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研究興趣

我們最主要的興趣是在研究演化的過程與其發生的機制。我們同時也使用演化的概念來研究基因體學、結構生物學、系統生物學、譜系學、以及生物地理學。

我們使用多樣的研究技術，從分子到個體層級、從DNA到蛋白質結構、從基因體到蛋白質體、從實驗操作到計算分析，另外也發展生物資訊方法與工具來解決上述問題。

目前研究方向

• 生物資訊工具及其應用

- 我們試圖發展一個簡單的方法讓使用者可以方便又便宜地辨識其所感興趣的微生物。在這些微生物的全基因體資訊已事先被定序的前提下，使用者只要指定一群他所需要辨識區分的物種，我們的演算法就可以設計出數個適當的引子，讓使用者只需透過PCR及電泳就可識別其目標物種。
- 我們也發展了一個新的偵測水平基因轉移(HGT)事件的演算法，可用來研究水平基因轉移事件對這些微生物在演化上的影響情況。

• 計算基因體學

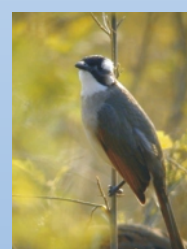
- 同義密碼子使用偏差是一個普遍存在於各類生物基因體中的現象，描述不同的同義密碼子其使用頻率有不同的偏好程度。我們試圖釐清密碼子在不同物種間，其使用偏好轉變的演化驅動力。我們也比較了病毒與宿主的密碼子使用偏差以探討他們之間的適應性演化關係。
- 我們研究了mir-302叢集以及C19MC叢集的演化歷史。在研究過程中，我們也偶然地發現數個在胎盤動物中microRNA透過L1 (一種反轉錄轉位子)協助，複製自己產生新的同源基因的事件。
- 另外，在與客家學院的合作計劃中，我們利用微陣列晶片所取得的基因體資料分析研究了台灣的客家人與福老人的遺傳結構與組成源流。

• 計算結構生物學

- 我們結合了分子動力學模擬 (MD)以及譜系學研究方法，來研究蛋白質結構的演化。

• 譜系學、系統分類學、生物地理學

- 台灣的黑頭翁與烏頭翁分布在中央山脈兩側，且型態各異。我們試圖利用次世代定序(NGS)收集它們的基因體資料，來研究它們的演化歷史以及種化的機制。





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Research Interests

Our major interest is in the processes and mechanisms of Evolution. We also use evolutionary concepts to study Genomics, Structural Biology, Systems Biology, Phylogenetics and Biogeography.

We use a wide range of research techniques,

from the molecular to the organismal level, from DNA sequences to protein structures, from genomics to proteomics, and from experimental to computational studies, including developing Bioinformatic methods and tools, to study these problems.

Current projects

• Bioinformatics Tools and Applications

- We attempted to develop a simple method for users to easily and costlessly identify their targeted micro-organisms as long as their whole genome sequences are available. After users designating their possible targeted micro-organisms, our method would design a few specific primers and users could simply use PCR and electrophoresis to discriminate these micro-organisms.
- We also developed another novel algorithm to detect horizontal gene transfer (HGT) events among these micro-organisms, which could be used to study the evolutionary impacts of HGT.

• Computational Genomics

- Synonymous codon usage bias (the differences in the occurring frequency of synonymous codons) is frequently found in various organisms' genomes. We attempted to clarify the evolutionary driving forces of the switch of codon usage preference in different organisms. We also tried to compare the codon usage bias of viruses and their hosts to investigate their adaptive evolution.

- We studied the evolutionary history of mir-302 cluster and C19MC (chromosome 19 microRNA cluster). Occasionally, we found several microRNA retrocopies emerged via L1-mediated retrotransposition events in placenta species.
- On the other hand, by cooperating with the College of Hakka Studies, we used microarray genotyping data to study the genetic structure and composition of genetic diversity in Taiwanese Hakka and Hoklo populations.

• Computational Structural Biology

- We incorporated molecular dynamics (MD) and phylogenetic analyses to study the evolution of proteins.

• Phylogenetics, Systematics, and Biogeography

The two morphologically diverged bulbuls *Pycnonotus sinensis formosae* & *P. taivanus* distributed in Taiwan are completely separated by The Central Mountain Range. We are working on their evolutionary history and speciation mechanism by genomic information collected from next generation sequencing (NGS) data.

