Introduction

Infectious diseases, including cancers, are common occurrences in populations. Devil Facial Tumor Disease, or DFTD, is a transmissible cancer among Tasmanian devils in which live cancer cells are transferred from one devil to another when they bite each other during social interactions, which means it is a frequency-dependent disease (Wells et al. 2017). When DFTD first emerged, it infected over 80% of the population and caused a substantial decline (Lazenby et al. 2018). DFTD is usually fatal due to its metastatic nature, and causes problems within the digestive system, oral cavities, and can lead to organ failure (Wells et al. 2017). The cells of DFTD exhibit polyploidy and can be diploid or tetraploid (Hamede et al. 2012). Devil populations lack genetic variation, which allows DFTD to downregulate the major histocompatibility complex, and prevents an immune response from occurring (Epstein et al. 2016).

Selection is a central topic in evolutionary biology and is a major driving force in the spread of DFTD. Strong selection could result in devil extinction, tumor extinction, or a state of equilibrium between the tumor and the host (Epstein et al. 2016). Disease prevalence within the population and genetic changes indicate that that Tasmanian devils are forming some kind of resistance to DFTD – which is what we will be exploring in our study.

Materials and Methods

*DRYAD*

For data collection, Dryad was extremely useful for collecting data from previous studies and for the papers themselves. I collected data primarily on Tasmanian devils and how DFTD affects them over time, as well as some papers that focused on *how* the devils are evolving in response to the cancer. Data was saved to my Projects folder and read into the R program on my desktop. Since the focus of this paper is testing whether Tasmanian devils are evolving some kind of resistance to DFTD, disease prevalence among individuals over time and genetic changes in devils as well as DFTD were our parameters.

*Disease prevalence*

The proportion of individuals affected over time was taken from a study by Wells et al. 2017 in which Tasmaninan devils were monitored over a 10-year period. Data that was available for individual devils was plotted over time against the presence of tumors. Changes in population structure have occurred after emergence of DFTD and may be affecting the prevalence within the population.

*Genetic changes*

The immune system of devils is a major factor that may be playing a role in the tolerance of DFTD, and two chromosomal regions have been studied to determine whether they are changing, or being selected for, among devil populations. The strain of DFTD, being diploid or tetraploid, was recorded and analyzed for its prevalence within the devil population (Hamede et al. 2012).

Results

*Disease prevalence*

Between July 2006 and November 2016, Tasmanian devils were captured and recaptured to monitor the presence of tumors (Wells et al. 2017). The data collected over the 10-year timespan indicates that DFTD prevalence increased in the population, but began to decrease somewhere in the middle of the study, and maintained this decrease until the end (Wells et al. 2017). Figure 1 displays the tumor prevalence among devils over 10 years. Tumor load was measured in cm3. Another study indicated that the force of infection had decreased among devils due to temporal effects (Wells et al. 2017). The size of the Tasmanian devil population began to stabilize within 5 years of the emergence of DFTD (Lazenby et al. 2018). One site, called West Pencil Pine, shows evidence of reduced impact of DFTD in the population (Lazenby et al. 2018). Additionally, the structure of devil populations changed substantially after the emergence of DFTD. Disease prevalence was extremely high in devils 3 years old and older, but remained relatively low in 1-2 year-olds (Lazenby et al. 2018). Breeding among 1-year-old females, in addition to increased numbers of pouch young, increased as a result of decreased numbers of adult devils (Lazenby et al. 2018).



Figure 1. Prevalence of DFTD among a population of Tasmanian devils from 2006-2016. Tumor load was measured in cm3. Measurements were taken from individual devils.

*Genetic changes*

There is evidence that DFTD may be evolving into a tetraploid strain instead of diploid, and may be less aggressive (Hamede et al. 2012). Counts taken from devil populations from 2006-2011 show that the number of tetraploid tumors are increasing (Fig. 2). Other possibilities that are contributing to resistance are two chromosomal regions, which appear to be under strong selection in Tasmanian devils (Epstein et al. 2016). These regions contained single nucleotide polymorphisms, or SNPs, with allele frequency changes when comparing pre- and post-disease samples (Epstein et al. 2016). Five genes in these regions are associated with cancer risk and immune function, along with immune system regulators, which is important to note because devil immune systems were initially evaded by DFTD with no form of immune response (Epstein et al. 2016). The MHC complex genotype of the tumor has remained the same, but the MHC complex genotype of the devils has changed since the emergence of DFTD (Hamede et al. 2012).



Figure 2. Prevalence of tetraploid tumor strains among Tasmanian devil populations from 2006 to 2011. (I’m hoping to make this into a histogram but couldn’t get it work so this is all I got)

Discussion

DFTD is still affecting a large portion of the Tasmanian devil populations. However, as of 2016, the prevalence of DFTD is decreasing. Over a 10-year timespan, prevalence of the disease increased, then steadily decreased, and the decline is expected to continue (Wells et al. 2017). This decline could be due to genetic changes occurring within DFTD tumors and the devils themselves. From 2006 until 2011, tetraploid strains of DFTD are increasing, even though there was a small decline from 2008 to 2009 (Ujvari et al. 2014). Tetraploid strains of DFTD could have a lower infection rate, therefore having a less severe impact on devil populations (Hamede et al. 2012). This is a possible explanation for lower disease prevalence, as well as an evolving resistance to DFTD. Selection for tetraploid tumors could be occurring because it allows for higher cell volume with slower development time (Ujvari et al. 2014). Tetraploid tumors are able to accumulate a higher number of mutations, which increases the probability of the tumor reaching a malignant state – but they are still considered to be less aggressive than diploid strains (Ujvari et al. 2014). Selection for a change in MHC complex of devil immune systems could also be occurring in order to allow an immune response to occur in response to DFTD, which did not occur when it first emerged (Hamede et al. 2012). Two chromosomal regions have been identified as being under strong selection in devils; both of these regions are involved in immune regulation and cancer risk, which supports the hypothesis that devils could be evolving some type of resistance to DFTD (Epstein et al. 2016). Overall, selection seems to be playing a role in each of these important processes and contributes to the resistance of devils to DFTD, or the evolution of DFTD itself – and could indicate a state of equilibrium that is being established between them.

References

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