NMR Structure Determination of KTM: A Rationally Designed Alpha-Conotoxin Targeting Parkinson's-Relevant Receptor Isoforms

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Abstract:
Validating Computational Results

KTM is a rationally designed alpha-conotoxin predicted to have optimal binding affinity for the rat α3β2 (rα3β2) nicotinic acetylcholine receptor (nAChR) isoform, which has >80% sequence homology with the human α6α4β3 receptor isoform implicated in Parkinson's Disease. Validation of computational accuracy will help adjust computational parameters to give more accurate predictions of receptor binding, which is critical to receptor understanding and effective drug development for neurodegenerative diseases such as Parkinson's. The NMR structure of KTM is currently being solved in order to validate computational results. Current progress indicates that the NMR structure follows the predicted structure, but is not as highly constrained as MII. Preliminary two-electrode voltage clamp electrophysiology (TEV) experiments confirm that KTM has affinity for rα3β2 on the order of MII, supporting the reliability of computational results.

How was KTM designed?

KTM is based on alpha-conotoxin MII, which has the highest binding affinity for rα3β2 known. The computational programs GAMPMS and Dockomatic were used to screen a peptide mutant library for optimal binding affinity for rα3β2.

Conclusions:
Reliable Computational Predictions

- TEV results indicate that KTM is a high-affinity antagonist of rα3β2
- TEV and NMR results indicate that computational results are reliable and can be used to predict lead compounds that will have high binding affinity for nAChR receptor isoforms

Future Work: How does KTM move?

- MD simulations to identify peptide dynamics and key binding features
- Refine TEV and NMR data

References


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