•Plant stress tolerance: Realising the global sustainable development goals

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Plant beneficial microbial communities (PGPB) influence plant fitness responses to pathogens and abiotic stress factors. The directed integration of the communities represents a promising sustainable solution to improve agricultural and forestry climate resilience [1, 2]. In natural settings plants are exposed to the enormous diversity of complex ever-changing signals. These factors may help or hinder plant adaptation to rapidly changing environments. Hence, the endophyte and biofilm community studies have to be performed against a background that integrates state-of-the-art observations at various scales. Here we present studies where plant microbiome interactions, examined at a finer scale, such as high resolution microscopy and next generation sequencing, are linked to the observations at the station for measuring ecosystems atmospheric relations (SMEAR Estonia) Fig. 1, 2 [3, 4]).

The SMEAR Estonia station http://smear.emu.ee/ system consists of different compartments (atmosphere, forests, lakes, peatlands, arable land). Concentration of matter or energy tell us about the "content" of the compartments. Fluxes of matter or energy tell us about the "change" of the "content" within the whole system. The dynamic of the system is mediated by a multitude of biological, chemical and physical processes. The processes act on multiple scales.

•Aim
•Understanding the dynamics and feedback of mechanisms between the plant PGPB ecosystem and environment via long-term, comprehensive and integrated phyllosphere, rhizosphere and atmospheric measurements
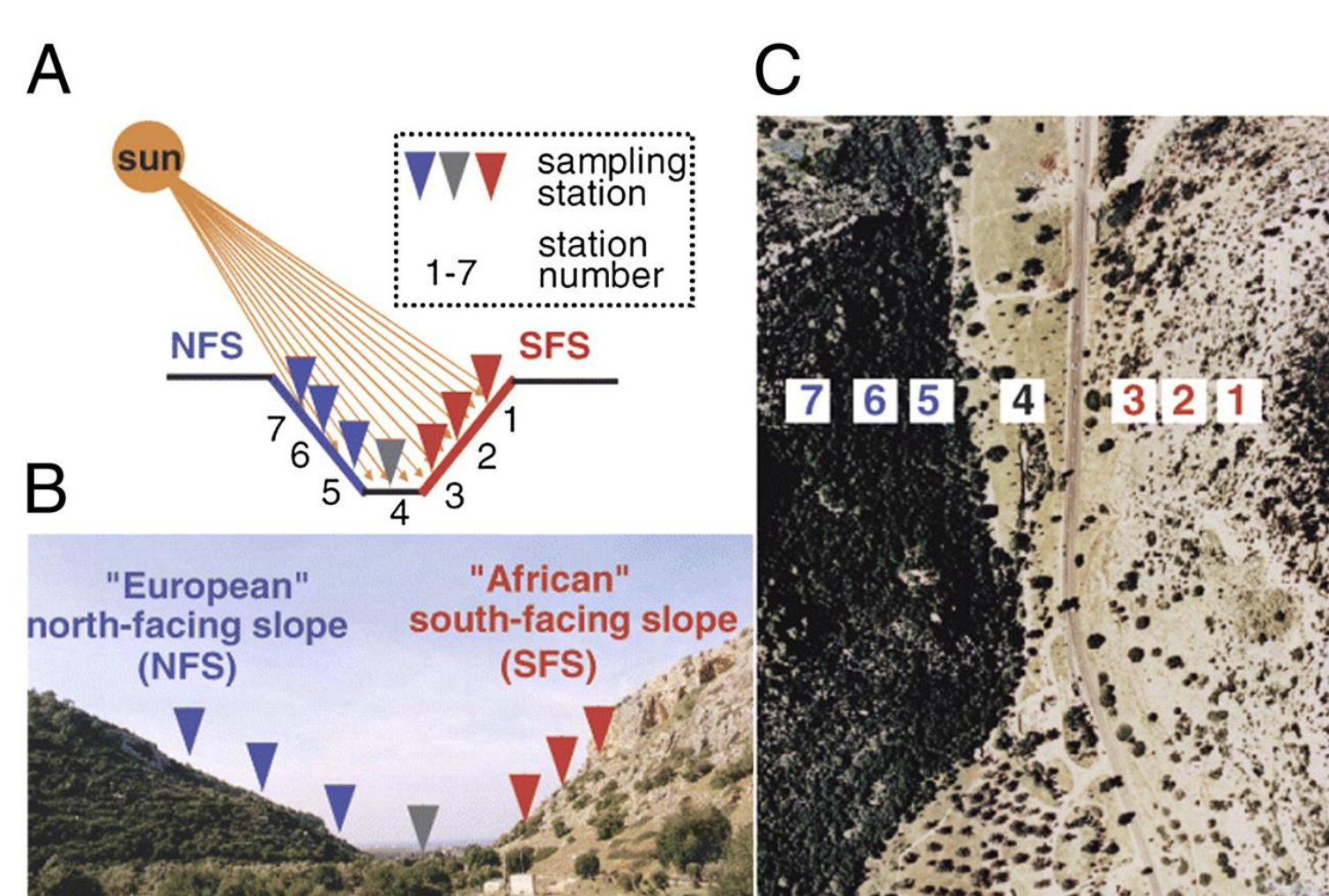

Fig 1 - The Evolution Canyon (EC) model. (A) Schematic diagram. (B) Cross section view of EC at Lower Nahal Oren, Mount Carmel. (C) Air view of EC (source: Nevo, 2012 Evolution Canyon," a potential microscale monitor of global warming across life, PNAS 109; 8) (Photo by E. Nevo).
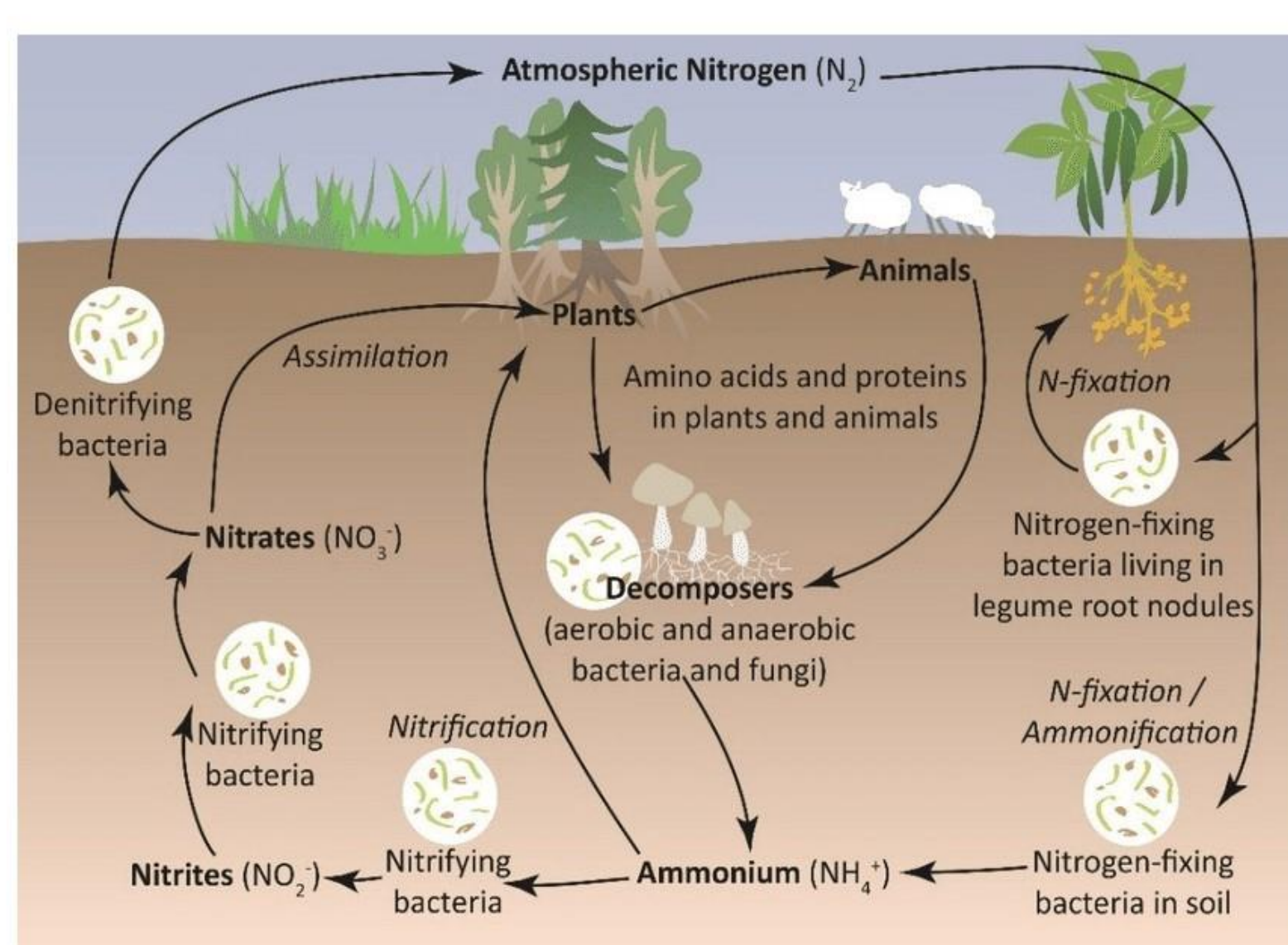

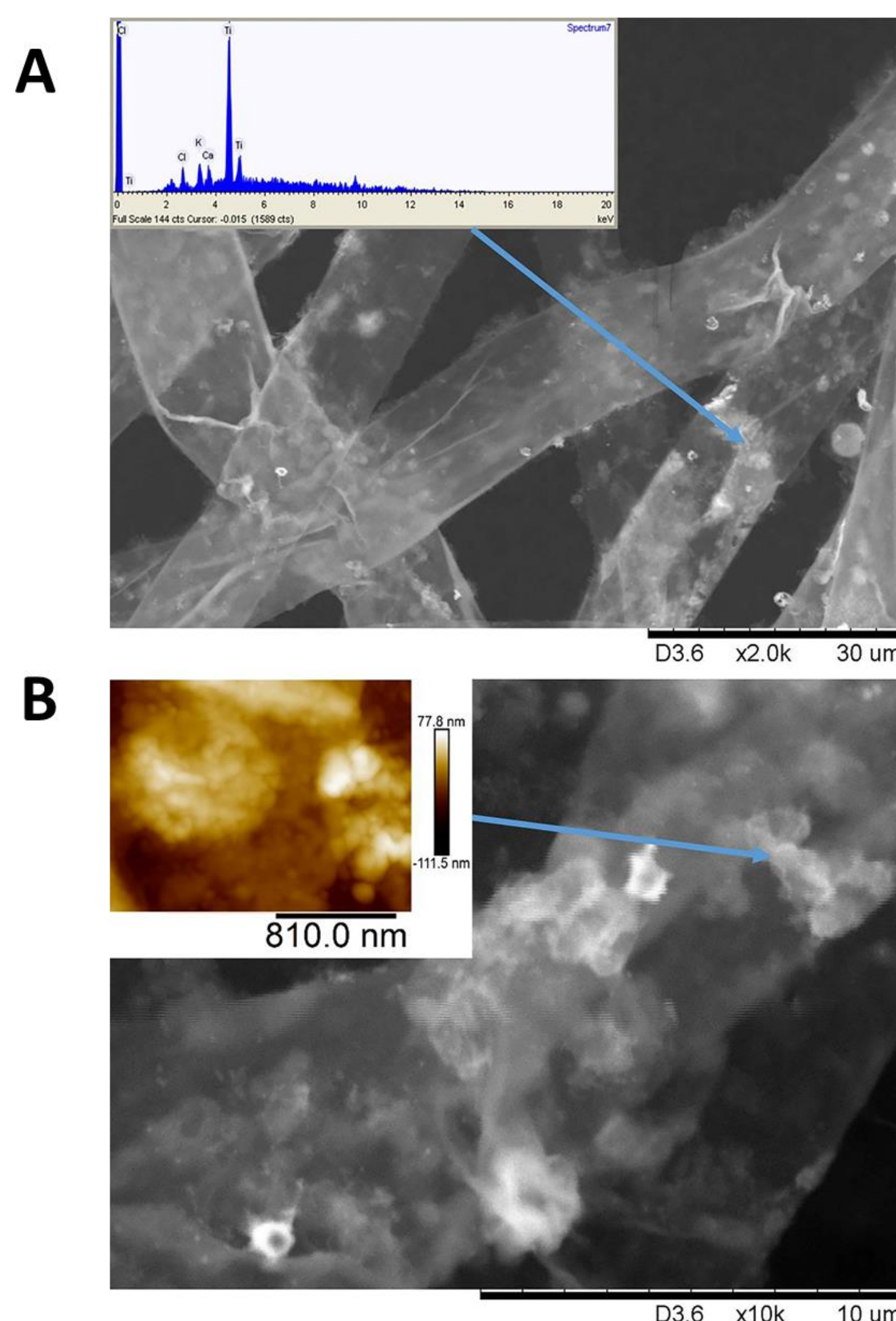**Fig 2-** Schematic figure for terrestrial nitrogen cycle

Fig 3 - PGPR –nanoparticle (NP) aggregates on plant root

•Typical scanning electron microscopy-energy-dispersive X-ray spectroscopy (EDS) images of PGPR cells grown with NPs for 24 hours on plant root after 6 hours of inoculation (**A**). and the characteristic aggregate sizes of 50–60 nm (**B**) (2)
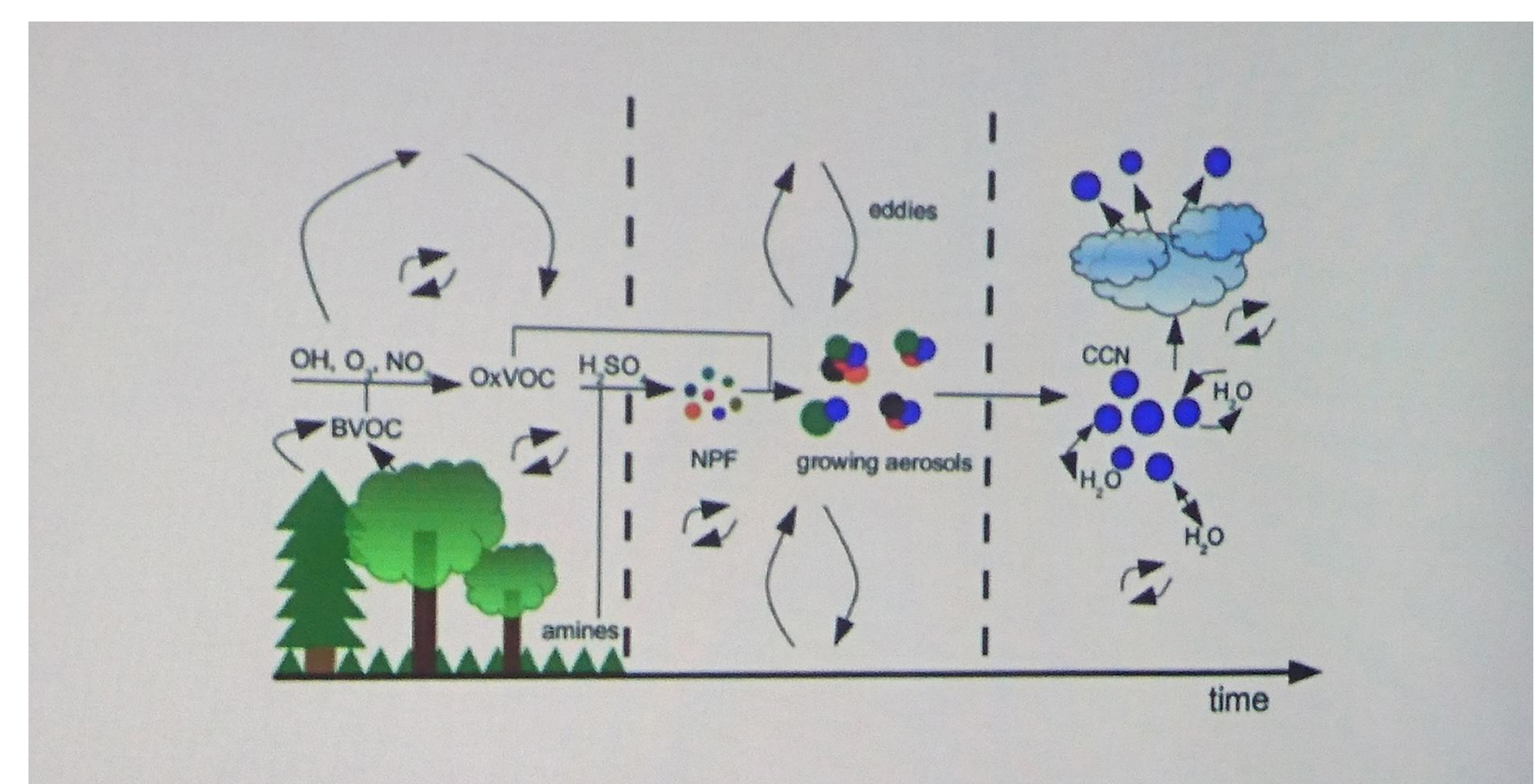

Fig 4 - Forests determine cloud formation

Results

•1. Bacterial inoculants are isolated from the roots of the EC wild progenitors of cereals [1, 2]. The harsh environment rhizobacteria which co-evolved with the host, most likely have assisted the wild progenitors to survive high levels of drought, UV, heat and nutritional deprivation over a long period of time.

•2. Bacterial consortia are formulated for seedlings inoculation considering Si nanoparticles ability to modulate the bacterial biomolecules surface (Fig.3).

•3. Nanointerface interactions between seedlings and the bacterial consortia on the rhizosphere and phyllosphere of seedlings are followed by integrating genomics, transcriptomics and metabolomics focusing on:
•a. Identification and dynamics of community structure
•b. Identification of dominant key metabolic pathways.

•4. Continuous measurements of ozone, carbon dioxide, water vapour, methane, nitrogen oxides and sulphur dioxide concentrations at two canopy layers.

•5. Atmospheric particulate matter and air ion measurements (Fig. 4).

•6. Soil variables measured using a diverse set of sensors and chamber systems.

•7. Continuously measured data covering key ecosystem traits (net primary productivity, individual plant growth, gas-exchange characteristics).

•**Conclusion** Integrating plant specific microbiome with the ecological background will enable development of efficient strategies based on ecological know-how.

References
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