A genome-scale metabolic model of the Gram-positive bacteria Corynebacterium glutamicum ATCC 13032 was constructed comprising 446 reactions and 411 metabolites, based on the annotated genome and available biochemical information. The network was analyzed using constraint-based methods. The model was extensively validated against published flux data, and flux distribution values were found to correlate well between simulations and experiments. The split pathway of the lysine synthesis pathway of C. glutamicum was investigated, and it was found that the direct dehydrogenase variant gave a higher lysine yield than the alternative succinyl pathway at high lysine production rates. The NADPH demand of the network was not found to be critical for lysine production until lysine yields exceeded 55% (mmol lysine (mmol glucose)(-1)).

The model was validated during growth on the organic acids acetate and lactate. Comparable flux values between in silico model and experimental values were seen, although some differences in the phenotypic behavior between the model and the experimental data were observed.

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