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A causal Bayesian network model of disease progression mechanisms in chronic myeloid leukemia

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Highlights

- A mathematical model of chronic myeloid leukemia based on causal Bayesian networks was developed to study disease progression mechanisms.
- Our results indicate that increase in Bcr-Abl expression levels is not sufficient to explain the phenotype of blast crisis.
- Positive feedback loops caused by secondary changes such as additional mutations are plausible candidates for disease progression mechanisms.
- Imatinib's potential to prevent disease progression seems to stem from its capability to reduce the accumulation of secondary changes by interfering with the proposed feedback loops, and to a lesser extent also from delaying increased Bcr-Abl expression.

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