明治大学グローバルCOEプログラム【現象数理学の形成と発展】

第10回 MEE SEMINAR

MATHEMATICAL ECOLOGY & EVOLUTION

2009年11月10日(火) 14：40～16：10

明治大学生田キャンパス第二校舎A館：A207

小田急小田原線　「生田駅」から徒歩10分
又は「向ケ丘遊園」駅北口から「明治大学正門前」行きバスで10分終点下車
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Adaptive evolution in humans revealed by the negative correlation between the two phases of molecular evolution: polymorphism and fixation

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Abstract:

Selective forces on amino acid substitutions may be different in the two phases of molecular evolution; polymorphism and fixation. Negative selection and drift may dominate the first phase whereas positive selection may become much more significant in the second. However, the conventional dichotomy of synonymous vs. nonsynonymous changes does not offer the resolution needed to correlate the two phases. We separated amino acid changes into 75 elementary types (1 bp substitution between their respective codons). The likelihood of each type of amino acid change to become polymorphic (PI, for polymorphic index), relative to synonymous changes, can then be calculated. Similarly, the likelihood of fixation (FI, for fixation index) conditional on common polymorphism is also calculated. Using Perlegen and HapMap data on human polymorphisms and the chimpanzee sequences as the outgroup, we compared the evolutionary dynamics of the 75 elementary changes in the two phases. We found a strong and significant ($p < 0.001$) negative correlation between FI and PI. Furthermore, only those changes with low PIs show FI > 1, which is often a signature of adaptive evolution. These patterns suggest that negative and positive selection operate more effectively on the same set of amino acid changes.

参加自由です。皆様のお越しをお待ちしております。

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