Synopsis 講座摘要

Herbgenomics –

Bridging Traditional Chinese Medicine and Modern Technologies

Herbgenomics is an interdisciplinary subject proposed by Professor Chen Shilin and his research team in which genomics and related omics are used to form the theoretical and technological basis for research on medicinal model organisms, genuine medicinal materials, targeted breeding of medicinal plants, molecular identification, bioactive metabolites synthetic biology and construction of herbal gene banks. In 2015, the team was invited by *Science* to publish a review titled *"Herbal Genomics: Examining the Biology of Traditional Medicines"* in its supplementary issue to elucidate the concept and application of herbgenomics. Apart from having sequenced more than 100 medicinal organism genomes so far including those of *Ganoderma lucidum, Panax ginseng*, *Salvia miltiorrhiza*, *Perilla frutescens, Selaginella tamariscina, Andrographis paniculate* and *Coptis chinensis*, the team has also released the "Global Pharmacopoeia Genome Database", an integrated and mineable database incorporating herb genomic data from international pharmacopoeias. In addition, Professor Chen has carried out quite a number of studies on the authentication of medicinal herbs, herbal drug safety, biosynthetic pathways of pharmacologically active ingredients and molecular breeding of good varieties. Relevant research findings were published in top-tier international academic journals including *Science, Nature Communications, Molecular Plants*, and *PNAS*. Being a focus area of TCM research and an important driving force for the modernisation of TCM, herbgenomics has been included in the undergraduate and postgraduate curricula of a number of universities and colleges in Mainland China.

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The team’s genomic research has laid a solid foundation for the application of species like *Ganoderma lucidum* and *Salvia miltiorrhiiza* as medicinal model organisms. In particular, their study on *Ganoderma lucidum*, in which genomics was used as the basis to elaborate how the genetic mechanism of traits contributing to high yield, fine quality, high disease resistance and high stress tolerance could enhance selection efficiency and accelerate the breeding process, was featured as one of the Research Highlights in *Nature China* and reported by *USA Today* in an article entitled “*Chinese ‘Mushroom of Immortality’ Genome Mapped*”. This new strategy was successfully deployed by the team to breed cultivars of medicinal herbs such as *Panax ginseng*, *Panax notoginseng*, *Perilla frutescens*, *Artemisia annua* and *Gastrodia elata*, which demonstrated that herbgenomics plays a pivotal role in molecular-assisted breeding.

“DNA barcoding system for identification of medicinal species” is another iconic study led by Professor Chen. Not only has it been included in the Pharmacopoeia of the People's Republic of China, it has also won a host of honours including Second Prize of The State Scientific and Technological Progress Award, 2016 Top 10 Medical Advancement in China, and the International Award for Contribution to Chinese Medicine from the World Federation of Chinese Medicine Societies in 2018.

本草基因組學與中醫藥現代化

本草基因組學（Herbgenomics）是由陳士林教授及他的研究團隊提出的交叉學科，旨在通過基因組學及相關技術，為藥用模式生物、道地藥材研究、基因組輔助育種、分子鑑定、中藥活性代謝物合成生物學、基因數據庫構建等提供理論基礎和技術支撐。2015 年，團隊應邀在《科學》增刊撰文，以‘Herbal Genomics: Examining the Biology of Traditional Medicines’為題，系統闡釋本草基因組學學科的內涵和應用。迄今，團隊已完成靈芝、人參、丹參、紫蘇、卷柏、穿心蓮、黃連等過百種藥用植物的全基因組測序，並在最近推出可挖掘的集成數據庫——「全球

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藥典草藥基因組數據庫」，蘊藏來自多國藥典的傳統藥物基因組數據。此外，陳教授在草藥物種鑒定、用藥安全、藥效成分生物合成途徑解析、優良品種分子育種等方面開展了大量研究，相關論文在《科學》、《自然通訊》、《分子植物》、《美國國家科學院院刊》等國際頂級期刊發表。本草基因組學乃中草藥研究的熱點領域，在中藥現代化發展中發揮著重要作用，更獲國內多所大專院校納入研究生和本科課程。

團隊通過全基因組研究，推動靈芝、丹參等形成藥用模式生物研究體系。其中，靈芝基因組研究工作獲《自然中國》選為中國最佳研究，《今日美國》亦以「揭秘中國『仙草』基因組」為題報導。是項研究以基因組遺傳信息為基礎解析高產量、高品質、抗病、抗逆等優良性狀的遺傳機制如何提高選擇效率，加快育種進程。團隊運用此方法成功選育人參、三七、紫蘇、黃花蒿、天麻等藥用植物的優良品種，引證本草基因組學在分子輔助育種領域中發揮重大作用。

「中藥材 DNA 條形碼鑒定技術體系」是陳教授的另一標誌性研究，不僅納入《中華人民共和國藥典》，更摘下國家科技進步二等獎、獲評為「2016 年中國十大醫學進展」，並於 2018 年榮獲世界中醫藥學會聯合會頒發的中醫藥國際貢獻獎。