Sample ID can be SK1, SK2, etc.

Plant germplasm: Gifu (genotype: Wild type) and Gifu\_mt\_symrk (genotype: mutant)

Compartment: Endosphere, Nodule, Bulk soil, Inoculant (Input)

STID: STID3

Responsible PI: Simona Radutoiu and Simon Kelly

Description: Lotus japonicus Gifu microbiome and root transcriptome from inoculation with LJSynCom and symbiont M.Loti. Samples are collected 2, 3, 5, 7, 10, 14, 21, 28, 35, 42 and 63 days after inoculation.

Syncom: SCID1

Strains in SCID1: Lj Syncom

Lotus Gifu, Lotus Gifu Symrk

Link to strains

SynCom:

Define new syncom with AM fungi. Bac + Fungi

What company -> strains table?

We know strains

MC: only undefined composition

Experimental protocol:

Link multiple protocols to STID3

PRD?

Seq.exp. transcriptome and microbiome; link to STID3

Strain:

Bac1 🡪 Description: M. loti

Fun1 🡪 AM fungi. Arbusuclar mychorrhiza

Microbial community:

MC5 🡪 Description: Sterile soil (SS) (I am not sure origin of this soil)

MC6 🡪 Description: Native Cologne Soil (this should have collection site information, it is Cologne in Germany but this is all I know)

MC7 🡪 SCID1 (LJSynCom) + Fun1 (SMA)

MC8 🡪 Bac1 + Fun1 (MA)

Nodule same as rhizosphere?

Inoculant?

Should I put in strain germplasm

Experimental protocol:

Lotus Japonicus Gifu incubation in different soils to figure out difference between native cologne soil and three other different communities (H20, LjSynCom + AM fungi, M.Loti + AM fungi) done in sterilized cologne soil.

Transcriptome of the plant was sequenced.

Phenotype: link to files.

Simon: Did you measure SFWg for individual plants in the same pot?

Individual plant per pot

Link from processed data to phenotype description

Link from raw data to phenotype description

In Phenotype description:

Description field

Abbreviation field

1. Put in strains
2. Phenotype description
   1. Description field
   2. Abbreviation field
3. Link from processed data to phenotype description
4. Link from raw data to phenotype description.