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When all identified strains of *M. cosmeticum* are considered, this species is clearly present in diverse geographic regions and in healthcare institutions. These findings suggest that it may be widely distributed in the environment and should be regarded, along with other rapidly growing mycobacteria species, as a potential pathogen.

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Ecoregional Dominance in Spatial Distribution of Avian Influenza (H5N1) Outbreaks

To the Editor: Recent articles in *Emerging Infectious Diseases* (1,2) and elsewhere (3,4) have highlighted the role of Anatidae migration in dispersal of the H5N1 subtype of highly pathogenic avian influenza (HPAI) virus. Although these articles point out that identifying the geographic origin of migrating waterfowl is needed to understand and predict pathogen dispersal, study analyses have been limited to pathways with nominal reference to climatic and vegetation patterns that control spatiotemporal patterns of this migration.

We propose that a better understanding of the threat of future spread can be obtained by identifying specific climatic and vegetation zones that are important in the life cycle of Anatidae, and which account for a disproportionately large number of HPAI outbreaks. The concept of ecoregions (5,6), i.e., distinct assemblages of natural communities determined by climate, geology, and evolution, is a useful zonal classification for evaluating HPAI outbreaks. A World Wildlife Fund classification delineating 825 terrestrial ecoregions (7), combined with a Google Earth map of 3,133 avian influenza outbreaks from November 24, 2003, to November 21, 2006 (8), provided the basis for this analysis.

All files were converted to shapefiles (Environmental Systems Research Institute, Redlands, CA, USA), and overlay analysis was performed by using ArcGIS software (Environmental Systems Research Institute).

The online Appendix Figure (available from www.cdc.gov/EID/content/13/8/1269-appG.htm) shows a choropleth map (display of quantitative or qualitative information about subentities in terms of symbols or colors) of ecoregions with numbers of avian influenza cases (each spatially and temporally isolated set of individual events, regardless of number of deaths, is recorded as a case). Panels A, B, and C of this figure show enlargements of specific ecoregions with large numbers of known cases in regions of Eurasia, Southeast Asia, and Africa, respectively. Twenty-five ecoregions, representing 8.8% of the terrestrial surface area, accounted for 2,407 (76.8%) cases. A total of 132 of 825 ecoregional classifications had ≥ 1 recorded case of an avian influenza outbreak, but most (83) had < 10 cases each.

Regionally, Southeast Asia has 12 ecoregions that collectively account for 1,651 cases (online Appendix Figure, panel B) that have occurred consistently, albeit cyclically, since 2003. Among these ecoregions, the freshwater wetlands of the Chao Phraya, Tonle Sap, and Red Rivers are known migratory waterfowl wintering habitats in which 719 cases were located. Recent phylogenetic evidence suggests that this area is a local hotspot for an endemic strain of avian influenza (H5N1) that demonstrates bidirectional dispersal among localities within the region (9).

In the Eurasian region (online Appendix Figure, panel A), 12 ecoregions accounted for 712 cases. The easternmost ecoregions, the Kazakh forest steppe (location of Lake Chany, an Anatidae habitat and breeding area) and the Kazakh Steppe, accounted for 132 cases, with the first case recorded

on July 18, 2005. Subsequent major outbreaks in this region occurred in July–August 2005 and December 2005–January 2006. Regions around the Black Sea, including Euxine-Colchic broadleaf forests (deltas of the Kizil and Yesil Rivers), westernmost Pontic steppe (Lake Sivash), and Balkan mixed forests (deltas of the Danube, Olt, and Siret Rivers) have been loci for outbreaks in the central Eurasian region since October 1, 2005. Additional outbreaks have occurred since October 21, 2005, in the Eastern Anatolia montane steppe and deciduous forests (location of Lakes Van and Urmia, and Karakaya and Keban Baraji Reservoirs). Mixed and broadleaf forests of central and western Europe account for the remaining European cases since October 19, 2005. Anatidae habitats in this area include freshwater wetlands formed by the Danube, Rhine, Rhone, and Saone Rivers, and the Baltic basin.

Two African ecoregions, the Nile Delta–flooded savanna (online Appendix Figure, panel A) and the West Sudanian savanna (online Appendix Figure, panel C), including part of the Lake Chad ecosystem, i.e., the Kano River and the Tiga Reservoir, accounted for 79 cases. The initial Sudanian savanna case was identified on January 10, 2006, and the initial Nile Delta case was identified on February 17, 2006.

Our results may be skewed by several confounding factors, e.g., low national surveillance capabilities resulting in unreported cases and effects of the poultry trade. Nonetheless, the findings have implications for global monitoring of avian influenza (H5N1) outbreaks. Although migratory pathways and the poultry trade should continue to be scrutinized, monitoring efforts should focus on wintering and breeding habitats of migrating waterfowl, especially wetlands located within ecoregions with a disproportionately large number of avian influenza outbreaks. These hotspots

are also likely to give rise to endemic local strains with regional dispersal characteristics (9).

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In Response: Ecoregions are large units of land that reflect the distribution of species and communities and are used to define priority areas for biodiversity conservation. In their letter (1), Sengupta et al. suggest that ecoregions could help explain the spatial distribution of observed outbreaks of HPAI (H5N1). Since most outbreaks they observed occurred in ecoregions with waterfowl habitats, they concluded that monitoring efforts should focus on these areas.

Habitat mapping is useful for predicting the spread of wildlife-associated diseases. However, because ecoregions are large areas where agriculture and other human activities abound, many confounding variables exist. To assume that ecoregions with HPAI (H5N1) outbreaks are chiefly characterized by the natural biotopes is too simplistic.

In addition, the authors assume that wild waterfowl are the main factors in the dispersal of HPAI (H5N1). Although wild birds are known to be involved in the dispersal of low pathogenic strains of avian influenza viruses (2,3), the precise role of these birds in the dispersal of HPAI (H5N1) viruses remains controversial. It is now clear that the expansion of HPAI (H5N1) in Asia and to Africa was primarily associated with the poultry trade (4), which is not represented on a map of ecoregions. Also noteworthy is that HPAI (H5N1) did not persist in wild birds after the spring of 2006, and no case has been detected in the wetlands of America despite the migration of wild ducks and waders from Siberia (their main breeding ground) to Asia, Europe, and North America.

We believe that human activity is the primary vehicle for the spread of HPAI (H5N1) virus. Rather than the monitoring of waterfowl habitats, increased surveillance of the legal and illegal trade of birds and bird products is more likely to help in predicting the spread of this virus.

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In Response: Sengupta et al. (1) discuss the role of ecoregions in the distribution of HPAI (H5N1) outbreaks. Although the concept of ecoregions is undoubtedly useful in global biogeography, we do not understand the point they are trying to make. In our article (2), which is cited in their letter, we undertook a descriptive study to determine whether spread of HPAI (H5N1) virus was consistent in time with ecologic drivers of bird migration and in space with distribution of major migratory flyways of Anatidae. It is obvious that the distribu-

tion pattern of Anatidae is dependent on ecologic variables, and some of these variables are summarized by the ecoregion concept.

However, apart from a strictly descriptive point of view, we do not see how the ecoregion concept applies to describe patterns in HPAI (H5N1) spread and distribution. Sengupta et al. list ecoregions where reports of HPAI (H5N1) were concentrated. However, what do they infer from this? They observe regions with many reports of HPAI (H5N1) and conclude that these ecoregions are at risk. We find this reasoning completely circular, and any geographic zonation would provide the same observation. They may mean that ecoregions define boundaries within which secondary spread of HPAI is more likely than across ecoregions. However, this hypothesis would need to be more clearly demonstrated and quantified before the ecoregion concept can be used for global monitoring of HPAI (H5N1) outbreaks.

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**Nephropathia
Epidemica in
Metropolitan Area,
Germany**

To the Editor: Old World hantaviruses (family *Bunyviridae*) are rodentborne pathogens that can cause hemorrhagic fever with renal syndrome (HFRS) (1). At least 3 different pathogenic hantavirus species have been detected in Europe: *Dobrava-Belgrade virus* (DOBV), *Tula virus*, and *Puumala virus* (PUUV) (1–3). Most human hantavirus infections in Europe are assigned to PUUV transmitted by bank voles (*Myodes glareolus*, formerly *Clethrionomys glareolus*). Although PUUV is thought to cause a mild form of HFRS, designated as nephropathia epidemica (NE), severe courses have been described with a case-fatality ratio of up to 0.6% (3).

Even though human hantavirus infections have sporadically been reported in Germany since 1983 (e.g., 4–7), clinically apparent hantavirus infections (HFRS, NE) did not become notifiable diseases in Germany until 2001. From 2001 through 2004, ≈140 to 240 cases per year have officially been documented in Germany; most were caused by PUUV. Regions endemic for PUUV have been identified in southern Germany, especially the Alb-Danube region (4,6,8). Since 2004, 2 aspects of the situation in Germany have changed. First, the number of clinical cases has increased dramatically to a total of 448 in 2005. Second, hantavirus infections have been observed in regions previously not recognized as endemic for hantaviruses (9). An increased number of human cases were also observed in other European countries (10).

Here we report the first, to our knowledge, documented PUUV-associated urban NE outbreak, which occurred in a city park in Germany. In 2005, a total of 89 cases were reported in the district of Cologne with