANG Huifeng, principal investigator at the Tianjin Institute of Industrial Biotechnology, CAS, has been working to design a microbe that can breathe in carbon dioxide and secrete some basic carbohydrates. (Photo by LU Li'na)

Seems that great prospects are in sight. How can we get there, however?

The wand JIANG holds in hand is computational biology.

According to JIANG, after years of efforts, the biological community has accumulated massive data from sequencing of various species/genes, as well as structure-functioning analyses and proteomics research. This has provided us a basis for prediction of potential reactions catalyzed by enzymes programmed by these genes.

“These data sets, however, are mostly fragmented and isolated from each other,” he explains. Therefore JIANG and his colleagues need to integrate these sets of data and analyze the mechanisms underlying different reactions, to predict which enzyme(s)/gene(s) of which species might be able to play the preconceived role in the pathway. “It is almost impossible to exhaust the whole library of data manually, testing the function of each gene one by one; and that is where we need computational biology,” he emphasizes.

Reactions in organisms are catalyzed by enzymes, which are mostly proteins. A pathway for biosynthesis can involve multiple reactions jointed together with nodes; and at each node appropriate enzyme(s) is (are) needed to catalyze the reaction. “Of course it is possible to identify such enzymes through experiments,” JIANG says: “but it takes too much effort and time to test all the potential candidates one by one. With computational biology it is much easier to find them out in the database.”

JIANG’s team are drawing on algorithms from massive data analysis to search for the candidate enzymes for each

node along the reaction pathways in design.

“We can narrow down to 10 or 20 proteins, for example for a certain node, and further examine their functioning in the reaction through experiments,” he continues: “In this way we can greatly increase the possibility of success without investing in too much effort.”

Computational biology also plays an important role in the design of the pathways, according to JIANG. “From the target substrate, carbon dioxide for example, to the target product, say butanol, with aid from computational biology we can screen in the database for all the possible pathways based on principles of organic chemistry and again, narrow down the candidate pathways. Subsequently we can focus on the shortlisted pathways to examine their feasibility and save us from the otherwise tremendous workload,” he explains. “Things are similar with biosynthesis. For example from the target substrate glucose to the target product adipic acid, the computer can automatically find out one or two dozens of potential pathways.”

“Sometimes we can find a similar enzyme that meets almost all the requirements except for one or two defects. For example, we might find a very good enzyme that functions rightly and efficiently in the reaction, unfortunately with the wrong substrate: it works with

acetone rather than pyruvateacid . In such cases we need to further analyze the structure of the enzyme to figure out if it is possible to modify it. Sometimes through multiple mutations we can hit the mark,” he says.

So far JIANG’s group has successfully determined the enzymes needed at critical nodes along the pathways from CO<sub>2</sub> to basic hydrocarbons containing one, two and three carbon atoms in their main chains, respectively.

After determining all the enzymes needed along the pathway, TIB scientists will know what genes are needed to produce these proteins or more exactly, what the optimal cell might look like. Starting from here they will be able to establish a bioreactor through optimizing a species of microbe via genetic engineering/modification.

“We will try our best to make the pathways as simple as possible,” JIANG says. Once the pathway design is finished, his TIB colleagues will take over the work to design and optimize the peripheral metabolic networks involved with the pathway. Only after that can they load the whole metabolic system into the cell and further optimize the cell factory. “In the end we will have an artificial cell that feeds on carbon dioxide in the atmosphere and secrete what we need, like butanol one day,” JIANG anticipates with a bright smile.

## Pathway in Design for CO<sub>2</sub> Recovery



With aid from computational biology and new biology, the dream to reclaim CO<sub>2</sub> from the atmosphere might come true. (Image by courtesy of Prof. JIANG H.)