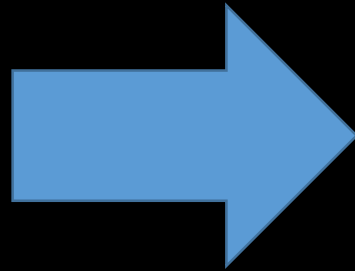
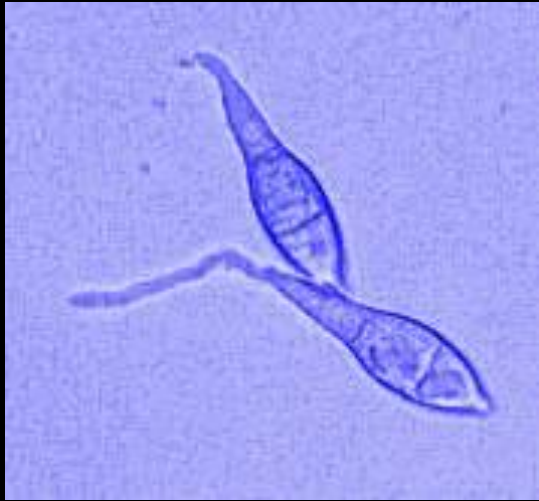


Exploring the phylogenetic evolution and
geographic transmission patterns of the rice
blast *Magnaporthe oryzae* in Africa

Margaret Wanjiku

Introduction

- **Rice blast** is caused by a fungal pathogen, ***M. oryzae***
- Reproduces both **sexually** and **asexually**
- Sexual reproduction was evident at the point of origin and the lineage here was largely genetically diverse
- As the pathogen spreads to other continents, it loses the sexual reproduction capability and becomes asexual
- The subsequent lineages are said to be **clonal** and tend to be less genetically diverse



Rice Blast

I-SEED



Image of rice field affected by rice blast from <https://ucanr.edu>

Hypothesis

Null hypothesis

- There is no genetic diversity of the pathogen within the African strains

Alternate hypothesis

- There is a genetic diversity of the pathogen within the African strains

Objectives

Main objective

1. To determine the possible point of entry of the *M. oryzae* pathogen to Africa and find any possible transmission patterns within Africa

Specific objectives

1. To investigate insights into the evolution of genes that are known to be important for virulence and pathogenicity
2. To examine the signatures of adaptation within the African strains

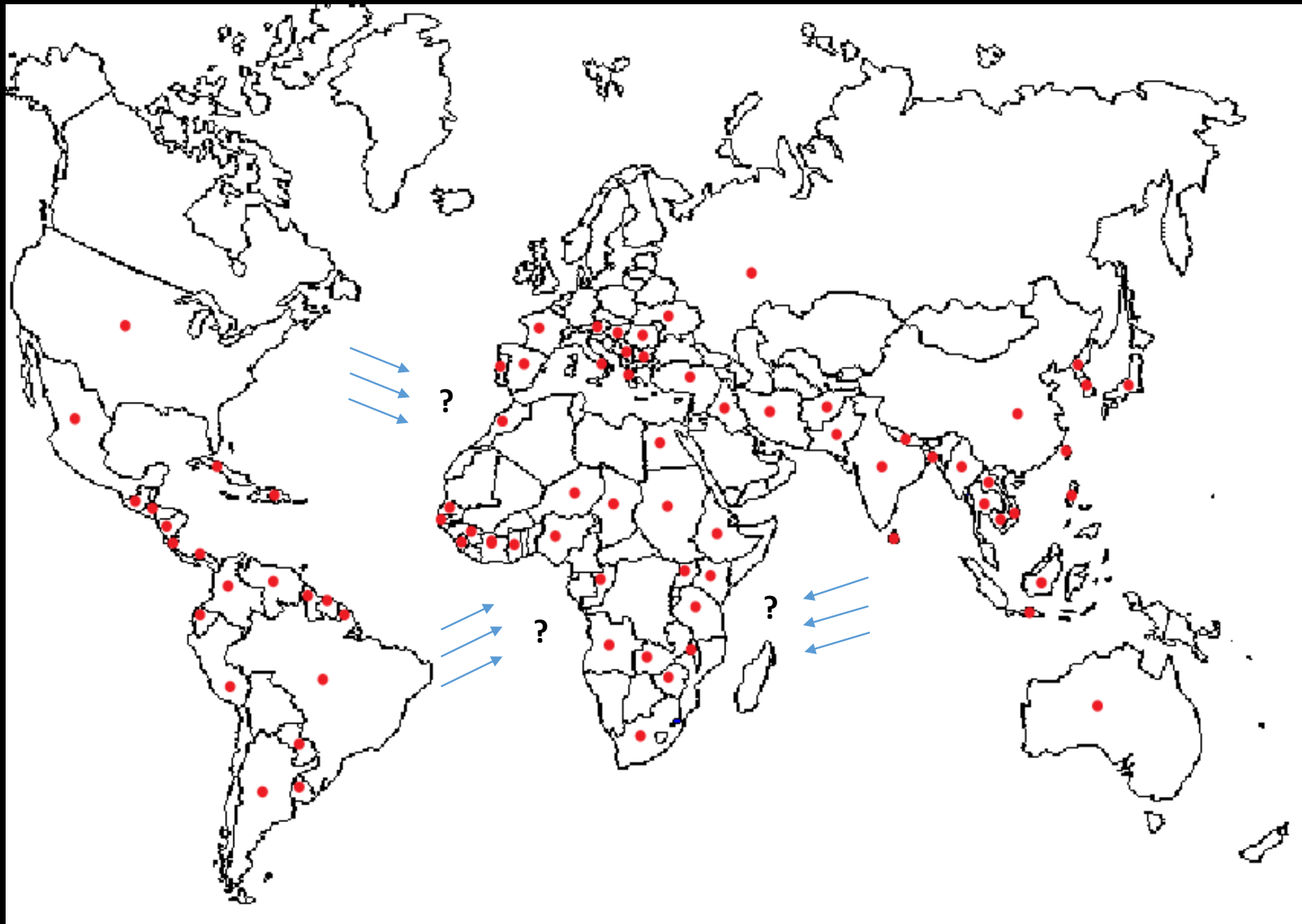
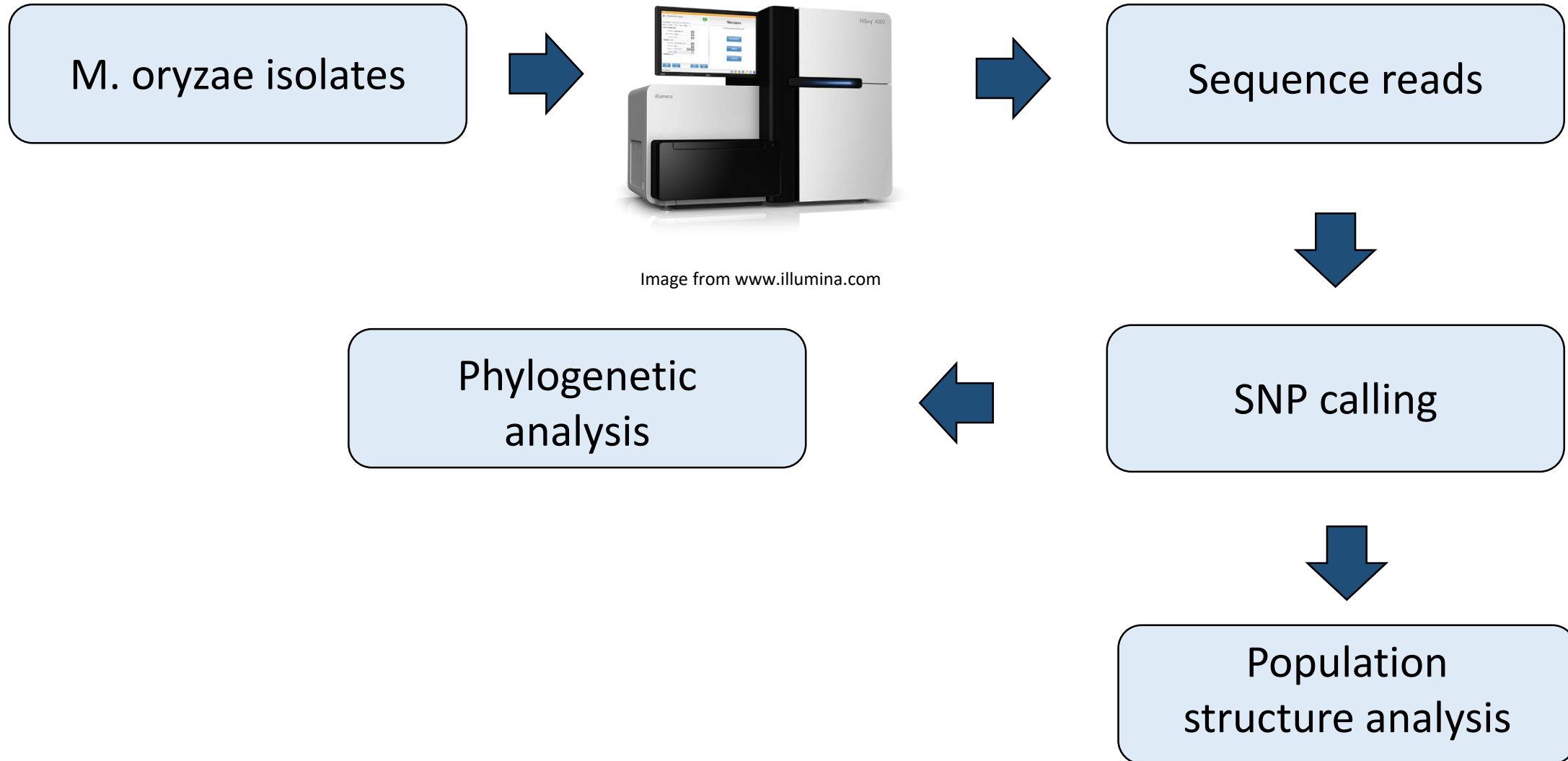


Image showing world wide distribution of rice blast from <https://www.researchgate.net>

Methodology



Conclusion

- Having a better understanding of the pathogen's **phylogeography** will help in informing future measures taken towards combating the spread and management of rice blast such as ;
 1. The development of more effective fungicides to control the disease
 2. Controlling the spread of the disease by preventing its movement through the wind by windborne spores, by water and on infected plant material
 3. Development of resistant varieties of rice
 4. Ensuring that the seeds planted by farmers are disease free

Work plan

[illegible]

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Thank you!