omit an important additional dimension. In birds, sexual dimorphism in singing and song learning varies greatly among species, and sex differences in brain morphology are the most extreme documented in any vertebrate [2,3]. Differences in female song-learning strategies might be even greater than those observed in male vocal learning, ranging from no learning to learning as much as males do [3,4]. Similar to males, individual females also vary in song complexity [5] and sharing levels [6,7].

In reviewing the functional basis of different song-learning strategies, the authors group Repertoire hypotheses, which suggest learning is advantageous where female preferences select for larger repertoires, and Sharing hypotheses, which suggest that learning songs shared with neighbours leads to selective advantage. Neither hypothesis considers female song [4,5,8] or learned song preferences [4]. The authors limit the role of females to selecting for increased male repertoire size (a preference that could result from unlearned biases). However, to identify the selection pressures on song learning, female singing and learned song preferences need to be incorporated. The study of female song offers additional advantages in this respect. Not only is interspecific variation in female song learning extreme, but in many species female song production is also restricted to certain social and ecological contexts (e.g. shortage of nest sites, or facultative polygyny) [5]. This high degree of inter- and intraspecific variation facilitates the isolation of the ecological and social factors that favour particular learning strategies.

We would like to stimulate the discussion further by postulating that, given the probable Australasian origin of oscine passerines [9] and the prevalence of female song in Australian birds [10], song in both sexes could be the ancestral condition. The real challenge for phylogenetic analyses might be to identify the factors that made it advantageous for females to give up singing. 'Song phylogenies' need to consider sex differences nested within species, and the coevolution between learned male song and learned female preference [4].

We support Beecher and Brenowitz in their quest to initiate comparative and phylogenetic analyses of song learning, but suggest that further insight can be gained through investigation of the poorly understood song-learning strategies of females.

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Emerging pathogens: fungal host jumps following anthropogenic introduction

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In a recent article in *TREE* [1], Woolhouse *et al.* discuss the importance of pathogens transgressing host species barriers as a source of new emerging pathogens and consequent epidemics. One of their main conclusions is that directly transmitted RNA viruses are the most probable pathogens to undergo host jumps. However, their conclusion is influenced by the frequent usage of the term 'host jump' in the literature, where it is usually used in connection with viral diseases. Selective usage of the term will therefore tend to underemphasize the significance of other pathogen groups that are equally likely to undergo host jumps. From a mycological standpoint, only two examples of fungal pathogens are considered in the table [1] from which the primary conclusion was drawn. These are *Phytophthora infestans* (the cause of potato blight) and *Cryphonectria parasitica* (the cause of chestnut blight).

In an earlier article in *TREE* [2], Anderson *et al.* consider emerging infectious diseases (EID) of plants and

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their possible causes. They cite both the fungal pathogens listed in [1], as well as ten other examples of EIDs (30% of the total number of EIDs cited) caused by fungi. Although the concept of pathogens infecting new hosts is discussed, the term 'host jump' is mentioned only once, and then only with respect to the tomato yellow leaf curl virus. Major factors driving EID of plants [2] were considered to be anthropogenic introduction of pathogens and weather changes.

The overlap between the examples and main conclusions in these papers [1,2] is insightful. Many of the examples, including both those pertaining to the fungal pathogens discussed by Woolhouse *et al.* [1], represent host jumps following anthropogenic introduction. Conversely, many of the pathogens introduced by humans (including most fungi) in [2] also involve host jumps, although these are not typically referred to as such. The 'host jump' – 'human introduction' interaction is not surprising as it exposes hosts to pathogens for which the hosts have no coevolved recognition or defense mechanisms.

Host jumps are common for fungal pathogens [3]. In some cases, these occur more commonly than does cospeciation (e.g. a study of *Puccinia* rusts of crucifers showed that patterns of cospeciation and coevolution with the hosts were rare, whereas host jumps to geographically associated hosts were frequent [4]). Among the many other examples is the rust pathogen *Puccinia psidii*, which jumped from native Myrtaceae to introduced *Eucalyptus* trees in South America [5]; *Cronartium ribicola*, an Asian Pine rust, jumped to new *Pinus* species in Europe and North America, causing a devastating epidemic that is still underway more than a decade after its introduction [6]; *Fusarium circinatum* resulted in the pitch canker disease epidemic on *Pinus radiata* in California, following its introduction into that area from native Mexican pines [7]; and various species of *Chrysoporthe* (previously *Cryphonectria cubensis*) cause devastating diseases of introduced *Eucalyptus* spp., as well as various native Myrtaceae and Melostomataceae, in South-east Asia, South America and Africa, jumping between these hosts [3,8].

Based on current trends, as well as RNA viruses, fungi are also likely to undergo increasing numbers of plant host jumps. This is due to the increasing spread of fungi worldwide as a result of anthropogenic movement, as well as global weather changes that negatively affect host-plant communities [2]. Hybridizations or recombination of introduced fungal pathogens with related resident fungi often result in strains that can infect an expanded range of hosts [8,9]. Many fungal pathogens also have relatively broad host ranges, identified as one of the factors common to organisms that are particularly prone to jump hosts [1].

Similar to viruses, fungal host jumps often cause significant disease epidemics, in many cases threatening the new hosts with extinction. The connection between host jumps and anthropogenic introduction lends new significance to the need for quarantine measures to prevent the accidental movement of fungi into new areas. The evolution of host jumps is a neglected concept in plant pathology that calls for more-focused attention (e.g. [10]), especially given its importance in EID.

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Sense and stability in animal names

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The way in which animals are given scientific names (zoological nomenclature) has recently attracted much media coverage (e.g. 'Turkey renames 'divisive' animals', http://news.bbc.co.uk/2/hi/europe/4328285.stm; and 'Bush has slime-mold beetle named after him', http://www.cnn.com/2005/TECH/science/04/14/bush.beetle.ap/). In addition to these and other stories, the proponents of the PhyloCode (http://www.ohiou.edu/phylocode/), an alternative system for naming organisms, have been pushing their cause relentlessly. The time seems appropriate to

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