



Title	Random control study looking at the use of 1320 nm Nd:YAG laser and intense pulsed light source for non-ablative skin rejuvenation in Chinese
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DMM-05 Random control study looking at the use of 1320 nm Nd:YAG laser and intense pulsed light source for non-ablative skin rejuvenation in Chinese

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Background:

Non-ablative rejuvenation with a 1320 nm Nd:YAG laser or intense pulse light source has generated much interest. Our objective is to study and compare the use of 1320 nm Nd:YAG laser/intense pulsed light source in non-ablative skin rejuvenation in Chinese

Method:

47 patients with Glogau classification type 2 photoageing were recruited into the study and were randomized to receive treatment with either 1320nm laser, or intense pulsed light source. All have received treatment at monthly interval for at least 4 months before assessment. All patients were assessed using a structure questionnaire for the degree of improvement in term of skin texture, pigmentation and wrinkle improvement. A cutometer was used for the objective measurement of skin elasticity and firmness

Result:

For subjective degree of improvement, 37% patients treated with 1320nm Nd-YAG recorded moderate to significant improvement as compare to 20% of those treated with IPL. However, in term of pigmentation, all patients treated with IPL recorded at least mild degree of improvement as compared to 33% in the cooltouch group. Cutometer assessment indicated significant improvement in firmness and elasticity of most of the important parameters for 1320nm Nd-YAG but only some of the parameters for IPL.

Conclusion:

1320nm Nd:YAG appears to be more effective in the improvement of wrinkle than IPL. However, in term of pigment reduction, IPL appears to be more superior. A combination approach using both 1320nm Nd:YAG and IPL can be particularly applicable in the use of non-ablative skin rejuvenation for Asian.

DMM-06 Bioinformatics data mining and statistical modeling on the molecular interactions between S-adenosylmethionine decarboxylase and its substrate

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Introduction & Method: S-adenosylmethionine Decarboxylase (AdoMetDC) is a rate-limiting enzyme in polyamine synthesis pathways. Significance of its conserved amino acids in relationship to function has been studied with respect to the molecular evolution and phylogenetic division of organisms. This paper attempts to use computational technologies to align and model for the homology of 28 species of AdoMetDCs using 1JEN, the human AdoMetDC, as the template; and to study the sites of molecular interactions, atom-atom interactions and bond-lengths, and docking energies between the 28 AdoMetDCs and 2 models of AdoMet. We have applied data from studies on conserved amino acid mutagenesis, and performed Gramm docking program (3D-models, bond-lengths and docking energies) and Afterdock statistics program (statistical analysis of group-distance-energy) to determine the most probable models for AdoMet and AdoMetDC interactions.

Result & Conclusion: Results indicated that the Pro225 and Pro246 of AdoMetDCs are involved in binding the adenine group of AdoMet and the Cys226 serves as an electron donor to facilitate the decarboxylation reaction, and the Ser68 undergoes serinolysis to form Pyruvol68, which in turn serves as an electron sink to break the C—COO⁻ bond from AdoMet. The sequential binding, activation and catalysis of the reaction are shown to be similar in all the 28 species of pyruvoyl-dependent AdoMetDC reactions, regardless of their highly variation of AdoMetDC amino acid sequences.

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