Projections of Climate Impacts on Vector-Borne Diseases and Valley Fever in Arizona

Building Resilience Against Climate Effects

December 2017

Coordinating Lead Authors

Matthew Roach (Arizona Department of Health Services, Office of Environmental Health), Heidi E. Brown (University of Arizona, College of Public Health).

Lead Authors

Robert Clark (University of Arizona, College of Public Health), David Hondula (Arizona State University, School of Geographical Sciences and Urban Planning), Joceline Lega (University of Arizona, Department of Mathematics), Quyymun Rabby (University of Arizona, College of Public Health), Nick Schweers (University of Arizona, College of Public Health), Joseph Tabor (University of Arizona, College of Public Health).

Suggested Citation

M. Roach, H. E. Brown, R. Clark, D. Hondula, J. Lega, Q. Rabby, N. Schweers, J. Tabor. (2017) Projections of Climate Impacts on Vector-Borne Diseases and Valley Fever in Arizona. A report prepared for the Arizona Department of Health Services and the United States Centers for Disease Control and Prevention Climate-Ready States and Cities Initiative.

ARIZONA DEPARTMENT OF HEALTH SERVICES

THE UNIVERSITY OF ARIZONA

CLIMAS Climate Assessment for the Southwest — A NOAA RISA TEAM

THE UNIVERSITY OF ARIZONA Institute of the ENVIRONMENT

Photo: Jo Vasquez

Table of Contents

Executive Summary

The Centers for Disease Control and Prevention (CDC) has developed the Building Resilience Against Climate Effects (BRACE) framework as a resource to health departments to aid in development of adaptation plans specific to their communities. The Arizona Department of Health Services, in collaboration with the University of Arizona, continued the BRACE framework with this overview utilizing climate predictions to estimate future infectious disease risk in Arizona.

This Projections document builds on the Vulnerability Assessment by focusing on two health hazards with infectious causes that are associated with climate and important to Arizona in particular: West Nile virus disease and Valley fever. These two diseases were selected because of their impact on Arizona as well as the state of the scientific evidence to build the projections. The Projections document is divided into two sections:

— Review of the Vulnerability Assessment: a brief review of the diseases of concern in Arizona described in the Vulnerability Assessment.

— The Projections: each disease is treated separately, first with a review of their link to climate followed by projections and limitations based on current scientific evidence.

   o For West Nile virus, the projections show an extension of the mosquito activity season and a location-specific change in mosquito abundance.

   o For Valley fever, development of quantitative projections continue to be a challenge due to scientific limitations.

Photo: Dan Ferguson

BRACE Framework

To facilitate state and local health departments' preparation for the health effects of climate-sensitive hazards, the CDC developed the Building Resilience Against Climate Effects (BRACE) framework. The BRACE framework outlines five steps (Figure 1) health officials can follow to develop plans and programs to communicate with the public and prepare for the health effects of climate-sensitive hazards with partner organizations. Sixteen US states and two large cities have begun efforts to implement the BRACE framework and complete the five-step process. The ultimate goal of the BRACE framework is to provide resources to health departments to aid in developing adaptation plans specifically suited for their communities.

Figure 1. Steps in the BRACE (Building Resilience Against Climate Effects) framework (Hess et al. 2014).

The Arizona Department of Health Services in collaboration with the University of Arizona completed step one of the BRACE framework for vector-borne diseases and Valley fever. The diseases reviewed were selected based on their burden in Arizona and the degree to which they will be affected by climate. This report informs the second step, Projecting the Disease Burden for those diseases identified in Step 1: the Vulnerability Assessment. Projecting the Disease Burden is a continuation of the BRACE framework with a greater focus on the overall health risks. In this document, we describe how climate models are used to identify how changes in environmental hazards may influence morbidity and mortality in Arizona. We focus on the same two diseases as the previous BRACE Step, West Nile virus disease and Valley fever, and provide evidence-based quantitative projections of climate impacts for West Nile virus vector abundance.

Vulnerability Assessment

Step 1: The Vulnerability Assessment provided a review of the evidence supporting climate-related infectious diseases in the Southwest and Arizona. The Assessment highlighted two diseases of concern due to their association with climate and their impact on Arizona and the US Southwest—West Nile virus disease and Valley fever. A US Census block level social vulnerability analysis was conducted, showing vulnerability across Arizona to be quite variable.

Climate Related Infectious Diseases in the US Southwest

Certain infectious diseases disproportionately affect the southwestern United States (Arizona, California, Colorado, Nevada, New Mexico, and Utah). Specifically, the vast majority of Valley fever and plague cases occur in this region (data extracted from CDC Summary of Notifiable Diseases, 2005-2014 and CDC 2013; Figure 2). Despite that this region is home to only 18.0% of the US population, it accounts for approximately 58.8% of Hantavirus Pulmonary Syndrome (HPS) and 30.1% of the West Nile virus cases.
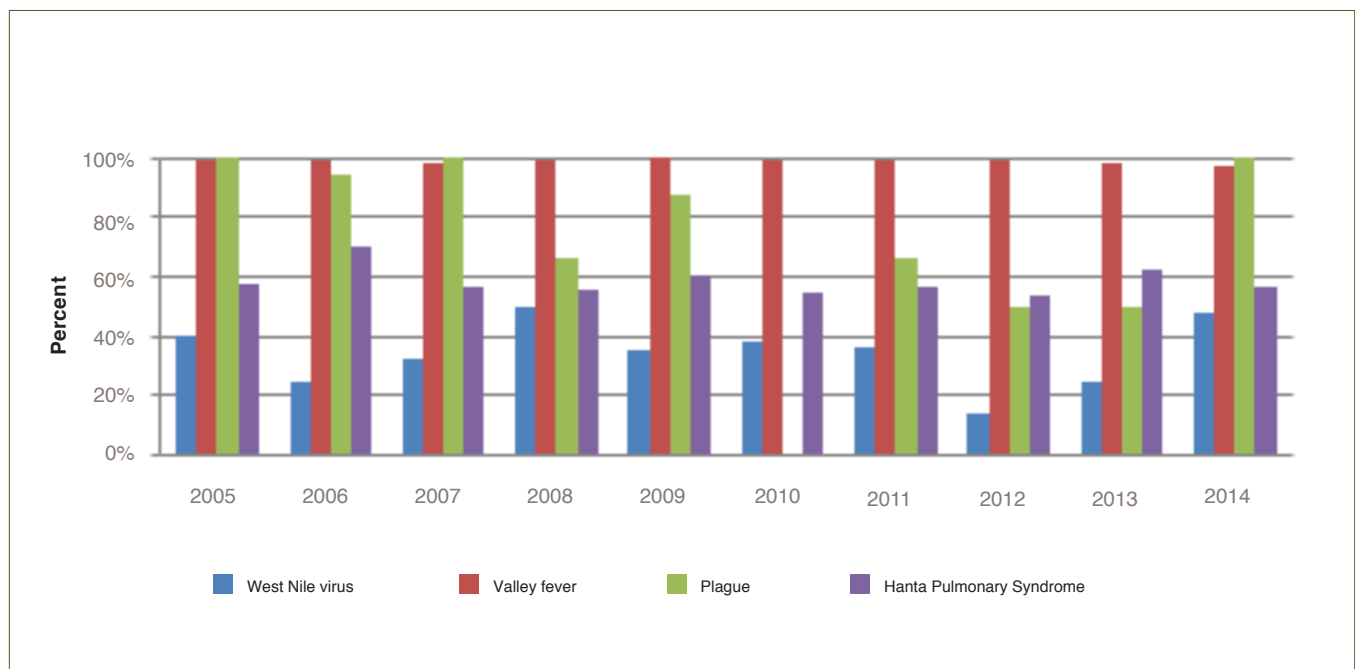

Figure 2. Incidence of selected vector-borne and zoonotic diseases occurring in the Southwest as a percentage of the total reported cases in the United States. The proportion of the West Nile virus disease, Valley fever, and Hantavirus Pulmonary Syndrome cases reported annually from the Southwest to the CDC are fairly consistent from year to year. The data for plague are more variable, as expected for a disease that rarely causes human cases (2 cases of plague were reported in the US in 2010; both in Oregon). *2010 Valley fever data do not include CO in estimate. Data source: CDC MMWRs 2007-2016.

Case Studies: Diseases of Concern

While Arizona accounts for approximately 2.1% of the total US population, 69.0% of Valley fever cases and 4.2% of West Nile virus disease cases were reported in Arizona from 2005 to 2012 (CDC Summary of Notifiable Diseases, 2005-2012). These two diseases, which inflict a considerable burden on the populations in the Southwest and Arizona, are strongly affected by climate, specifically temperature and precipitation. Within Arizona, both diseases tend to be reported with higher incidence in southern counties (Figure 3).

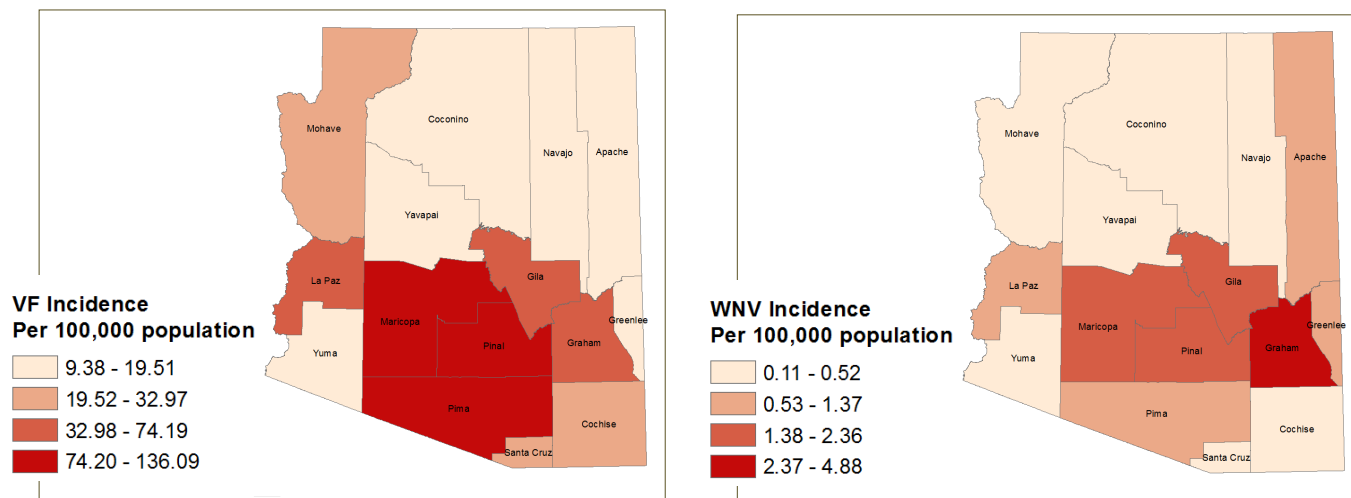# Incidence of Valley Fever and West Nile Virus per 100,000 by County, 2001-2014

Figure 3. Maps of Valley fever and West Nile virus disease in Arizona.

West Nile Virus (WNV) disease is a vector-borne zoonotic disease maintained in an avian cycle by multiple mosquito species (Greer et al. 2008). Humans and horses do not develop sufficiently high viremia to infect mosquitoes; thus, while they may contract the disease, they are not an integral part to maintaining disease transmission. Approximately 2,500 cases of WNV disease occur in the US each year (estimated from CDC Summary of Notifiable Diseases, 2005-2014) with symptoms including acute febrile illness with headache, myalgia or arthralgia, and gastrointestinal issues (Hayes et al. 2006).

Mortality is rare, occurring among those who develop the more severe West Nile neuroinvasive disease (~ 1 % of all cases with a ~ 20% case fatality rate; Sejvar 2007).

Mosquitoes of the *Culex* genus are the primary WNV vectors. In Arizona and the Southwest, two species, *Cx. tarsalis* and *Cx. quinquefasciatus*¸ are implicated (CDC 2013a; Reisen et al. 2008a). *Cx. quinquefasciatus* is generally considered an urban species, utilizing artificial containers for immature life stages (Bowden et al. 2011; DeGroote and Sugumaran 2012). *Cx. tarsalis* tends to be associated with agriculture and rural areas (Bowden et al. 2011; DeGroote and Sugumaran 2012; Cardenas et al. 2011).

Coccidioidomycosis (aka Valley fever) is a fungal disease endemic to the Southwest US (CDC 2015; Figure 2). Common symptoms include fever, difficulty breathing, coughing, or acute or subacute pneumonic illness (Petersen et al. 2004; Galgiani et al. 2016). Symptoms in most patients with early infection will subside without antifungal therapy. However, when the disease has progressed to complicated pulmonary disease and disseminated infection, long-term antifungal therapy is often required (Galgiani et al. 2016). Of those infected, only 40% develop disease symptoms that might be diagnosed. Nearly all people infected develop lifelong immunity. The number of reported cases in Arizona has been increasing over time (Figure 4). Improved diagnosis and surveillance resulting from changes in reporting requirements and increased awareness among physicians and the general population likely contributed to the observed changes. Although susceptible residents moving to the endemic areas or increased soil disturbance from construction activities are also likely contributors, they do not account for the magnitude of the increase in cases nor match the temporal changes in growth.
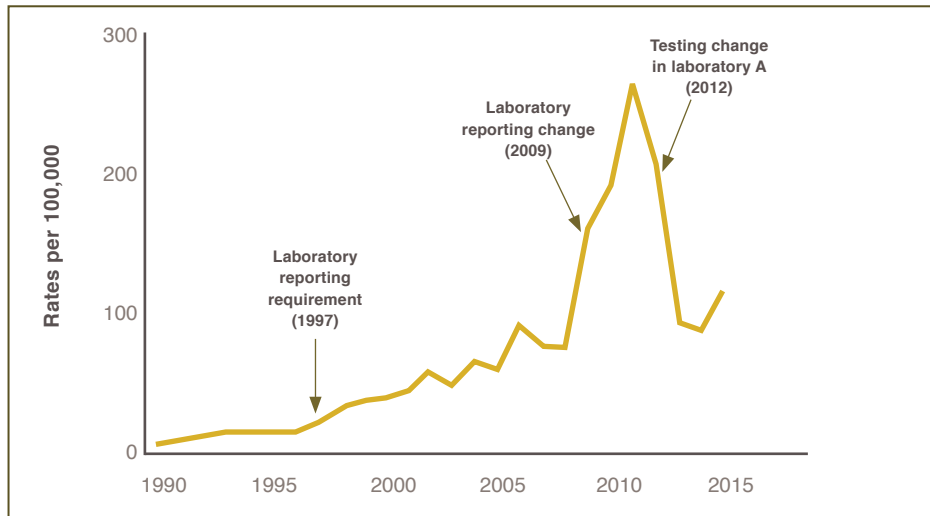
Figure 4. Reported cases of Valley fever in Arizona per 100,000. Until 2012, the reported number of cases has been increasing though changes in reporting requirements and diagnostics greatly influence observed trends. Source: ADHS 2015 Valley Fever Annual Report.

The agents that cause Valley fever are soil borne fungi, *Coccidioides* spp. They are more commonly associated with desert habitats (Maddy et al. 1960). Since the 1940s, environmental sampling results have indicated that rain facilitates fungal growth and subsequent drying allows the spores to mature and be disseminated (Emmons 1942). Temporally and spatially specific case data also show seasonal trends associated with dry and wet periods. In Arizona, a peak of cases are reported in May and another in September for Tucson, while a September peak is often reported in Phoenix (Hugenholtz 1957; Tamerius and Comrie 2011).

Projecting Disease Burden and Climate

After assessing key public health vulnerabilities in BRACE Step 1, projecting disease burden is the second step of the BRACE framework. Ideally, this step includes developing quantitative estimates of future disease burden which can facilitate ranking and prioritizing health outcomes. These estimates would then feed into the rest of the BRACE framework to help assess interventions, develop and implement an adaptation plan and, finally, to evaluate and improve the quality of those adaptation activities.

BRACE Step 2: Projections

As outlined by BRACE, projecting disease burden, involves first developing a causal pathway to understand the process by which the disease will be affected by climate. This causal pathway helps model development by identifying components which should be included, provided there are data available for parameterizing the models. Each disease system for which projections are to be generated must be modeled separately. When models for a given disease can be created, empirical data about vector, host, and pathogen temperature response are derived from new studies or the established literature. Models are tested on current data to confirm they are adequately depicting the disease system and a baseline is generated which can be compared with future estimates. Next, global climate models are downscaled to provide input data for models of future disease risk. Finally, the error or uncertainty of the estimates should be described and discussed with respect to the disease system.

The success of developing a model to estimate future burden of disease relies on the ability to explicitly model how the current system responds to climate. Quantitative analysis on weather patterns and the resulting impact on health for each specific hazard are difficult to perform due to the complexity of health outcomes and limitations in weather specific empirical data to build the models. Although models for direct effects like heat-related illness have been created, fewer models exist for vector-borne diseases.

West Nile Virus

The abundance (how many) and distribution (where they occur) of mosquitoes are dictated by the climate they experience. The immature (egg, larval, and pupal) stages of mosquitoes require aquatic environments to complete their development. Depending on the species, human activities (e.g., agriculture, home watering, and neglected pools), precipitation, or naturally occurring water bodies may be sources for immature habitat. Temperature also influences the abundance and distribution, the speed of immature development, the survival of all stages, and the host seeking and dispersal behavior of adults. While upper and lower temperature thresholds halt development and reduce survival of all mosquito life stages, warming is usually associated with faster development. Disease occurs where a greater abundance of mosquitoes increases the probability of susceptible individuals being bitten if the bites are infectious.

Projecting vector-borne disease burden requires quantitative estimates of how vectors, hosts, and virus currently respond to climate stressors and estimates of how they will respond and adapt to future climate stressors. Most of the work in projecting future vector-borne disease risk is limited to the expected responses of the vector (i.e., modeling entomologic risk rather than disease occurrence) because vectors can be reared in the laboratory under constant temperatures and their development rates recorded. By applying future climate scenarios to the empirically derived development rates, we can then project future vector abundance, assuming no adaptation occurs. Similarly, taking into account the extrinsic incubation period (time it takes for a vector to become infectious after feeding on an infectious blood meal), we can estimate the proportion of vectors that might be infectious. Again, controlled experiments in the laboratory help to parameterize models which include the effects on the pathogen.

Humans present an additional challenge as they too will respond to the weather they by going indoors, applying insecticides or wearing protective clothing, and reducing breeding sources (Figure 5). Similarly, birds, which are important hosts for West Nile virus, may change their behavior (e.g., nesting, roosting at different times of day) in response to weather. Although vectors are weather sensitive, the vector-borne diseases are not expected to cause major epidemics in the US if the public health infrastructure is maintained or improved (Gubler et al. 2001). This reinforces the importance of a vulnerability assessment and the capacity of a population to respond with respect to estimating future disease burden. While the tools exist to confidently model mosquito abundance in response to climate, without being able to model human behavior, we are still limited in being able to predict changes in disease risk (Eisen and Moore 2013).
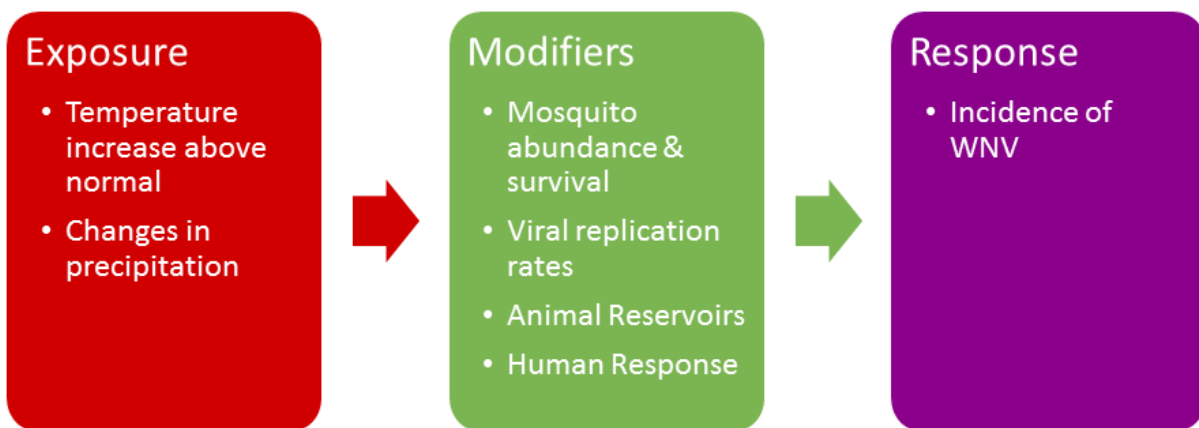

Figure 5. Causal pathway for projecting vector-borne disease burden: Mosquito vector, WNV. Conceptually, temperature and precipitation changes are the exposure to which mosquitoes, and hosts are subjected; the interaction of those results in changes in the incidence of WNV disease.
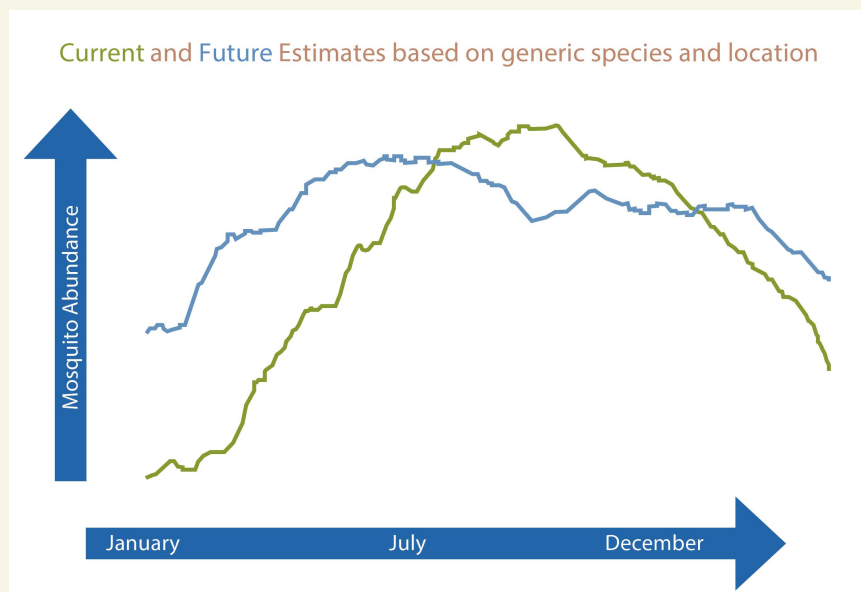
State of the Science

Limiting the discussion to changes in entomologic risk help focus on the piece of the puzzle with the most quantitative data available. Fluctuations in weather patterns affect infectious diseases, such as vector-borne diseases, in three primary ways: increased range and/or abundance of vectors and reservoirs, prolonged transmission cycles, and introduction into new regions due to migration patterns of animals and people (Gage et al. 2008; Greer et al. 2008).

Generally, precipitation augments available breeding habitat and the associated changes in humidity influence mosquito survival. However, there is mixed understanding associated with predicting the magnitude and timing of future precipitation events (Paz and Albersheim, 2008). Increasing temperatures are expected to shorten the developmental time of mosquitoes thereby shortening generation times, potentially increasing mosquito abundance. How long a mosquito survives is critical to disease transmission as a female mosquito must first take an infectious blood meal, survive the time period for the virus to replicate and migrate to the salivary glands, then successfully feed a second time. This period of time, known as the extrinsic incubation period, is also influenced by temperature.

Additional modifying factors include host behavior: whether there are sufficient and abundant maintenance hosts and whether humans engage in protective behavior. The outcome of the interaction between mosquito-virus-host and the innate characteristics of each (e.g., is the vector competent, how virulent is the pathogen, are the humans susceptible?) is disease.

This generic annual abundance graph is the average of 30 simulations using one of the WNV vectors and smoothed over 30 days. It is illustrative of two key trends: 1) extension of the season and 2) changes in abundance. As evidenced by the blue line, warmer temperatures are expected to result in mosquitoes becoming active earlier in the season and remaining active longer into the fall. With a disease like WNV in which the transmission is understood to build-up in avian hosts before spilling over to humans (Hamer et al. 2009, Kilpatrick et al. 2006), this translates to both a greater abundance yielding an increased probability that hosts will be bitten and, perhaps more importantly, an increased period in which mosquitoes are actively seeking hosts and potentially becoming infected. This graph also shows an interesting mid-summer phenomenon in certain areas where a dip in abundance, (blue line: future climate) potentially due to a negative effect of extremely high summer temperatures that affect adult survival. Thus, while generally it is assumed that increased temperatures will result in increased vector abundance, in some regions there may be a decrease in vector abundance, both with indeterminate implications on disease transmission.

Current and Future Estimates based on generic species and location

Mosquito Abundance

January   July   December

Figure 6. Schematic of vector abundance over a year. This figure provides a generic annual abundance of mosquitoes under current and future climate. Shown are model estimates of mosquito abundance, based on empirically derived temperature-dependent growth rates coupled with daily temperature and precipitation survival rates.

Quantitative models of climate impacts on WNV vector abundance generally show that changes are not uniform across the U.S. necessitating local evaluations and planning. Generally across the US, a northerly expansion is expected (Chen et al. 2013; Harrigan et al. 2014; Hongho et al. 2012). Certain areas can be expected to experience an increase in vector abundance while other areas might see decreases at certain times of the year (Morin and Comrie 2013; Brown et al. 2015). Both in the spring and fall, warmer temperatures are expected to result in an extension of the period mosquitoes are active.

Less understood is how the decreases in mid-summer mosquito abundance impact WNV transmission. The question remains as to whether the chain of transmission can be broken such that incidence will go down, despite the extension of the season into the spring and fall. This question is of particular importance in places like Arizona where temperatures often reach near 104 degrees Fahrenheit – a threshold at which adult mosquito mortality increases.

There are limited studies on the impact of changing temperatures on the extrinsic incubation period, but generally warmer temperatures result in a shorter extrinsic incubation period (Dohm et al. 2002; Kilpatrick et al. 2008; Reisen et al. 2006). This has specifically been evaluated with respect to the high temperature decrease in abundance observed in some areas, where, while adult survival was negatively impacted, the extrinsic incubation period was shortened yielding a net effect of proportionally more infectious mosquitoes (Hartley et al. 2012; Brown et al. 2015).
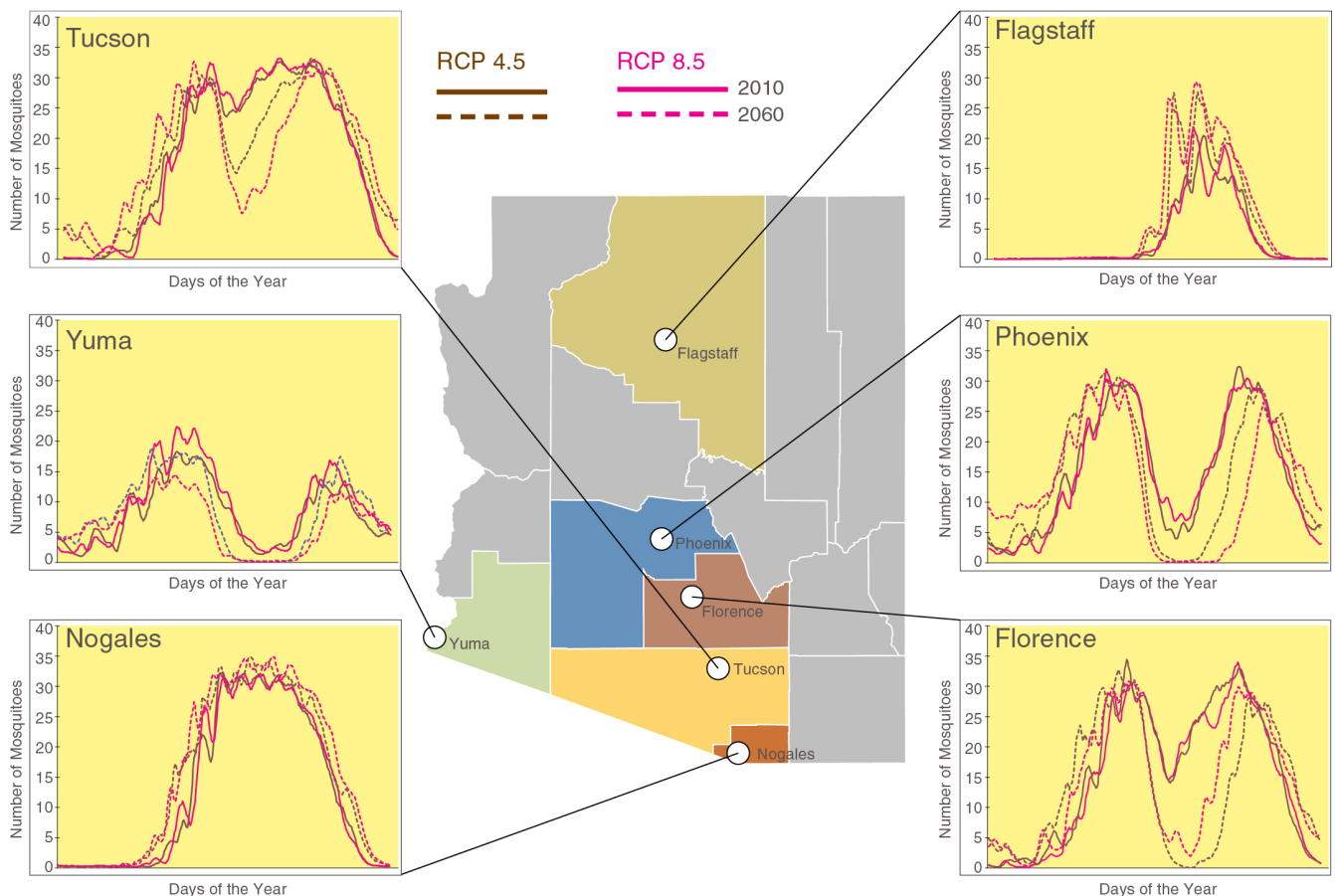
Arizona Projections

Using daily temperature and precipitation, a simulation model can be used to estimate daily abundance for the two primary West Nile virus vectors in Arizona, *Cx. quinquefasciatus* and *Cx. tarsalis* (Morin and Comrie 2010; Brown et al. 2015). The model is parameterized using temperature dependent growth and death rates. In the model, precipitation data are used to create habitat for the immature life stages. However, for these *Culex* species, the role of precipitation is limited as they are common in larger, more permanent bodies of water, which is also accounted for in the model. For example, *Cx. tarsalis* is associated with agricultural irrigation (Hayes et al. 2005), while *Cx. quinquefasciatus* is associated with larger artificial bodies of water such as neglected swimming pools (Reisen et al. 2008b; Harrigan et al. 2010). Due to the association between temperature and mosquito development and survival, future vector abundance can be estimated using downscaled data from global climate models.

For six cities in Arizona (Fig. 7 a & b: Flagstaff, Florence, Nogales, Phoenix, Tucson and Yuma), *Cx. tarsalis* and *Cx. quinquefasciatus* abundances were estimated under current (2010) and future (2060) climate for two representative concentration pathways (RCP's 4.5 (moderate emission scenario) and 8.5 (high emission scenario)). These cities were selected for their size as well as their geography (urban/rural, and across the state). The spatial resolution for the projections in these 6 locations was 1/8 degrees, which is about 9 miles at Arizona latitudes (~81 mi^2, 196 km^2). The two RCPs provide a high (RCP 8.5) and moderate (RCP 4.5) estimate for future climate. For RCP 4.5 and 8.5, daily minimum, maximum, and average temperature as well as precipitation values were generated for 2010 (baseline) and 2060. All available models were simulated, however, for the summary graphs here, the mean across all models for each location/time period combination is presented.

a. Current and Projected *Culex tarsalis* Abundance

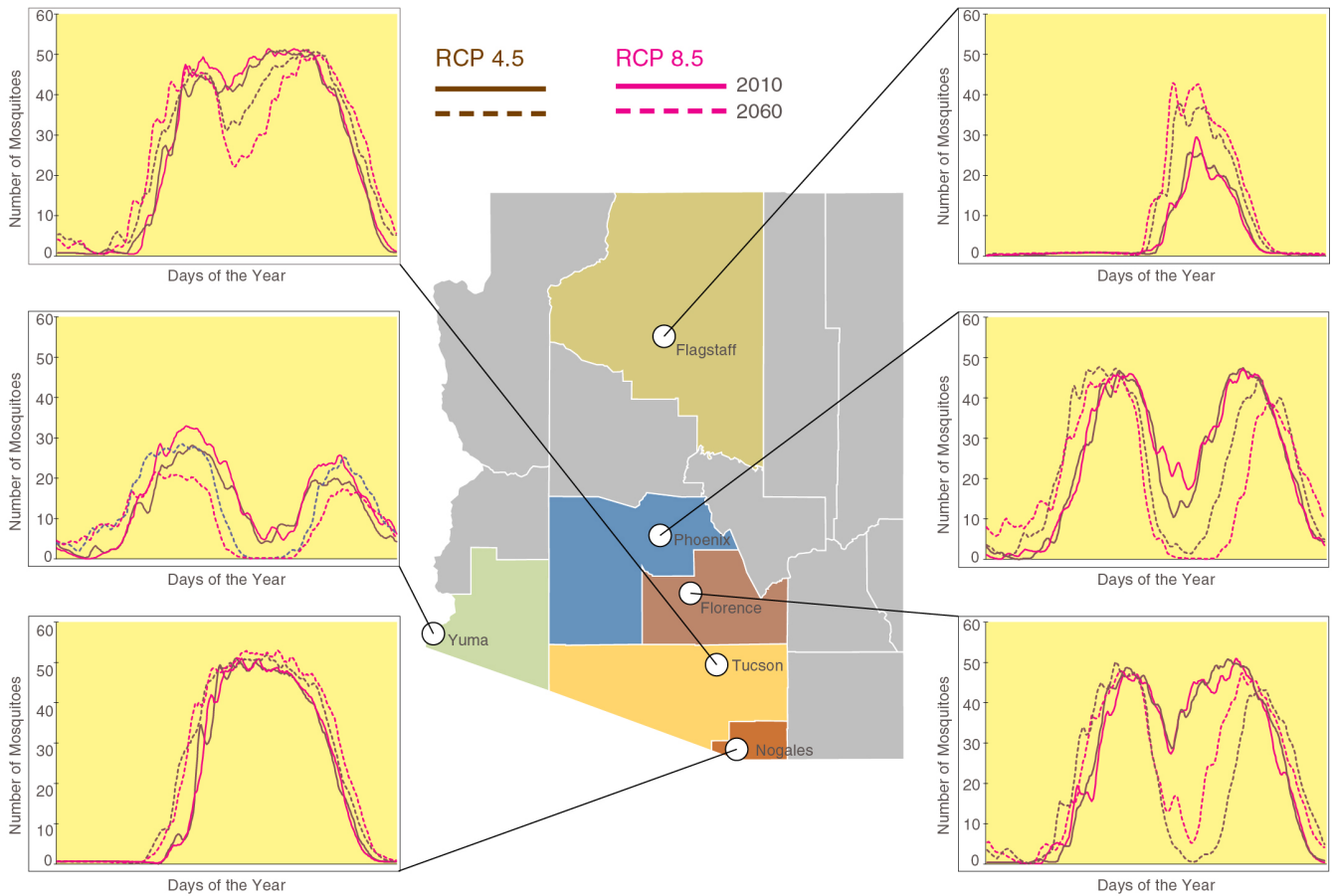# b. Current and Projected *Culex quinquefasciatus* Abundance

Figure 7. Estimated *Culex tarsalis* (a) and *Culex quinquefasciatus* (b) abundance for six Arizona cities for RCP 4.5 (brown) and 8.5 (magenta) under current (2010: solid) and future (2060: dashed) climate. Notice that the mid-summer temperatures have a negative effect on vector abundance in Phoenix, Florence, Tucson and Yuma for both species. Based on these estimates, seasonal mosquito dynamics in Florence in 2060 might begin to more similarly mirror current Phoenix vector dynamics. Nogales seems relatively unchanged with respect to abundance, while Flagstaff might expect increases in vector abundance.

Two patterns emerge from these projections of WNV mosquito abundance in six urban areas across Arizona. First, an elevation, quasi climate, effect where higher (cooler) cities like Flagstaff (elevation: 6,909 ft.) and Nogales (elevation: 3,832 ft.) have a single-hump curve while lower (hotter) cities like Yuma (141 ft.) and Phoenix (1,086 ft.) have a bimodal curve where the summer populations are adversely effected as the summer temperatures reach and exceed adult mosquito survival thresholds. The mid-summer reduction in vector populations has been corroborated by observations in Arizona vector control data (Brown personal communication). Secondly, as evidenced by the wider curves (dashed lines), there is an extension of the season across all locations with mosquito populations growing earlier in the year and lasting longer into the fall. Changes in the duration of the vector season that have been reported elsewhere (Brown et al. 2015) are also evident among these predictions. While these models are just of mosquito abundance, how this may translate to disease transmission is unknown.

Table 1. Summary of Vector Abundance Predictions for Urban Areas in Arizona.

Location	Current	Mid-Century
High Elevation (cooler) Urban Areas (e.g., Nogales, Flagstaff)	Unimodal distribution of WNV vectors with the season lasting from June to September, peaking in July-August.	Extension of the season with some areas experiencing increased abundance.
Medium Elevation Urban Areas (e.g., Tucson, Florence)	Primarily a unimodal distribution of WNV vectors with some mid-summer reduction in abundance observed. WNV season starts early spring (February/April) and lasts through November, with a late summer peak.	Extension of the season with some areas experiencing a more pronounced mid-summer dip in vector abundance.
Low Elevation (hotter) Urban Areas (e.g., Phoenix, Yuma)	A bi-modal distribution of WNV vectors with the season – some mid-summer reduction observed. Trapping is almost year round with a break in the WNV season only in December/January.	Extension of the season with some areas experiencing a pronounced, potentially crashing, mid-summer change in vector abundance.

* Information regarding current observations were provided with thanks to Marlene Gaither, Environmental Health Program Manager III, Coconino County Public Health Services District for input of the current WNV season in higher elevations; to Christopher Reimus, Environmental Health Services, Pinal County Environmental Health and David Ludwig, Environmental Services, Pima County Health Department for their input on WNV seasonality in medium elevation areas, and to Kirk Smith, Vector Control Division, Maricopa County Environmental Services Department and Joey Martinez, Vector Control Specialist, Yuma County Health for their expertise on vector control in lower elevation areas.

Limitations

While models provide some insight, the most important message is that the shape of these curves and the degree of vector season extension will be dependent on the temperature and precipitation, i.e., the local information. It is also important to note that these predictions do not estimate disease incidence, rather vector abundance (entomologic risk). To transmit WNV, a female mosquito must first take an infectious blood-meal, survive long enough to become infected and then successfully find and feed on an uninfected host. The degree to which warming-associated decreases in mosquito abundance are compensated for by changes in the percent infected is yet to be determined with location specific precision. Human behavior, such as the management of breeding sites, window screens, use of insect repellant, also have a dampening effect on disease transmission.

Models are limited by the quality and quantity of data available to create them (Hosking and Campbell-Lendrum 2012; Rodo et al. 2013). While there is the tendency to think of "the mosquito" or "the virus" there are multiple species and even populations with varying competence (capacity to become infected and transmit virus) and virulence (ability to cause harm). Moreover, vector and pathogen adaptation are rarely, if ever, considered when making projections due to a gap in knowledge as to how quickly and to what threshold they may adapt.

Finally, the timing of the precipitation and warming events is critical to vector life cycles, but there is considerable uncertainty in those predictions. Winter rains will have a different effect than summer rains on vector abundance, as will winter versus summer warming. In addition, the magnitude of events is critical. For example, a flushing effect of excessive precipitation events has been observed which negatively effects abundance by washing out immature mosquitoes (Koenraadt and Harrington 2008). Both the uncertainty of magnitude and timing of events as well as the subsequent implications for vectors is an area of active research for both the climate and vector research communities.

Valley Fever

Projecting Valley fever incidence under future climate projections is considerably more challenging than other diseases due to the scarce temporally and spatially explicit environmental data on *Coccidioides* positive and negative sites. While there are thousands of cases each year which have allowed us to understand the epidemiology of Valley fever, our understanding of the ecology of the pathogen is limited (Figure 8).
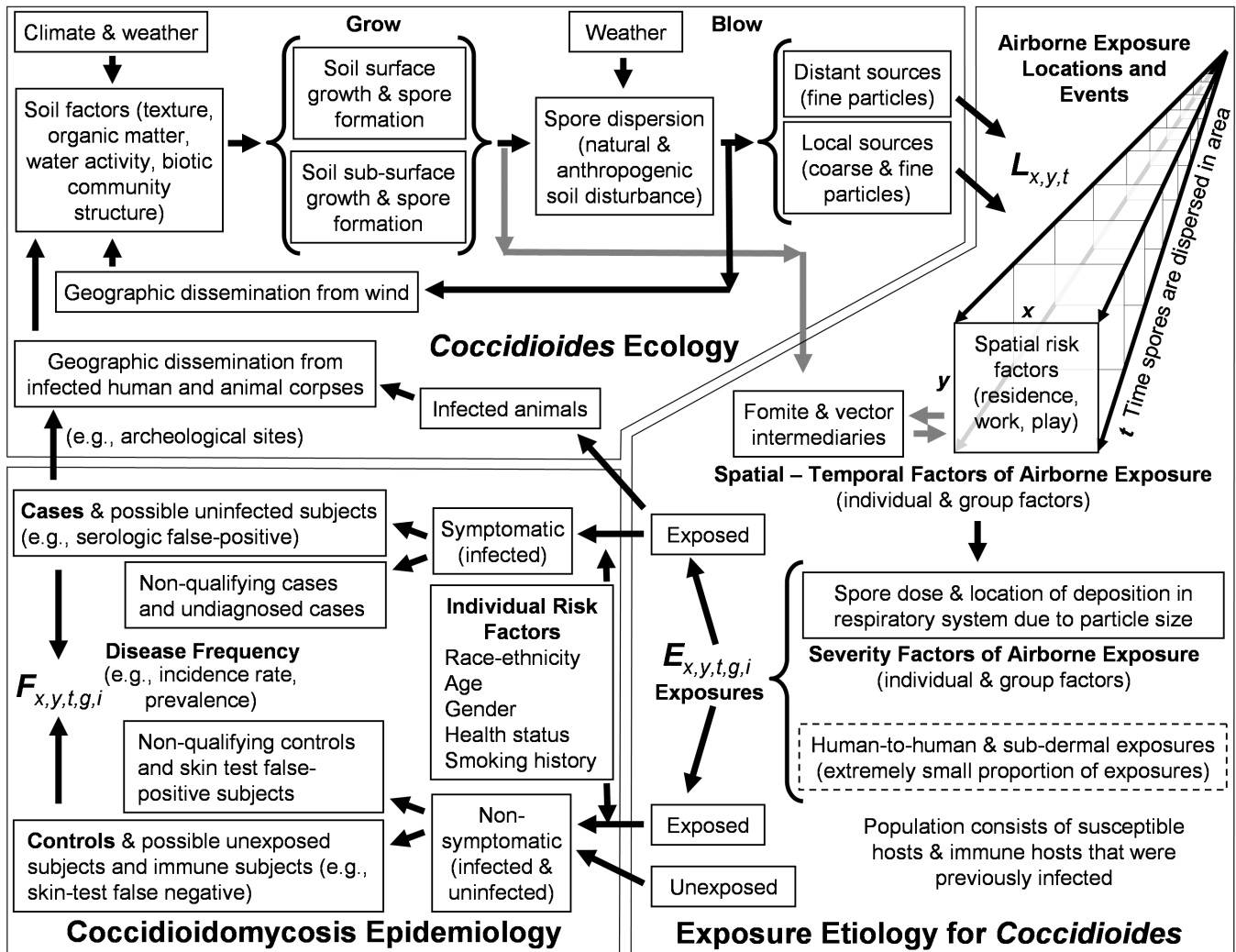

Figure 8. Ecological and epidemiological causal diagram of known and hypothesized determinants of growth, dispersion, exposure, and infection for *Coccidioides* spp. in North, Central and South America (reproduced with permission from Tabor and O'Rourke, 2010).

Some outbreak investigations highlight limited areas of risk for exposure, such as during construction or other soil disturbances in certain areas (e.g., Peterson et al. 2004, Cummings et al. 2010). The cost of sufficient sampling and detecting viable *Coccidioides* spp. in the environment limits the ability to develop valid models of occurrence and distribution that will allow predicting exposure risk. Early laboratory investigations found that competition with other soil microbes might play a significant role in determining the successful growth of *Coccidioides* spp (reviewed by Kolivras et al. 2001 and by Kirkland and Fierer 1996). Not being able to incorporate the interaction between fungal species in the soil further increases the uncertainty with respect to future disease projections. Because not all construction, dust storms, or archeological digs are associated with Valley fever outbreaks, the key to identifying why soil disturbance in certain areas resulted in disease may be contingent upon more precise delineation of areas where the pathogen is most likely to occur naturally.

State of the Science

While results vary by study location (e.g., southern California versus Arizona), researchers have found significant associations between Valley fever incidence and weather. The Grow and Blow hypothesis describes the association generally, where fall precipitation facilitates fungal growth and subsequent drying allows the spores to form. These are then aerosolized when the winds blow across areas where the fungus grows. In Pima County, Arizona, a strong association was found between Valley fever incidence and precipitation during the normally arid spring/early summer 1.5–2 years prior (Comrie 2005). In Maricopa County, Arizona, Valley fever incidence was predicted by drought indices, wind, temperature, precipitation, and the concentration of particulate matter smaller than 10µm (Park et al. 2005). In Kern County, California, it was not weather, rather the prior disease incidence that best predicted Valley fever incidence (Talamantes et al. 2007). The complicated association between climate and Valley fever incidence indicated by these and other studies makes regional predictions too unreliable given the current understanding and available data.

A literature review and unpublished laboratory results (Joseph Tabor) suggest that soil, physical, and chemical factors at the sub-meter scale may help predict the occurrence of *Coccidioides* spp. A systematic research approach (Figure 9) is proposed to identify and predict sub-meter growth and transport processes that are dependent on soil and animal host relationships. Ideally, these findings can be scaled-up using environmental data such as soil maps and satellite imagery, to develop predictive models.
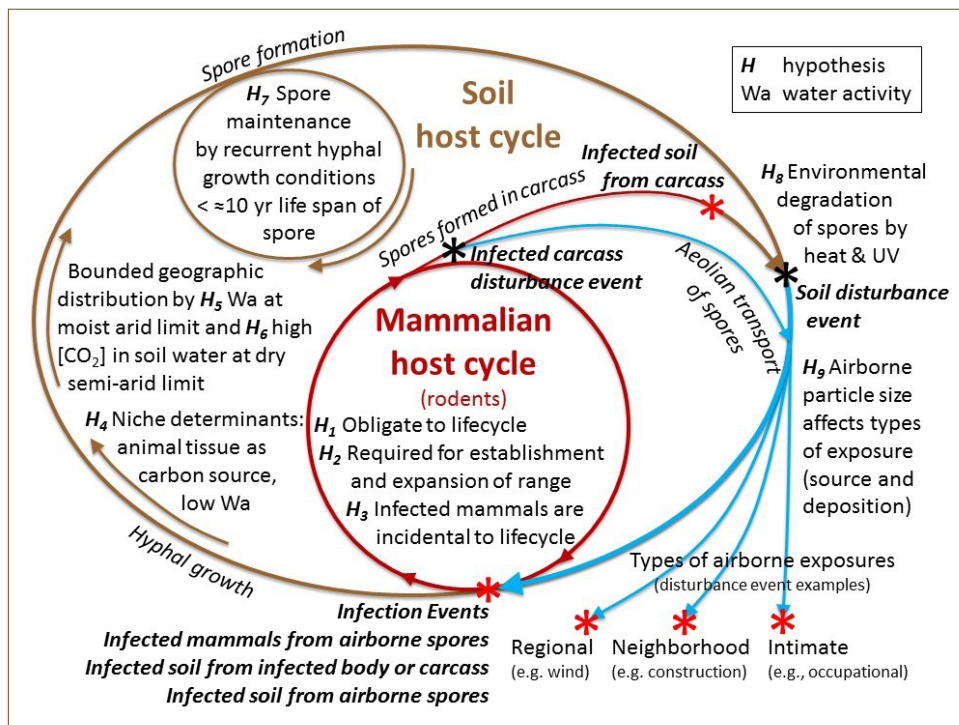

Figure 9. Hypothesized causal pathway for predicting valley fever burden. The exposures are weather related changes that may influence fungal growth and host behavior.

Arizona Projections

At best, projections for Valley fever in Arizona are qualitatively based on extrapolating from where the disease currently occurs. If the climate in one city becomes like the climate in the other (e.g. Tucson becomes hotter and dryer like Phoenix) then seasonal disease occurrence may become more similar. If the climate in either city becomes significantly cooler and/or wetter (e.g. Flagstaff) or dryer and/or hotter (e.g. Yuma) then the incidence of disease may decrease. Conversely, if other areas become similar to Phoenix and Tucson then higher incidence of disease is likely.

Limitations

While what we understand about this pathogen and its lifecycle in the desert soil leads us to expect an association with climate, the data available make quantifying this association challenging. Finding an association between incidence over time and climate is unlikely because of the nature of incidence data.

References

Arizona Department of Health Services (2015). "Valley Fever Annual Report." Office of Infectious Disease Services. Bureau of Epidemiology and Disease Control.

Brown, H.E., Young, A., Lega, J., Andreadis, T.G., Schurich, J., Comrie, A. "Projection of climate change influences on U.S. West Nile virus vectors" Earth Interactions 19:1-18.

Centers for Disease Control and Prevention (2013). Increase in Reported Coccidioidomycosis — United States, 1998–2011. *MMWR*. 62: 217-218.

Centers for Disease Control and Prevention, Summary of Notifiable Diseases, 2005-2012

> 2005: McNabb, S.J.N., Jajosky, R.A., Hall-Baker, P.A., Adams, D.A, Sharp, P., Anderson, W.J., Aponte, J.J., Jones, G.F. Summary of Notifiable Diseases --- United States, 2005. *MMWR*. 2007. 54(53): 2-92.

> 2006: McNabb, S.J.N., Jajosky, R.A., Hall-Baker, P.A., Adams, D.A, Sharp, P., Worsham, C., Anderson, W.J., Aponte, J.J., Jones, G.F., Nitschke, D.A, Rey, A.,. Wodajo, M.S. Summary of Notifiable Diseases --- United States, 2006. *MMWR*. 2008. 55(53): 1-94.

> 2007: Hall-Baker, P.A., Nieves, E., Jajosky, R.A., Adams, D.A, Sharp, P., Anderson, W.J., Aponte, J.J., Jones, G.F., Aranas, A.E., Rey, A., Lane, B., Wodajo, M.S. Summary of Notifiable Diseases --- United States, 2007. *MMWR*. 2009. 56(53): 1-94.

> 2008: Hall-Baker, P.A., Nieves, E., Jajosky, R.A., Adams, D.A, Sharp, P., Anderson, W.J., Aponte, J.J., Aranas, A.E., Katz, S.B., Mayes, M., Wodajo, M.S., Onweh, D.H., Baillie, J., Park, M. Summary of Notifiable Diseases --- United States, 2008. *MMWR*. 2010. 57(54): 1-94.

> 2009: Hall-Baker, P.A., Groseclose, S.L., Jajosky, R.A., Adams, D.A, Sharp, P., Anderson, W.J., Abellera, J.P., Aranas, A.E., Mayes, M., Wodajo, M.S., Onweh, D.H., Park, M., Ward, J. Summary of Notifiable Diseases --- United States, 2009. *MMWR*. 2011. 58(53): 1-100.

> 2010: Adams, D.A, Gallagher, K.M., Jajosky, R.A., Ward, J., Sharp, P., Anderson, W.J., Abellera, J.P., Aranas, A.E., Mayes, M., Wodajo, M.S., Onweh, D.H., Park, M. Summary of Notifiable Diseases — United States, 2010. *MMWR*. 2012. 59(53): 1-111.

> 2011: Adams, D.A, Gallagher, K.M., Jajosky, R.A., Kriseman, J., Sharp, P., Anderson, W.J., Aranas, A.E., Mayes, M., Wodajo, M.S., Onweh, D.H., Abellera, J.P. Summary of Notifiable Diseases — United States, 2011. *MMWR*. 2013. 60(53): 1-117.

> 2012: Adams, D.A, Jajosky, R.A., Ajani, U., Kriseman, J., Sharp, P., Onweh, D.H., Schley, A.W., Anderson, W.J., Grigoryan, A., Aranas, A.E., Wodajo, M.S., Abellera, J.P. Summary of Notifiable Diseases — United States, 2012. *MMWR*. 2014. 61(53): 1-121

> 2013: Adams, D.A, Fullerton, K., Jajosky, R.A., Sharp, P., Onweh, D.H., Schley, A.W., Anderson, W.J., Faulkner, A., Kugeler, K. Summary of Notifiable Infectious Diseases and Conditions — United States, 2013. *MMWR*. October 23, 2015. 62(53): 1-119.

> 2014: Adams, D.A., Thomas, K.R., Jajosky R., Foster, L., Sharp, P. Onweh, D.H., Schley, A.W., Anderson, W.J. Summary of Notifiable Infectious Diseases and Conditions — United States, 2014. *MMWR* Morb 2016:63: 1-152

Chen, C.C., Jenkins, E., Epp, T., Waldner, C., Curry, P.S., Soos, C. (2013). "Climate change and West Nile virus in a highly endemic region of North America." *International Journal of Environmental Research Public Health* 10(7): 3052-3071.

Comrie, A. (2005). "Climate factors influencing coccidioidomycosis seasonality and outbreaks." *Environmental Health Perspectives* 13(6): 688-692.

Cummings, K. C., McDowell, A., Wheeler, C., McNary, J., Das, R., Vugia, D.J., Mohle-Boetani, J.C. (2010). "Point-source outbreak of coccidioidomycosis in construction workers." *Epidemiology and Infections* 138: 507–511.

Dohm, D.J., O'Guinn, M.L., Turell, M.J. (2002). "Effect of environmental temperature on the ability of *Culex pipiens* (Diptera : Culicidae) to transmit West Nile virus." *Journal of Medical Entomology* 39(1): 221-225.

Eisen, L. and Moore, C. (2013). "*Aedes* (Stegomyia) *aegypti* in the continental United States: A vector at the cool margin of its geographic range." *Journal of Medical Entomology* 50(3): 467-478.

Emmons, C.W. (1942). "Isolation of *Coccidioides* from soil and rodents." *Public Health Reports* 57(4): 109-111.

Gage, K. L., Burkot, T. R., Eisen, R. J., Hayes, E. B. (2008). "Climate and vectorborne diseases." *American Journal of Preventative Medicine* 35(5): 436-450.

Galgiani, J.N., Ampel, N.M., Blair, J.E., Catanzaro, A., Geertsma, F., Hoover, S.E., Johnson, R.H., Kusne, S., Lisse, J., MacDonald, J.D., Meyerson, S.L., Raksin, P.B., Siever, J., Stevens, D.A., Sunenshine, R., Theodore, N. (2016). "Infectious Diseases Society of America (IDSA) Clinical Practice Guideline for the Treatment of Coccidioidomycosis". *Clinical Infectious Diseases* 63(6): e112-46.

Greer, A., Ng, V., Fisman, D. (2008). "Climate change and infectious diseases in North America: the road ahead." *Canadian Medical Association* 187(6): 715-722.

Gubler, D.J., Reiter, P., Ebi, K.L., Yap, W., Nasci, R., Patz, J.A. (2001). "Climate variability and change in the United States: potential impacts on vector and rodent-borne diseases." *Environmental Health Perspectives* 109(2): 223-233.

Hartley, D.M., Barker, C.M., Le Menach, A., Niu, T., Gaff, H.D., Reisen, W.K. (2012). "Effects of temperature on emergence and seasonality of West Nile virus in California." *American Journal of Tropical Medicine and Hygiene*. 86: 884–894.

Hamer, G.L., Kitron, U.D., Goldberg, T.L., Brawn, J.D., Loss, S.R., Ruiz, M.O, and others (2009). "Host selection by *Culex pipiens* mosquitoes and West Nile virus amplification." *American Journal of Tropical Medicine and Hygiene* 80(2): 268-278.

Harrigan, R.J., Thomassen, H.A., Buermann, W., Cummings, R.F., Kahn, M., Smith, T.B. (2010). "Economic conditions predict prevalence of West Nile virus." *PLoS ONE* 5(11): e15437.

Harrigan, R.J., Thomassen, H.A., Buermann, W., Smith, T.B. (2014). "A continental risk assessment of West Nile virus under climate change." *Global Change Biology* 20(8): 2417-2425.

Hess, J.J., Saha, S., Schramm, P.J., Conlon, K.C., Uejio, C.K., Luber, G. (2014). "Projecting Climate and Disease Burden: A Guide for Health Departments. Climate and Health Technical Report Series." Climate and Health Program, Center for Disease Control and Prevention.

Hongoh, V., Berrang-Ford, L., Scott, M.E., Lindsay, L.R. (2012). "Expanding geographical distribution of the mosquito, *Culex* pipiens, in Canada under climate change." *Applied Geography* 33: 53–62.

Hosking, J., Campbell-Lendrum, D. (2012). "How well does climate change and human health research match the demands of policymakers? A scoping review." *Environmental Health Perspectives* 120(8).

Hugenholtz, P.G. (1957). Climate and coccidioidomycosis. In *Proceedings of Symposium on Ccoccidioidomycosis, Phoenix, AZ.* Atlanta: Public Health Service Publication 575: 136-143.

Kilpatrick, A.M., Kramer, L.D., Jones, M.J., Marra, P.P., Daszak, P. (2006). "West Nile virus epidemics in North America are driven by shifts in mosquito feeding behavior." *PLoS Biology* 4(4): e82.

Kilpatrick, A.M., Meola, M.A., Moudy, R.M., Kramer, L.D. (2008). "Temperature, viral genetics, and the transmission of West Nile virus by *Culex pipiens* mosquitoes." *Plos Pathogens* 4(6): e100009

Photo: Daniel Griffin

Kirkland, T. N., Fierer, J. (1996). "Coccidioidomycosis: a reemerging infectious disease." *Emerging Infectious Diseases* 2: 192-9.

Koenraadt, C.J., Harrington, L.C. (2008). "Flushing effect of rain on container-inhabiting mosquitoes *Aedes aegypti* and *Culex pipiens* (Diptera: Culicidae). " *Journal of Medical Entomology* 45(1):28-35.

Kolivras, K.N., Johnson, P. S., Comrie, A. C., Yool, S. R.. (2001). "Environmental Variability and coccidioidomycosis (valley fever)." *Aerobiologia* 17: 31-42.

Maddy, K.T., Crecelius, H.G., Cornell, R.G. (1960). "Distribution of *Coccidiodes immitis* determined by testing cattle." *Public Health Reports* 75:955-96.

Morin, C.W., Comrie, A.C. (2010). "Modeled response of the West Nile virus vector *Culex quinquefasciatus* to changing climate using dynamic mosquito simulation model." *International Journal of Biometeorology* 54: 517-529.

Morin, C.W., Comrie, A.C. (2013). "Regional and seasonal response of a West Nile virus vector to climate change." *Proceedings of the National Academy of Sciences* 110(39): 15620-15625.

Park, B. J., Sigel, K., Vaz, V., Kinatsym K., McRill, C., Phelan, M., Colman, T., Coomrie, A.C., Warnock, D.W., Galgiani, J.N., Haijeh R.A. (2005). "An epidemic of coccidioidomycosis in Arizona associated with climate changes, 1998-2001." The *Journal of Infectious Diseases* 191:1981-7.

Paz, S., & Albersheim, I. (2008). "Influence of warming tendency on *Culex pipiens* population abundance and on the probability of West Nile Fever outbreaks (Israeli case study: 2001–2005)." *EcoHealth* 5(1), 40-48.

Petersen, L.R., Marshall, S.L., Barton-Dickson, C., Haijeh, R.A, Lindsley, M.D., Warnock, D.W., Panackal, A.A., Shaffer, J.B., Haddad, M.B., Fisher, F.S., Dennis, D.T., Morgan, J. (2004). "Cocciodioidomycosis among workers at an archeological site, northeastern Utah." *Emerging Infectious Diseases* 10(4): 637-642.

Reisen, W.K., Fang, Y., Martinez, V.M. (2006). "Effects of temperature on the transmission of West Nile virus by *Culex tarsalis* (Diptera: Culicidae)." *Journal of Medical Entomology* 43(2): 309–317.

Reisen, W.K., Lothrop, H.D., Wheeler, S.S., Kennsington, M., Gutierrez, A., Fang, Y., Garcia S., and Lothrop, B. (2008a). "Persistent West Nile Virus transmission and the apparent displacement St. Louis Encephalitis virus in southeastern California, 2003-2006." *Journal of Medical Entomology* 45(3): 494-508.

Reisen, W. K., Takahashi, R. M., Carroll, B. D., Quiring, R. (2008b). "Delinquent mortgages, neglected swimming pools, and West Nile virus, California." *Emerging Infectious Diseases* 14(11): 1747:1749.

Rodo, X., Pascual, M., Doblas-Reyes, F.J., Gershunov, A., Stone, D.A., Giorgi, F., Hudson, P.J., Kinter, J., Rodriguez-Arias, M.A., Stenseth, N.C., Alonso, D., Garcia-Serrano, J., Dobson, A. (2013). "Climate change and infectious diseases: Can we meet the needs for better prediction?" *Climate Change* 118(3-4):625-640.

Tabor, J.A., O'Rourke, M.K. (2010). "A risk factor study of coccidioidomycosis by controlling differential misclassification of exposure and susceptibility using a landscape ecology approach." *Science of the Total Environment* 408(10):2199-2207.

Talamantes, J., Behseta, S., Zender, C.S. (2007). "Fluctuations in climate and incidence of coccidioidomycosis in Kern County, California." *Annals of the New York Academy of Science* 1111: 73-82.

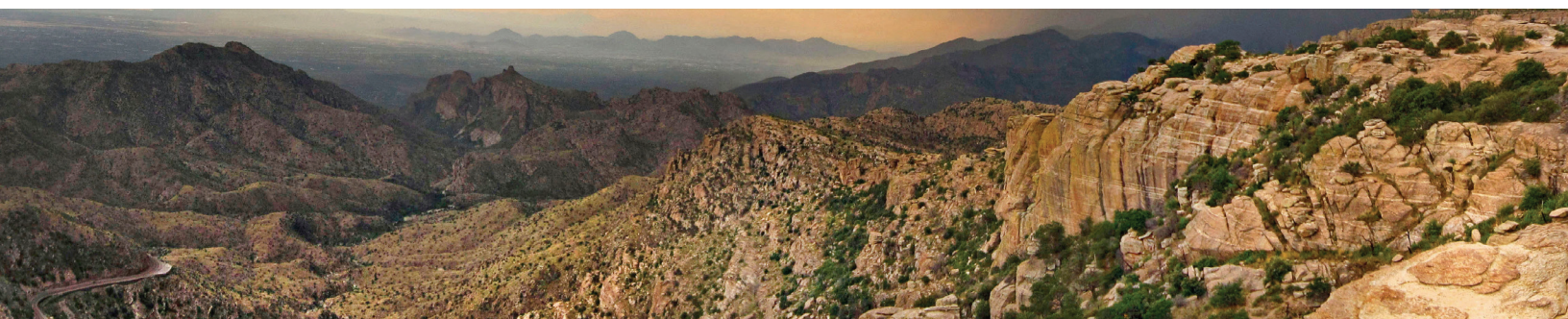Tamerius, J.D., Comrie, A.C. (2011). "Coccidioidomycosis incidence in Arizona predicted by seasonal precipitation." *PloS One* 6(6): e21009.