



# Testing soil for the presence of *Aphanomyces euteiches*

## *A. euteiches* is the causal agent of Aphanomyces root rot in peas

### Introduction

The protocol is designed to be used with soil samples to detect the presence of *Aphanomyces euteiches*, the causal agent of pea root rot. The procedure uses disease assessment to determine the presence of the pathogen and its risk level, thereby supporting informed decisions regarding crop management, variety selection and rotation.



### Objectives

One of the aims of the COUSIN project is to evaluate pea (*Pisum sativum*) crop wild relatives against root rot disease. This disease is a limiting factor for pea cultivation in the Nordic countries, and the evaluation will involve testing several accessions of pea wild relatives, such as *Pisum fulvum*, in the field and in greenhouses. The aim is to identify sources of resistance that can be used in the crossing to breed new pea cultivars with resistance or tolerance to

the root rot disease. The first step in this process is to establish a method of detecting the presence of the disease in the soil in order to evaluate the crop wild relatives. We have established a protocol for testing soil from fields in the greenhouses, which will help us select fields for evaluating pea crop wild relatives.





## Results

A representative soil sample is collected from the field to be evaluated for the presence of *Aphanomyces euteiches*. Seeds of a susceptible cultivar are then sown in the soil sample. It is an advantage to have control pots filled with soil from a field with known problems with *Aphanomyces euteiches*. The soil samples are sieved first to remove stones, and then plastic pots are filled with the soil. Ten seeds are planted in each pot and watered. After five weeks, the seedlings are removed from the soil and washed. The symptoms of the disease are assessed. The results show that the protocol is successful in identifying fields contaminated with the pathogen causing root rot disease in peas.

## Recommendations

Developing robust evaluation methods for crop wild relatives can significantly accelerate the transfer of their beneficial traits to cultivated crops. In the case of peas (*Pisum sativum*), for example, wild relatives represent a valuable reservoir of genetic diversity, particularly with regard to traits such as disease resistance, adaptation to abiotic stress, and improved nutritional quality. Systematic phenotyping, controlled disease screening and efficient crossing strategies are essential for identifying useful alleles and transferring them into elite breeding material. Refinement of evaluation protocols and pre-breeding approaches enables breeders to leverage wild germplasm more effectively, thereby enhancing the resilience, productivity, and sustainability of modern pea cultivars.

## Further reading

- Kimberly Zitnick-Anderson, Lyndon D. Porter, Linda E. Hanson, and Julie S. Pasche. Identification, Laboratory, Greenhouse, and Field Handling of *Aphanomyces euteiches* on Pea (*Pisum sativum*). *Plant Health Progress* 2021 22:3, 392-403.
- Rubiales et al. 2019. CH20 - Advances in breeding of peas. In: Hochmuth G (Ed), *Achieving sustainable cultivation of vegetables*, Burleigh Dodds Science Publishing Limited, Cambridge, UK.

