SUMMARY & CONCLUSION
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The present investigation was conducted with an aim to identify novel candidates as anti-mycobacterial agents. Emergence of MDR-TB and XDR-TB has become serious problem because of its resistance against the existing four lines of drugs. Therefore, developing new effective drugs from plant-based natural sources has become challenge for the researchers. After a lean period of over 30 years in the process of anti-TB drug discovery now many molecules have been developed and they are in different stages of the drug development process. This is becoming possible mainly because of better understanding of the *Mtb* drug targets, publication of many research works, and advancement of the computational technologies.

The computer assisted molecular docking methods were extensively used to find out plant-based effective anti-mycobacterial compounds present in *Azadirachta indica* (neem), *Ginkgo biloba* (a gymnosperm) and *Camellia sinensis* (tea) along with few antimicrobial compounds available in DrugBank database to identify anti-TB compounds.

Sheltered and efficient utilization of nature based compounds can guarantee that plant-based solutions are more agreeable with organic frameworks. The utilization of extracts of a few plants, alone or in combinations with regular tuberculosis pharmaceuticals proves to be effective. However, because of complexities in the structure of phytochemicals and its bioactivities, the mechanism of actions is not properly understood. These favorable activities of the plant extracts in several metabolic pathways were reported by many researchers from last many years.

The present research study again proves that the structure of plant natural compounds are similar to those of bioactive antibacterial compounds and evaluates its action with anti-tuberculosis medicine. These findings could be therapeutically significant for people suffering from TB. The ten active compounds, finally selected in this study showed desired biological activities on multiple validated molecular targets. Lead compounds were screened as a novel plant-based anti-TB compounds through molecular docking analysis.
and were confirmed as potential anti-mycobacterial agents with appropriate drug-like properties compared to the standard antimicrobial compounds viz., grepafloxacin and norfloxac</p><p>CADDD approach provided information on binding energies and binding interactions of the compounds to predict their anti-<i>Mtb</i> activities. These compounds need to be extracted from the sources or synthesize in the chemistry lab and test for their pharmacokinetic and pharmacodynamics effectiveness through various pre-clinical trials.

Structure-based drug discovery methods were applied to identify mode of interaction of therapeutic target and previously unknown bio-activities for known plant-derived data. It is significant to highlight that while finding bioactive anti-tuberculosis compounds; identification of the plant-derived compounds is also important and it will add information to chemical synthesis of novel and unique natural products which could be valuable food supplement, dietary supplements or an anti-<i>Mtb</i> medicine. In future, the results could be useful as substructures for molecular dynamic simulations and wet lab experimental studies which will not only proceed to the new vision of drug design and discovery but may offer an effective therapy for TB.

Plant-derived natural compounds have been regarded as the best sources of medicines for the treatment of many diseases including tuberculosis. Almost 80% of the world population use traditional medicines and generally, prefer plant-based drugs for primary health issues. Effective and safe use of plant-based natural products can ensure that plant-based medicines are relatively more harmonious with biologic systems.

In this work a combinatorial library was created from natural compounds, (particularly from Neem, <i>Gingko biloba</i> and Tea and some molecules from DrugBank having antimicrobial property) with antibacterial activity and their derivatives through <i>in silico</i> approaches. The selected molecules from the library were subjected to interaction study through computational approaches using relevant software against four well known drug targets of <i>Mycobacterium tuberculosis</i>. The resultant molecules with potential multiple
receptor interactions could be offered as lead molecules for subsequent synthesis and validation.

Computer-aided multi-target drug discovery approach successfully identified plant-derived active compounds with the potential to inhibit the at least three of the four important targets of \textit{Mtb} selected for the study. Some earlier reports highlighted the combined effect of plant extracts and conventional drugs that significantly enhanced the action as compared to individual drug treatment. Hence, this plant-based study might be useful in future to understand the anti-tuberculosis drug interactions.

The selected lead compounds in this structure-based study were without any predicted toxicity and showed the best binding affinity with the multiple protein targets. Therefore, the lead compounds are expected to be effective as anti-tuberculosis drugs after subsequent testing and validation. The present study could aid in the development of potential new chemical entities originated from nature for tuberculosis treatment.

In conclusion, the study using CADDD was successful in screening some new candidate molecule as anti-\textit{Mtb} agents along with knowledge of plant extracts, which possess anti-\textit{Mtb} activity by the computer-aided multi-target approach of structure-based drug designing. The idea behind use of structure-based drug discovery approach was to prevent huge cost involvement and hectic work of wet lab based conventional drug discovery approach. Through \textit{in-silico} approaches, this study could able to generate and confirm an inexpensive scheme available to the academic institutes and developing countries for identifying novel plant-based natural anti-mycobacterial compounds for the betterment of human health.