Clarification in response to the question:

In order to characterize the diet of different deer species and understand their preferences in relation to vegetation availability and landscape composition, it is important to identify as many species in the samples as possible. The samples are likely to contain specimens of grasses, herbs, shrubs, trees as well as agricultural crops. The comparison of these different groups is an important part of our management questions, so it is critical that the analyses outcomes reflect the composition of the consumed biomass adequately.

Because of the variable affinity of the different plant groups to different primers, the pilot project used two primers – ITS2 and RbcLa. If you intend to use other primers, please explain why, and how a comprehensive species coverage will be achieved.

In addition to identifying the major diet components, we are also interested to assess, whether deer consume any rare plant species. That's why it is also important to be able to detect species which only occur in the samples in low quantity. Please comment on the ability of the methods to detect low quantity, e.g. single-read species.

The required outputs are:

- Full list of identified species with their read quantity for each sample
    - Species level identification for majority and genus level identification for all the taxons
- Evidence of quality control – checking for amplification and read quality, alignment with a reference library; handling of any unexpected results
- Comprehensive report of the factors affecting the diet composition
    - Statistical analysis of the effect of deer species; male x female preferences and location/woodland type are the minimum requirements

Please note that the samples will be supplied in two separate batches, 100 samples in mid-February, and another 100 samples in mid-April (exact dates subject to deer cull). We will require an interim report in early March in order to review the preliminary results of the first batch of samples, verify the plant species identified, and discuss if any adjustments are required to further analyses.

Because this study is still of experimental nature, we require assurance of the robustness and accuracy of the method. We require that minimum of 10 specimens of plant species, which are either abundant and/or of particular interest in the study area are sequenced to confirm the match with the samples and genome library. NE / FE will identify the priority specimen species and can provide the specimen samples at the time of the interim review.

Chapter title

Please describe how you will achieve to deliver the three main outputs. List skills and expertise of your team for all three output areas, as well as examples of outputs of previous similar projects.