Evolution can beat disease

Evolutionary principles and tools harbour the potential to revolutionize the struggle against medical challenges such as antibiotic resistance, infectious disease and cancer.

Darwinian evolution explains the proliferation of microbial and viral systems. These systems are characterized by groups of genetically related individuals that carry different beneficial mutations. Their evolutionary dynamics follow the traditional model of clonal interference — high mutation rates provide plenty of genetic variation for selection to act on, driving the rise or fall of clones. Clonal interference is typical of large populations of asexual organisms subject to strong selection; it has been demonstrated in microbial and viral systems but drives the evolution of cancer and adaptive immune repertoires as well. In a previous issue of *Nature Ecology & Evolution*, Lässig et al. argued that the complexity of these evolutionary dynamics can be exploited to predict, and ultimately control, evolution (*Nat. Ecol. Evol.* **1**, 0077; 2017).

In this issue, we publish two Comments that explore how evolutionary principles and methods can transform infectious-disease management and control cancer progression. Russell and de Jong explain how an understanding of pathogens' fitness landscapes is essential to circumvent the evolution of resistance to antibiotic treatment and to design effective influenza vaccines. von Loga and Gerlinger argue that the ability of tumours to evolve is a neglected but essential problem in cancer medicine.

Sequencing data have revealed tremendous genetic variation in different parts of tumours in most cancer types. This intratumour genetic heterogeneity is the fuel for Darwinian selection. Nevertheless, both neutral evolution and selection can operate in the same tumour in different regions or at different times. Thus, characterizing genetic intratumour heterogeneity is a useful first step, but is not the finish line. To develop therapies that control cancer evolution and stop tumour progression we must identify the multiple selection pressures in primary tumours and metastases, and understand how they shape cancer genotypes and phenotypes.

Factors such as high recombination rates and host population structure add complexity to the evolutionary dynamics of pathogens. Similarly, chromosomal alterations and the spatial structure of solid tumours make the study of cancer evolution particularly challenging. Evolutionary biologists rely on powerful tools such as phylogenetic methods, population genetics and computer simulations of evolutionary models. With modifications to accommodate the complexity of pathogens and cancer, such tools can be applied to understand the evolutionary dynamics of these systems. We can then use that knowledge to develop refined therapies that control pathogen and cancer evolution and prevent acquisition of drug resistance.

Another evolutionary problem shared by pathogens and cancer cells is the selective pressure imposed by the immune system. Incorporating an understanding of the evolutionary trajectories of the host's immune system in response to microbial or viral infection or vaccination may help to improve vaccine design. Similarly, once we understand how the cancer genome changes in response to immune surveillance, we can design therapies that harness the immune system to fight tumour progression.

Both Comments call for evolutionary biologists, disease researchers and clinicians to join forces to control disease. The development of evolutionary tools to address the specifics of systems such as pathogens or cancer can only be achieved if evolutionary biologists and disease researchers work together. Similarly, applying evolutionary principles and methods to analyse the tremendous amount of data being generated in hospitals requires cross-talk between researchers and clinicians. Ultimately, translating evolutionary knowledge into novel therapeutics that control evolution is an ambitious goal that requires the united efforts of evolutionary-disease researchers and physicians.

The need to integrate basic evolutionary research and medicine to fight disease defines the mission of the International Society for Evolution, Medicine and Public Health (ISEMPH), whose annual meeting takes place this month in Groningen, The Netherlands, in conjunction with the sixteenth European Society for Evolutionary Biology Meeting. This year's ISEMPH meeting includes the popular topics of pathogens, antibiotic resistance and cancer, but also others perhaps less familiar to the evolution community, such as the immune system, microbiome, sexual health and ageing. We shall be there and look forward to engaging with basic researchers and clinicians alike. ❐

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