

SHORT  
COMMUNICATIONS

## Methanol and Glucose Metabolism in *Beijerinckia mobilis*

K. V. Smirnova<sup>\*,\*\*</sup>, S. N. Dedysh<sup>\*\*\*</sup>, V. N. Khmelenina<sup>\*</sup>, and Yu. A. Trotsenko<sup>\*\*,1</sup>

<sup>\*</sup>*Skryabin Institute of Biochemistry and Physiology of Microorganisms,  
Russian Academy of Sciences, pr. Nauki 5, Pushchino, Moscow oblast, 142290 Russia*

<sup>\*\*</sup>*Pushchino State University,*

*pr. Nauki 3, Pushchino, Moscow oblast, 142290 Russia*

<sup>\*\*\*</sup>*Winogradsky Institute of Microbiology, Russian Academy of Sciences,  
pr. 60-letiya Oktyabrya 7, k. 2, Moscow, 117811 Russia*

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Bacteria of the genus *Beijerinckia* are nonsymbiotic aerobic chemoheterotrophs and diazotrophs that are able to utilize a broad range of polycarbon substrates, preferably sugars [1]. Due to their acidotolerance (ability to survive at pH 3.0–4.0), these bacteria are widespread in acidic soils, although they also occur in neutral soils. There are four *Beijerinckia* species with a suitable taxonomic description: *B. mobilis*, *B. indica*, *B. derxii*, and *B. fluminensis*. However, their physiology and metabolism are as yet poorly understood [2–4]. Our recent investigations have shown that *B. mobilis* can grow autotrophically on methanol and formate [5]. This prompted us to study the enzymes involved in the metabolism of methanol and glucose in this facultative methylotroph.

Enzyme activity was measured, as described in [6, 7], in extracts of *B. mobilis* cells grown on methanol and glucose. As is evident from the table, *B. mobilis* possesses all the enzymes necessary for oxidation of methanol to CO<sub>2</sub> via formaldehyde and formate, i.e., for methylotrophic growth. The presence of highly active phosphoribulokinase and ribulose 1,5-bisphosphate carboxylase/oxygenase suggests that the methanol carbon is mainly assimilated at the level of CO<sub>2</sub> via the ribulose bisphosphate (RuBP) pathway. Transketolase and transaldolase are involved in reactions that convert glyceraldehyde-3-phosphate into xylulose-5-phosphate, which results in the regeneration of ribulose-1,5-bisphosphate, the primary acceptor of CO<sub>2</sub> (see figure). The reaction catalyzed by ribulose 1,5-bisphosphate carboxylase/oxygenase produces, in addition to 3-phosphoglycerate, phosphoglycolate, which is then dephosphorylated to glycolate. The last compound transforms into glyoxylate, glycine, and serine via a shunted variant of the serine pathway. Since the activity of NADH-dependent hydroxypyruvate reductase, serine-glyoxylate aminotransferase, and glycerate kinase

is low, the serine pathway plays a minor role in assimilation of the methanol carbon at the level of formaldehyde. *B. mobilis* does not have 3-hexulose-6-phosphate synthase, suggesting that the ribulose monophosphate pathway is not involved in the primary assimilation of formaldehyde.

In contrast to fructose-1,6-bisphosphate aldolase and fructose-1,6-bisphosphatase, which are involved in gluconeogenesis, some enzymes involved in carbon metabolism (ATP-dependent 6-phosphofructokinase, glucose-6-phosphate dehydrogenase, and 6-phosphogluconate dehydrogenase) were suppressed in the methanol-grown culture. Growth on glucose was found to activate ATP-dependent glucokinase, 6-phosphofructokinase, fructose-1,6-bisphosphate aldolase, and 6-phosphogluconate dehydrogenase (NADP<sup>+</sup>-dependent). This circumstance suggests that *B. mobilis* catabolizes glucose with the involvement of both the glycolytic and the pentose phosphate oxidative pathways. At the same time, the absence of 2-keto-3-deoxy-6-phosphogluconate aldolase activity indicates that hexose phosphates are not metabolized via the Entner-Doudoroff pathway.

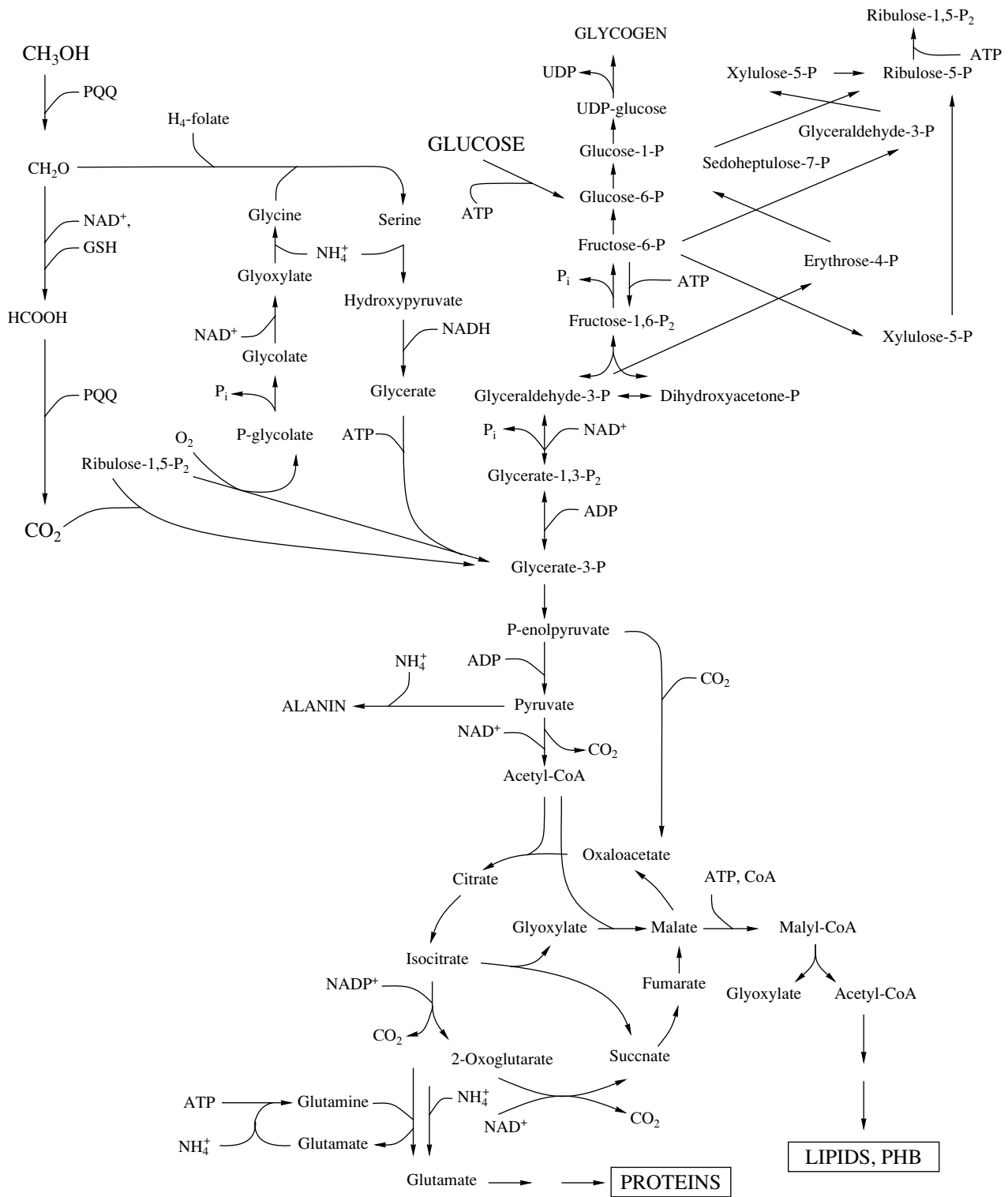
The *B. mobilis* cells grown on methanol exhibited low activity with of pyruvate dehydrogenase and tricarboxylic acid cycle enzymes (such as citrate synthase, isocitrate dehydrogenase,  $\alpha$ -ketoglutarate dehydrogenase, and malate dehydrogenase), indicating that the Krebs cycle mainly performs a biosynthetic function during methylotrophic growth of *B. mobilis*. The low activity of isocitrate lyase and malate synthase in the cells grown on methanol as compared to those grown on glucose suggests that the glyoxylate bypass plays a minor role in methylotrophic growth of *B. mobilis*.

Ammonium is assimilated by *B. mobilis* with the involvement of NADPH-dependent glutamate dehydrogenase, alanine dehydrogenase, and the glutamate cycle. The presence of highly active phosphogluco-

<sup>1</sup> Corresponding author; e-mail: trotsenko@ibpm.pushchino.ru

Activity of the enzymes involved in the metabolism of methanol and glucose in *B. mobilis*

| Enzyme                                     | Cofactor                | Activity with |         |
|--|-------------------------|---------------|---------|
|  |                         | methanol      | glucose |
| Methanol dehydrogenase                     | PMS                     | 27            | 0       |
| Formaldehyde dehydrogenase                 | PMS                     | 17            | 0       |
|  | NAD <sup>+</sup> , GSH  | 210           | 0       |
| Formate dehydrogenase                      | NADP <sup>+</sup> , GSH | 108           | 0       |
|  | PMS                     | 32            | 0       |
| Phosphoribulokinase                        | NAD <sup>+</sup>        | 0             | 0       |
|  | ATP                     | 103           | 3       |
| Ribulose 1,5-bisphosphate carboxylase      |                         | 160           | 30      |
| Phosphoenolpyruvate carboxylase            |                         | 103           | 47      |
| 3-Hexulose-6-phosphate synthase            |                         | 0             | 0       |
| Hydroxypyruvate reductase                  | NADH                    | 18            | 10      |
|  | NADPH                   | 0             | 0       |
| L-Serine-glyoxylate aminotransferase       |                         | 63            | 40      |
| Phosphoglycolate phosphatase               |                         | 25            | 12      |
| Malyl-CoA synthase/Malyl-CoA lyase         | ATP, CoA                | 49            | 56      |
| Glycerate kinase                           | ATP                     | 64            | 40      |
| Transaldolase                              |                         | 86            | 94      |
| Glucose-6-phosphate dehydrogenase          | HAD <sup>+</sup>        | 10            | 322     |
|  | HADP <sup>+</sup>       | 24            | 349     |
| 6-Phosphogluconate dehydrogenase           | NAD <sup>+</sup>        | 0             | 0       |
|  | NADP <sup>+</sup>       | 16            | 345     |
| Fructose-1,6-bisphosphate aldolase         | NADH                    | 133           | 215     |
| Fructose-1,6-bisphosphatase                |                         | 31            | 64      |
| 6-Phosphofructokinase                      | PP <sub>i</sub>         | 0             | 0       |
|  | ATP                     | 54            | 41      |
| 2-Keto-3-deoxy-6-phosphogluconate aldolase |                         | 0             | 0       |
| Pyruvate dehydrogenase                     | NAD <sup>+</sup>        | 143           | 212     |
| Pyruvate kinase                            |                         | 100           | 96      |
| Citrate synthase                           |                         | 22            | 130     |
| Isocitrate dehydrogenase                   | NAD <sup>+</sup>        | 0             | 0       |
|  | NADP <sup>+</sup>       | 68            | 67      |
| 2-Oxoglutarate dehydrogenase               | NAD <sup>+</sup>        | 286           | 295     |
| Malate dehydrogenase                       | NADH                    | 250           | 700     |
|  | NADPH                   | 357           | 296     |
| Isocitrate lyase                           |                         | 35            | 225     |
| Malate synthase                            |                         | 20            | 188     |
| Glutamate dehydrogenase                    | NADPH                   | 0             | 0       |
| Alanine dehydrogenase                      | NADH                    | 49            | 201     |
|  | NADPH                   | 206           | 188     |
| Glutamate synthase                         | NADH                    | 78            | 362     |
|  | NADPH                   | 0             | 0       |
| Glutamine synthetase                       | ATP, Mg <sup>2+</sup>   | 48            | 44      |
| Glucokinase                                | ATP                     | 97            | 104     |
| Phosphoglucomutase                         |                         | 101           | 131     |
| UDP-glucoylphosphorylase                   |                         | 140           | 81      |
| Glycogen synthase                          |                         | 72            | 199     |
| Acetoacetyl-CoA reductase                  | NADPH                   | 73            | 120     |



Pathways of methanol metabolism in *Beijerinckia mobilis*

mutase, UDP-glucopyrophosphorylase, glycogen synthase, and NADPH-dependent acetoacetyl-CoA reductase confirms their involvement in the synthesis of reserve biopolymers, such as glycogen and polyhydroxybutyrate.

The comprehensive metabolic characteristics of *B. mobilis* schematically presented in the figure are important for understanding ecophysiology and the role of this facultative methylotroph in natural microbial communities [1, 5].

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