

Introduction

American elms are highly appreciated ornamental trees because of their umbrella shape and high resistance to urban stresses. However, two alien pathogens have decimated a large part of the world elm population through two successive pandemics of the so-called Dutch Elm Disease (DED). The two pathogens are the closely related species *Ophiostoma ulmi* and *O. novo-ulmi*. The former is moderately virulent and caused the first wave of DED from the 1910s to the 1940s, whereas the highly virulent *O. novo-ulmi* is responsible for the second wave of DED since the 1960s (Figure 1, Nierhaus-Wunderwald, 1999; Brasier, 1996). Both species have a similar life cycle and require a vector (elm bark beetle) to infect healthy elms (Figure 2).

Several studies investigated genomic factors that influence virulence in *O. ulmi* and *O. novo-ulmi*, but none clearly identified and characterized any genes or alleles that can be implicated in this phenotype (e.g. El-Touil et al., 1999; Bowden et al., 1996). A century after the first published report of DED (Moreau, 1967; Schwarz, 1922), we still do not have much data on the physiological, molecular or genomic bases of virulence. In addition, no effective cure has been developed yet. Nevertheless, *O. novo-ulmi* is a good model organism for studying tree pathogens as it is genetically tractable.

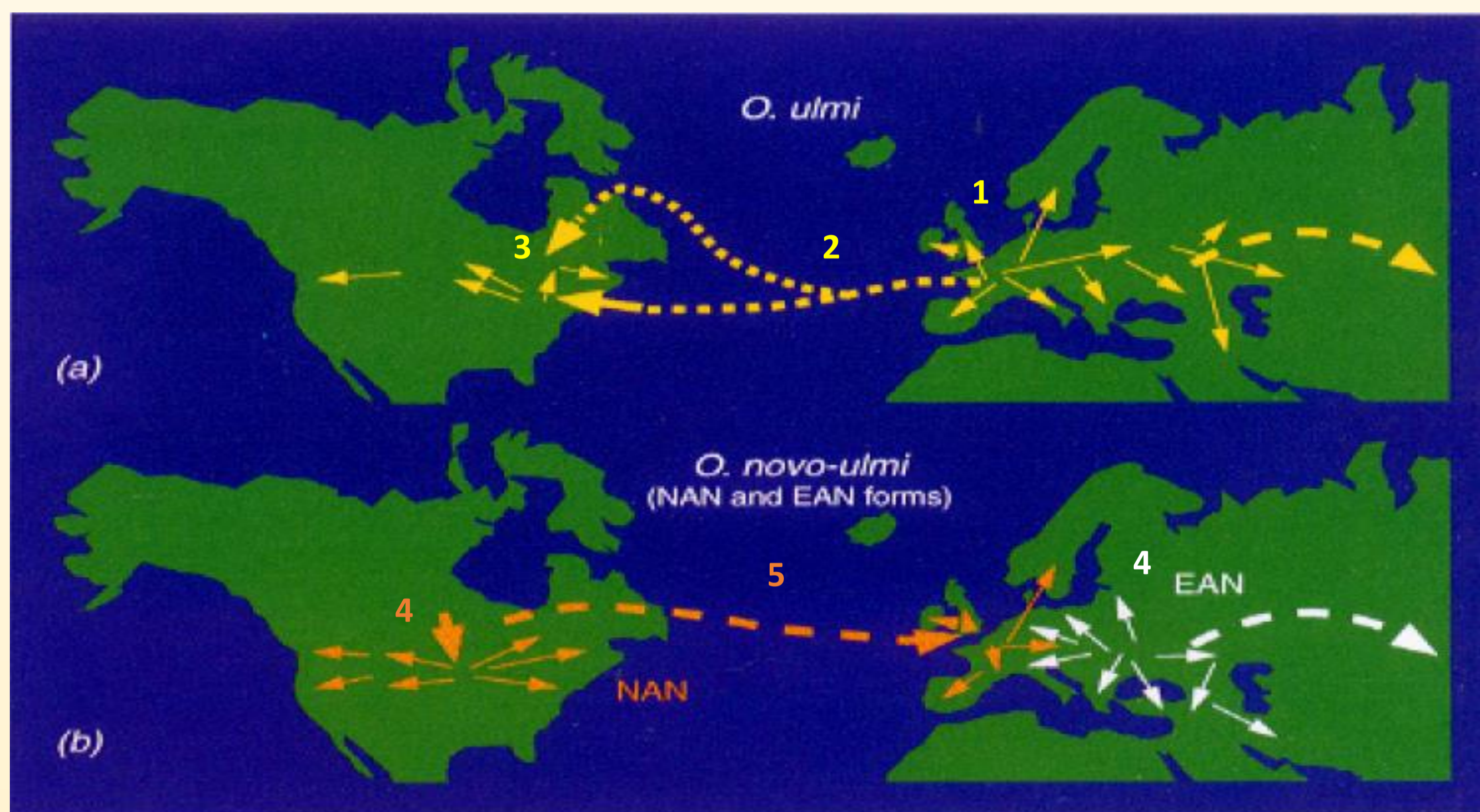


Figure 1: Proposed migration of the two species that induce DED. Simple arrows represent natural migration due to the vector and dotted arrows represent migration due to human activity. (a) migration of *O. ulmi*; (b) migration of *O. novo-ulmi*. NAN: subspecies *americana*; *O. americana* and EAN: subspecies *novo-ulmi* (Brasier, 1996).

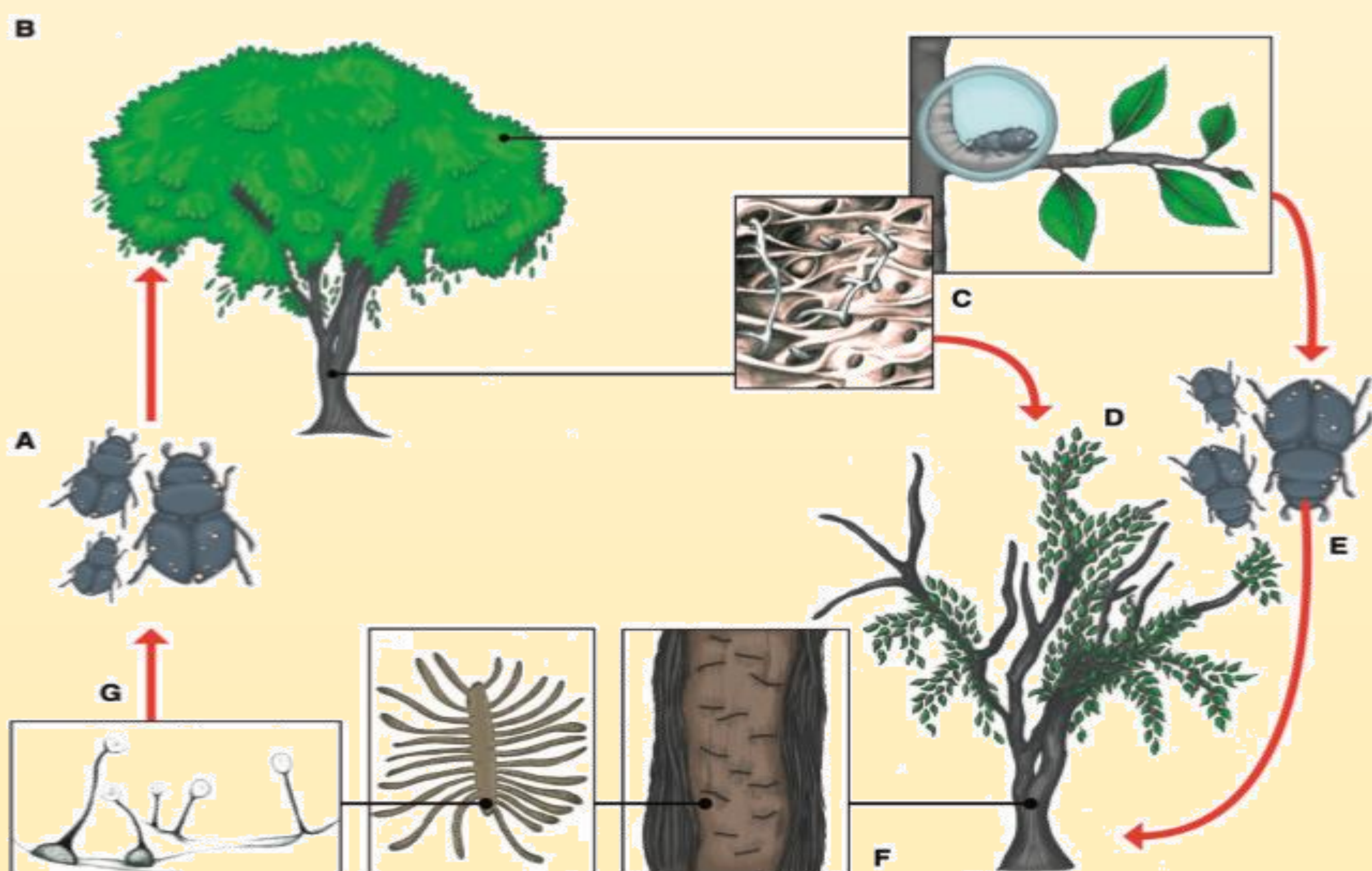


Figure 2: Life cycle of *O. novo-ulmi*. (a) Elm bark beetles carry spores of *O. novo-ulmi* on their exoskeleton. (b) Young adult beetles are attracted by healthy elms (*Ulmus*) on which they feed. (c) This allows infection by *O. novo-ulmi* which disseminates in xylem vessels (d) and induces wilting. (e) Infected elms attract female elm bark beetles which lay eggs in galleries under the bark (f). *O. novo-ulmi* invades galleries (g) where it develops spore dispersion structures: synnemata (asexual) or perithecia (sexual). When elm bark beetle progeny are mature, they will carry fungal spores on their exoskeleton and allow the dispersion of *O. novo-ulmi* to healthy trees. (Comeau et al., 2015)

References

Nierhaus-Wunderwald (1999), WSL FNP p1-6; Brasier (1996), Forest Research p20-28; Brasier (1991), Mycologia 115: 151-161; Khoshraftar et al. (2013), BMC Genomics 14:162; Forgetta et al. (2013) J Biomol Tech 24: 39-49; Schwarz (1922), Willie Commelin Scholten 5: 1-73; Miles & Wayne (2008), Nature Comm 1: 1-73; Moreau (1967) Revue Forestière Française 5: 309-331; Kile & Brasier, 1990, Mycol Res 94: 514-522; Comeau et al. (2015), Genome Biol Evol 7: 410-430; Et-Touil et al. (1999), Molec Plant-Microbe Interac 12: 6-15; Bowden et al. (1999), Molec Plant-Microbe Interac 9: 556-564.

Objective

Virulence of *O. novo-ulmi* has been reported to be a quantitative phenotype (Kile and Brasier, 1990) which is itself the result of several more discrete traits (Figure 3).

The objective of my PhD project is to identify genomic factors underlying the high virulence and fitness of *O. novo-ulmi* (Figure 3).

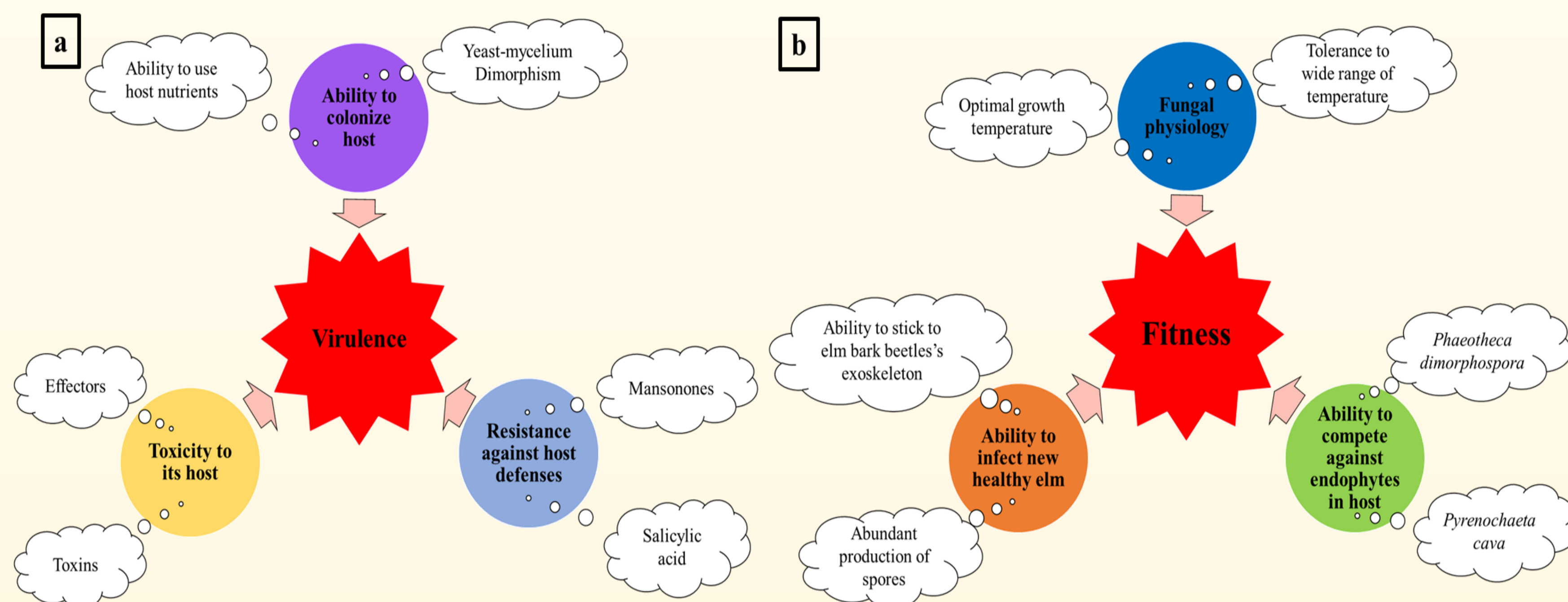


Figure 3: Schematic representation of traits that may contribute to (a) virulence and (b) fitness. Colored circles indicate global trait that can participate in virulence or fitness. Uncolored bubbles are examples for each global phenotype in colored circle.

Methods

- Quantitative Trait Locus (QTL) mapping of virulence by analysis of the F1 progeny of a cross between *O. ulmi* and *O. novo-ulmi* (Figure 4). This technique allows to localize loci possibly implicated in virulence or traits that contribute to it.

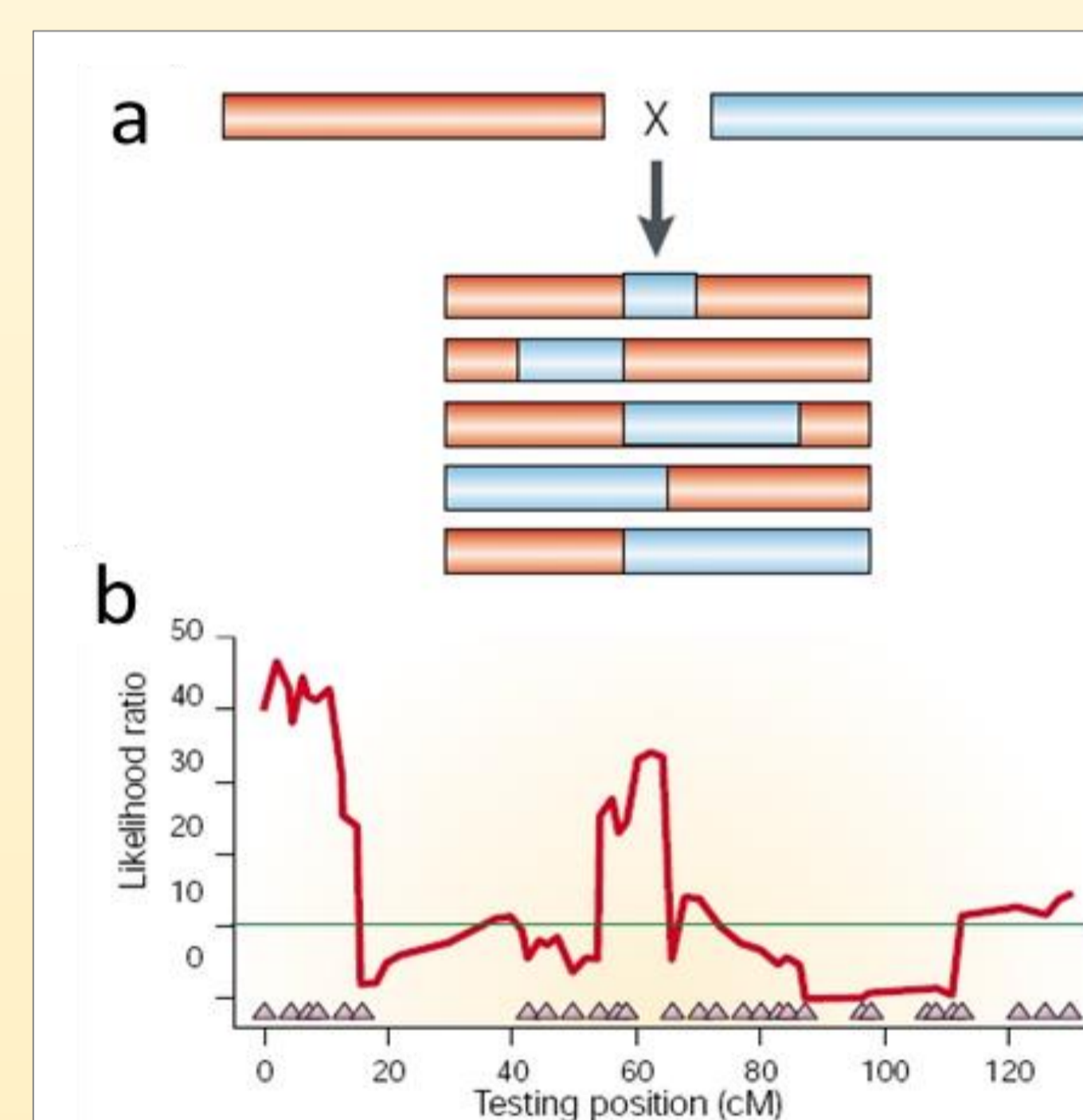
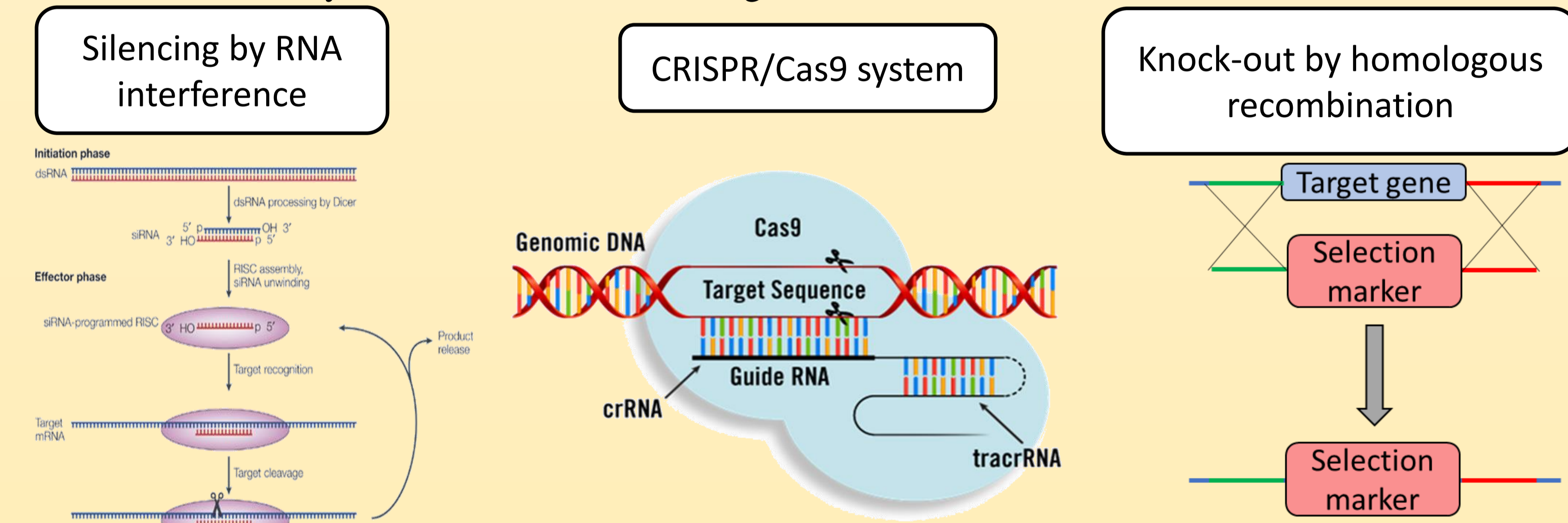


Figure 4: Example of QTL mapping (Miles and Wayne, 2008). (a) cross between 2 genetically distant parent allows recovery of a progeny with a mixture of genomic alleles from the 2 parental stains. (b) Association of the genotype to the phenotype of interest in each progeny individual. LODscore is the probability that the phenotype is linked to the genotype. The graph represents the genomic position of a QTL locus that could be implicated in the analyzed phenotype.

Parental strains: *O. ulmi* W9 (moderate virulence) and *O. novo-ulmi* (EAN) H327 (high virulence).

Genomes of parental strains previously sequenced, assembled and annotated (Khoshraftar et al., 2013, Forgetta et al., 2013, Comeau et al., 2015).

- Functional analysis of candidate virulence genes involved in virulence in *O. novo-ulmi*.



Expected results and perspectives

Genes identified in the first part of the research will be implicated in traits contributing to virulence presented in Figure 3. Moreover, we expect to identify regulatory genes implicated in many different functions (transcription factors, signaling cascades, etc...).

Understanding of virulence mechanisms will allow us to figure out challenges faced by *O. novo-ulmi* during elm infection. Thereby, we will learn a lot on the host-pathogen interaction leading to DED and maybe find a new way to control this disease. Moreover, *O. novo-ulmi* is a good model organism to study tree pathogens. This PhD project will bring new critical information on DED but also on other tree diseases.

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