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Fungal commposition after vaccination of *Ulmus glabra*

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FORMAS

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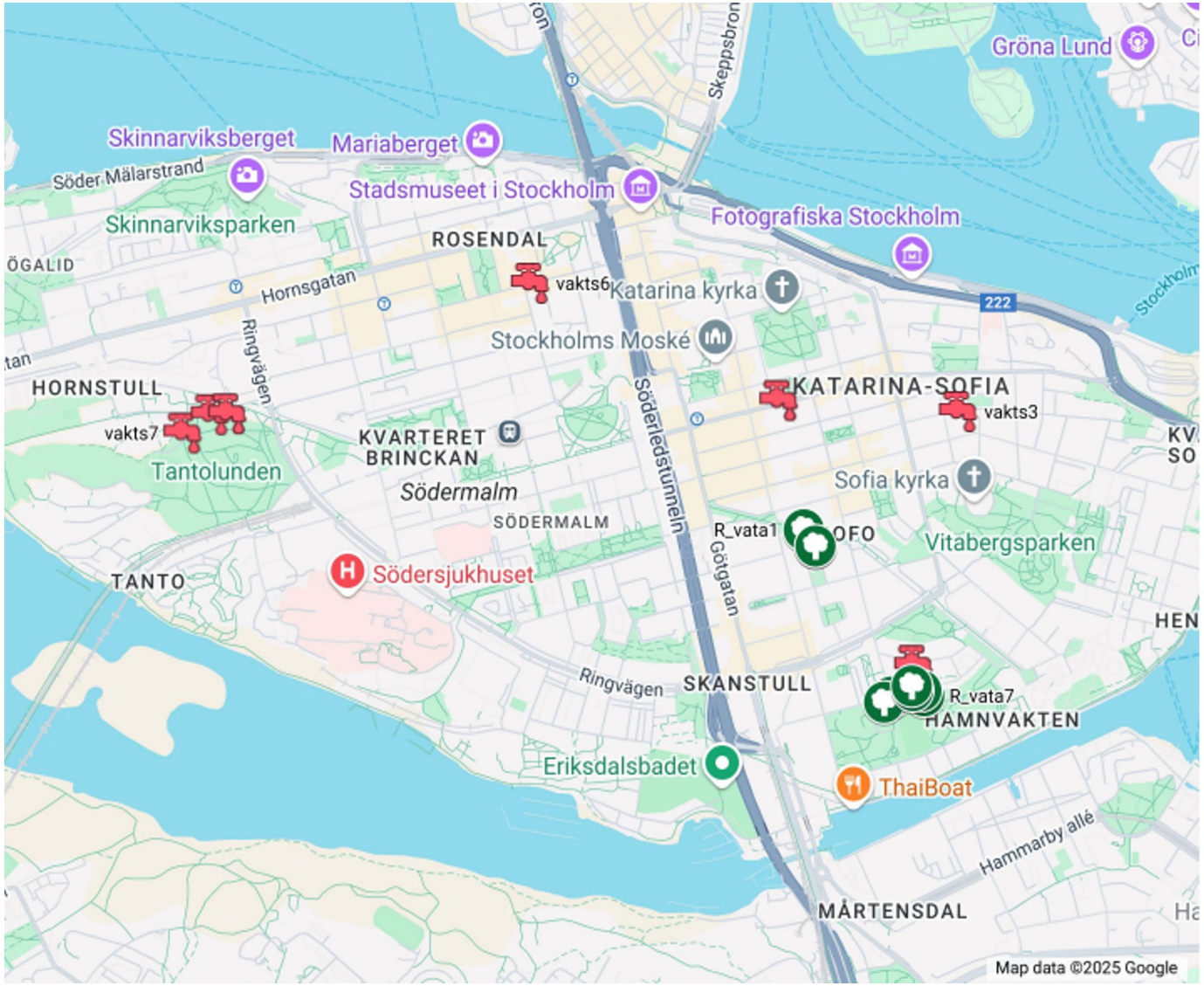
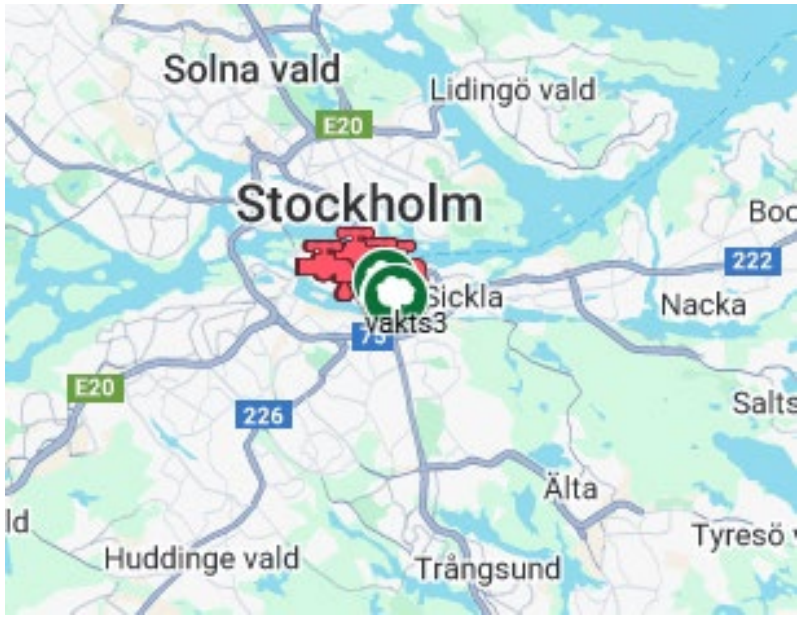
Study sites in Stockholm





Ulmus glabra

- 10 vaccinated
- 10 unvaccinated

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Methods

- twigs for sampling
- the samples for DNA extraction from **wood** and **bark**
- fungal DNA amplified using primers ITS4ngs and ITS1catta included a 10–12 base multiplex identifier (MID)
- Amplicons were pooled into sequencing libraries, followed protocols for the PacBio third-generation sequencing platform
- Sequencing was conducted on the PacBio RSII platform at the University of Oslo Sequencing Centre.

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Results across 40 samples (wood and bark)

- 85662 sequences
- 3214 OTUs
- On average the dataset consisted of 171± 30.3 (mean±SE) OTUs per sample

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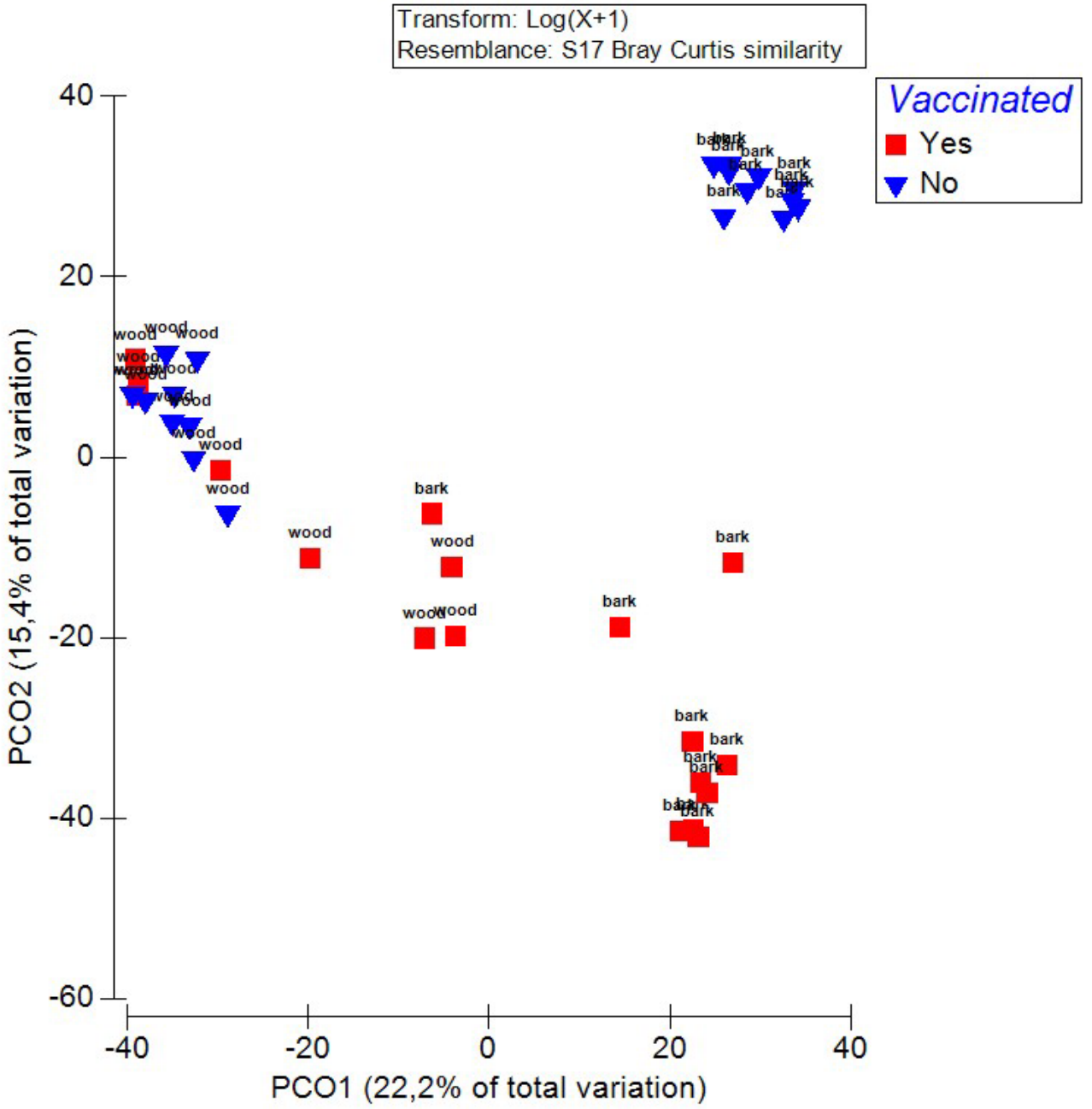
Species composition between vaccinated and unvaccinated trees



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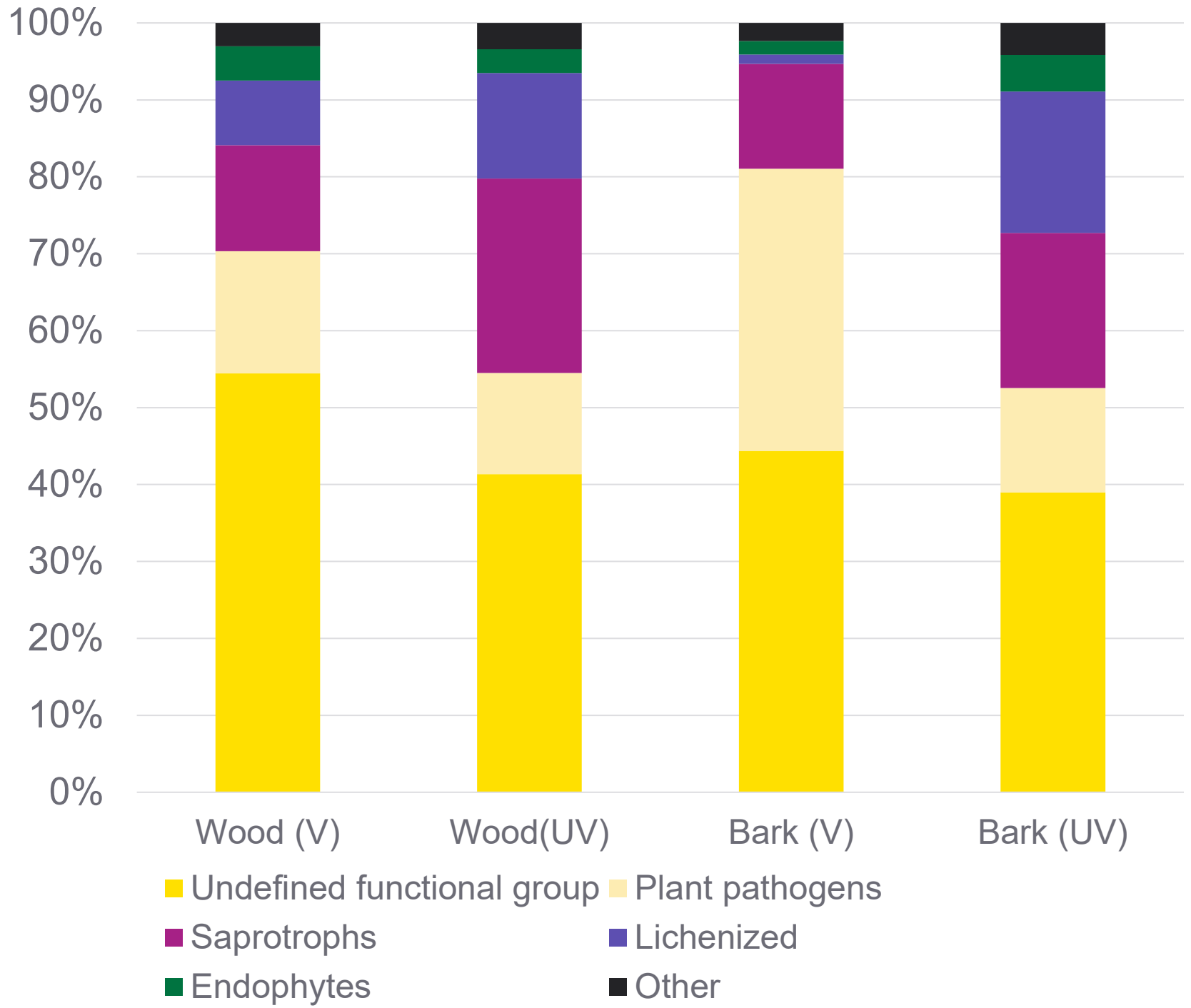
The relative abundance of different functional groups between vaccinated (V) and unvaccinated (UV) wood and bark samples of *U. glabra*



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Overall fungal richness and diversity

- vaccinated trees had a significantly lower overall residual fungal richness in both
  - bark ($F=291.7$; $p<0.05$)
  - wood ($F=21.3$, $p<0.05$)

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Relative abundance of *O. novo-ulmi*

- significantly lower in vaccinated trees when compared with unvaccinated trees
- percentage of *O. novo-ulmi* did not differ significantly between the bark and wood samples

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Most significant taxa identified to species level on unvaccinated

- *Cladosporium sphaerospermum* – xerotolerant saprotroph
- *Ophiostoma novo-ulmi* – pathogen
- *Seltsamia ulmi* – saprobic, particularly on elm bark and wood

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Taxa that were identified to species level, the indicators of vaccinated *Ulmus glabra*

- *Xenosonderhenia syzygii* – exact ecological impact is still being studied
- *Knufia cryptophialidica* – black yeast (extremotolerant rock-inhabiting fungus)
- *Neocatenulostroma microsporum* – endophyte, saprobe, or potential plant pathogen

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