NEXTRAD - General Progress Summary

Please provide a public summary of the progress of the project (the summary will be used in dissemination activities by TETTRIs on the 3PP):

Summary Requirement	Description
Context and overall objectives	The NEXTRAD project is aiming to test and implement new genomic technologies to increase our ability to estimate species diversity in areas with high number of species or hot spots of biodiversity. In the project we are also interested in transferring this knowledge to botanists and taxonomist working of these areas, as an additional tool for assessing biodiversity. In the project, we are doing these activities in the Macaronesian region and targeting a group of legumes from the genus *Lotus*. Most of the species in *Lotus* are of recent origin and many are considered endangered, given their low abundance and restricted distribution. A crucial step to achieve these goals was a good representation of the species and populations of this group.
Work performed and main achievements	During the first stage of the project, we focused our attention in obtaining a good representation of the species and the different localities of their distribution. We performed field work to collect these underrepresented areas, particularly from the Canary Island archipelago. We also gathered specimens from previous projects, from herbaria, seed banks, and cultivated plants. We achieved the most extensive collection of *Lotus* to date, including sampling at population level (multiple specimens per locality) of the endangered species. This level of sampling will allow us to estimate the levels of genetic diversity and provide us with a finer level of information that could be useful for the future conservation of these species. We also achieved the preparation of nearly 200 samples that we will use to test the genomic approaches in the next stage.
Outlook for the remaining activities in the project	The remaining project will focus on two main activities. From one side, we will analyze the data that we will receive back from the two genotyping tools we are testing in the project. Once we analyzed these data sets, we will have a fair assessment of the advantages and limitations of these approaches. Then, we will organize a workshop where we will share our experience with Lotus and engage taxonomists and botanists from the Macaronesian region. We also plan to invite representatives of the government and local authorities involved in the management of the protected areas where the endangered *Lotus* species are localized.
Images attached to support the summary for publication	Photos of the field work and the communication activities https://drive.google.com/drive/folders/1JzMY-_9ONWL5vFQkG1gDx2yc5RGLDOVc?usp=sharing