

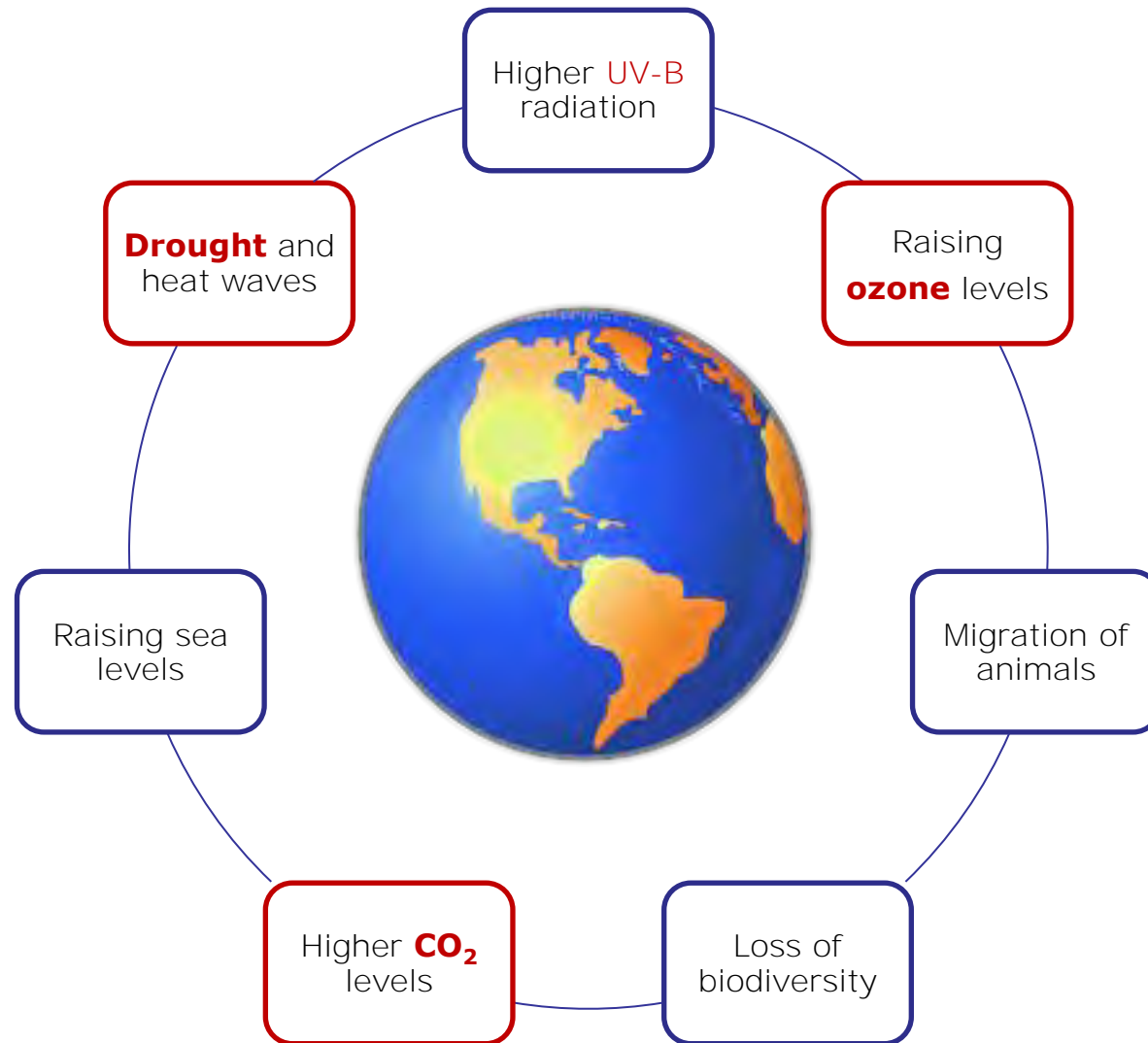


Common ragweed (*Ambrosia artemisiifolia*):

Systems biology to understand the reaction of the allergenic pollen to air pollutions and climate change

Ulrike Frank

Impact of climate changes and global warming



Questions to be answered:

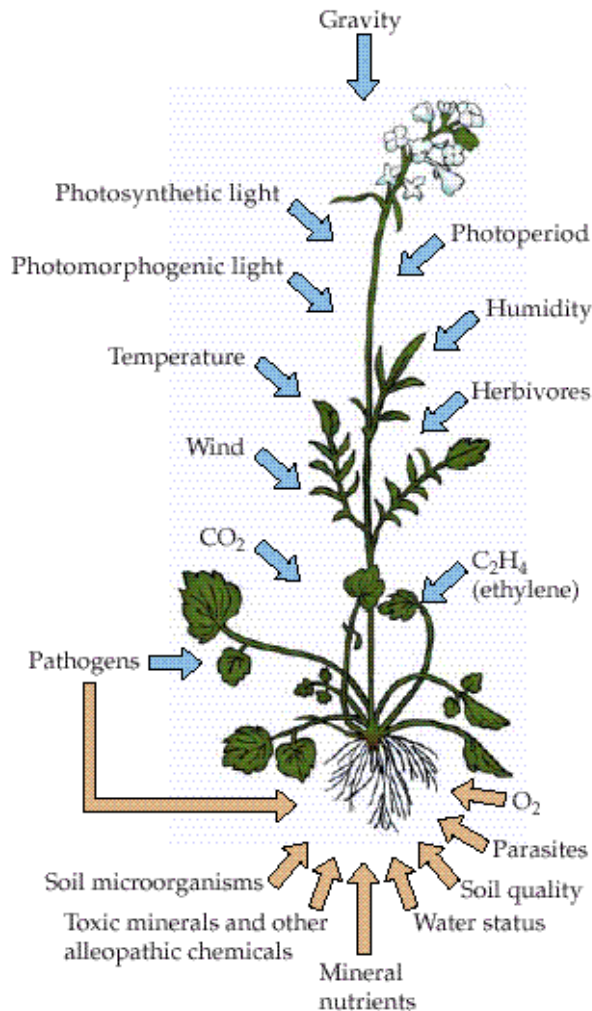
- Does European ragweed pollen have a **modified allergen set**?
- Do **climatic parameters** influence the allergenicity of ***Ambrosia*** pollen?
- What is the impact of **long distance transport** on the pollen allergenicity?
- **Which allergens** are induced under **which environmental conditions**?
- Due to a **profiling** of allergenicity induction (**transcript-, protein-, and metabolite level**) new, **unknown allergenic components** should be identified and characterized as basis for immunotherapy

Hypothesis: The allergenic potential in plant components depends on environmental conditions

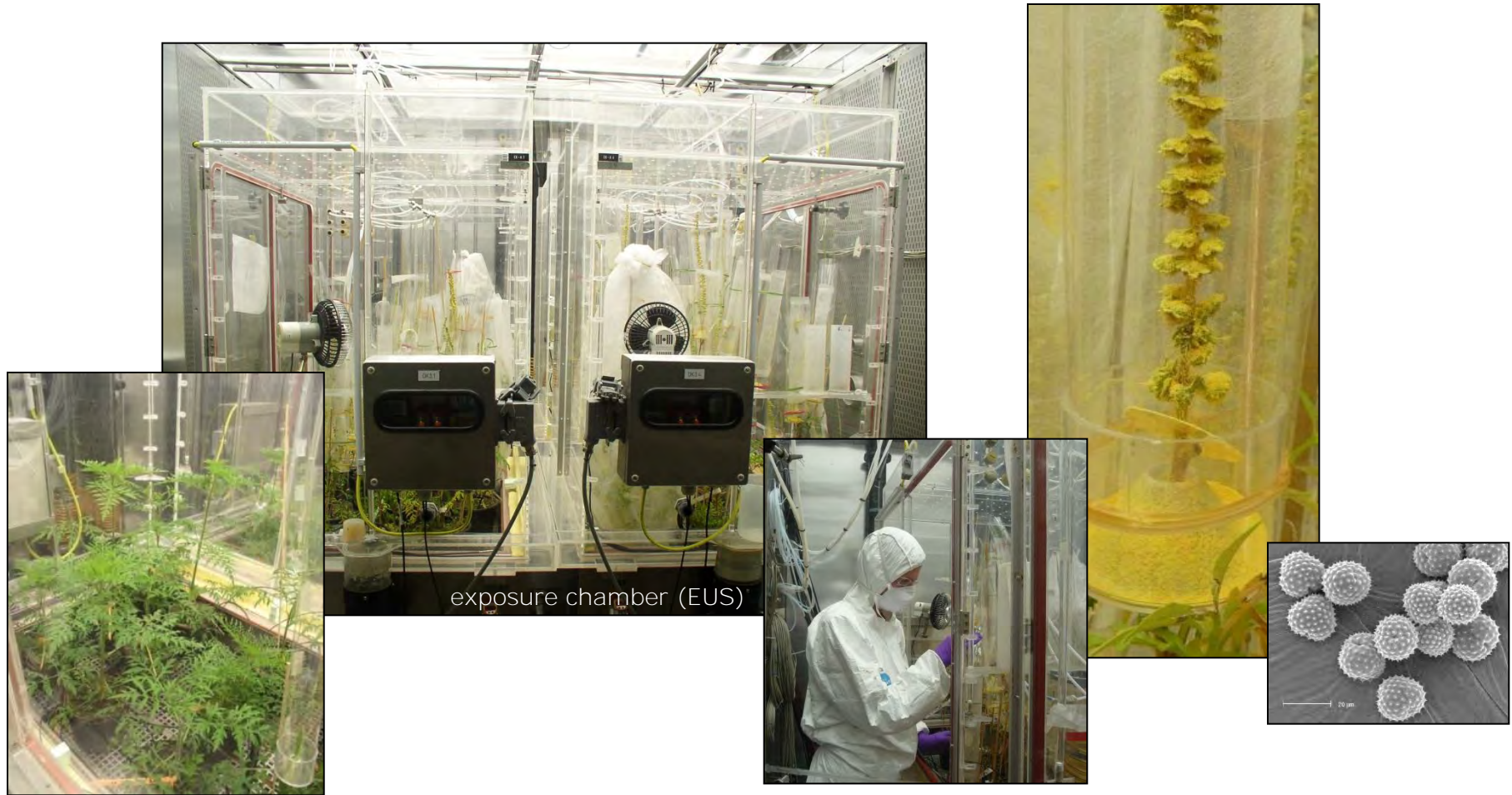
Example: 25% of all plant allergens are related to the pathogenesis-related proteins (PR) = stress proteins

Aim:

Investigate the impact of environmental and climatic parameters on the induction of potentially allergenic components in *Ambrosia* pollen



Ambrosia – growth in exposure chambers under climate change parameters

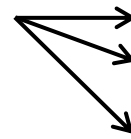


Treatments: elevated **ozone**, **CO₂**, **NO₂** and **drought**

Ambrosia – environmental impact on genes and proteins

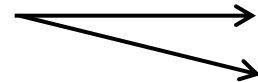
Systems biology of *Ambrosia*:

Genes ? → Transcriptomics



454-sequencing
SuperSAGE
Illumina

Proteins ? → Proteomics



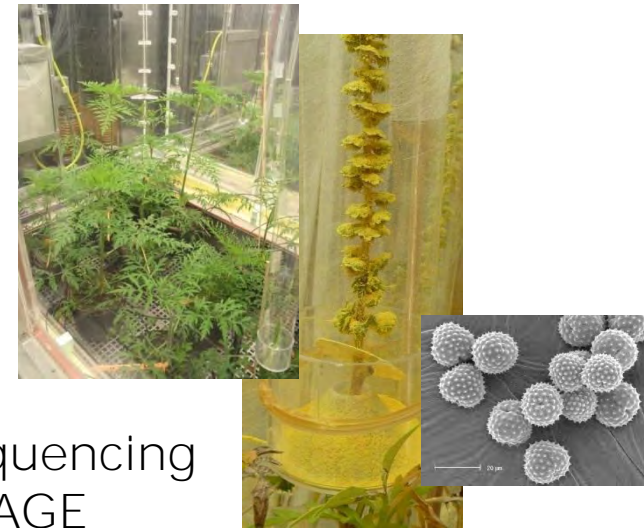
2D-DIGE + LC-MS/MS
ICPL-analysis + LC-MS/MS

Metabolites ? → Metabolic profiling → HPLC

Morphology and surface structure ? → SEM; ATR-FTIR

Allergens ? → Amb a 1 – Amb a 11 → ELISA

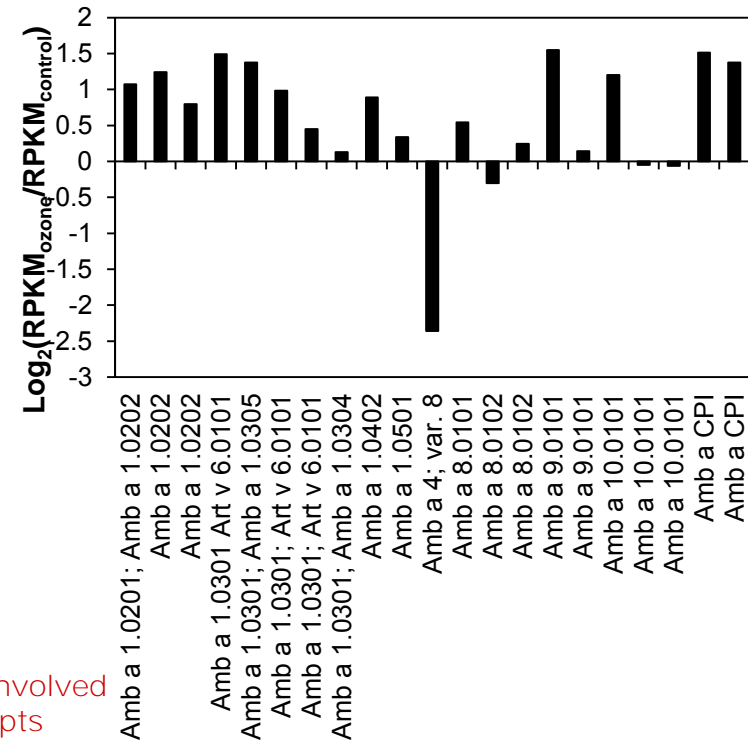
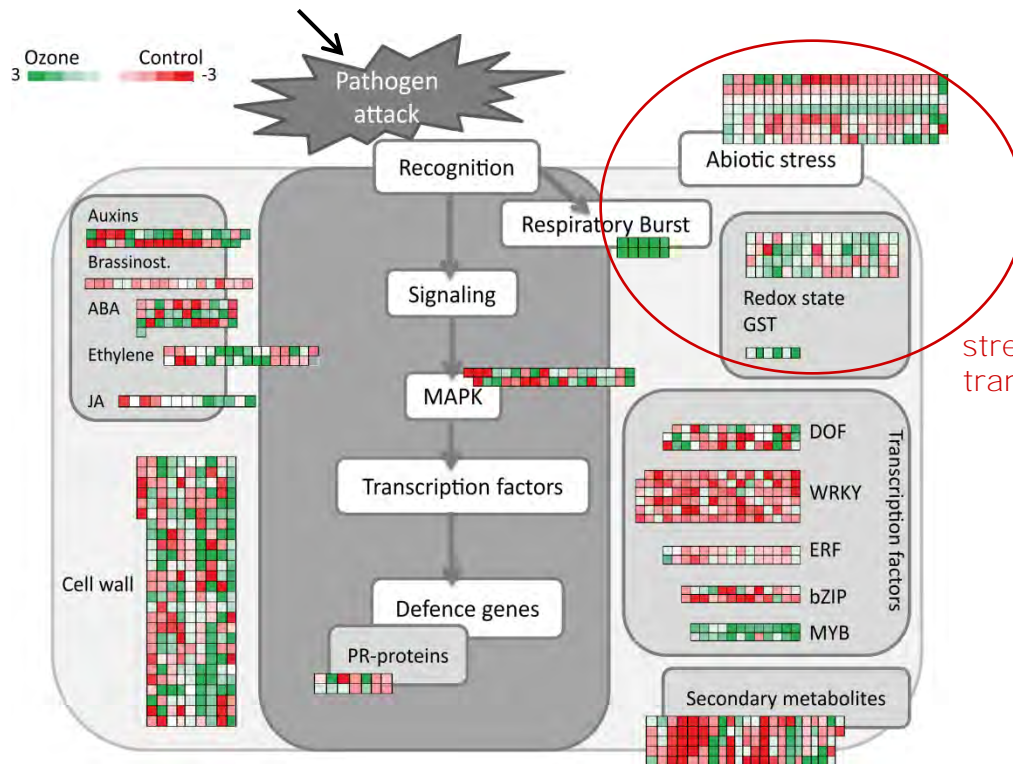
Immunoblotting



TRANSCRIPTOMIC DATA

Ozone induces allergen- and stress related transcripts (454-Sequencing)

Arabidopsis thaliana approach
 non-red. Protein Allergen approach



RPKM: Reads per kilobase per million mapped reads

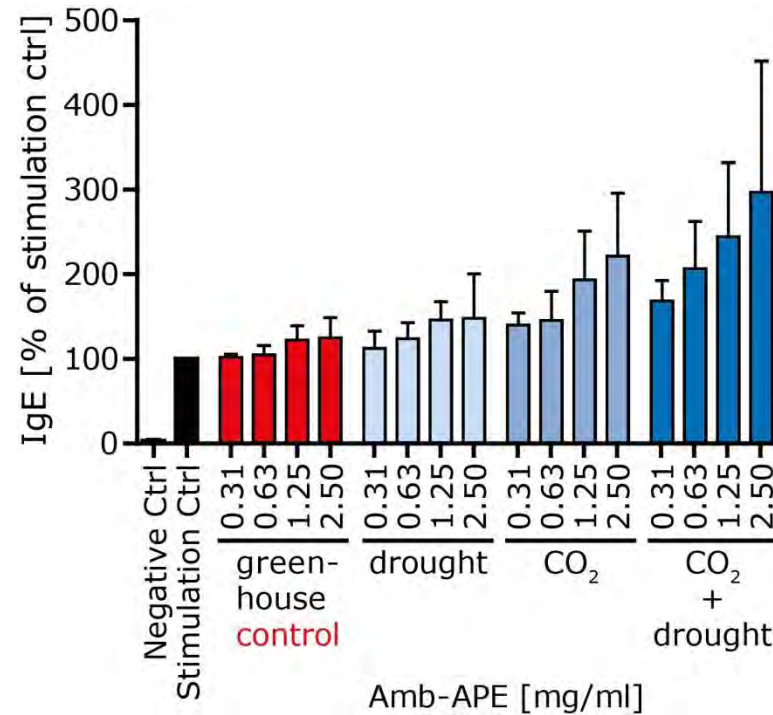
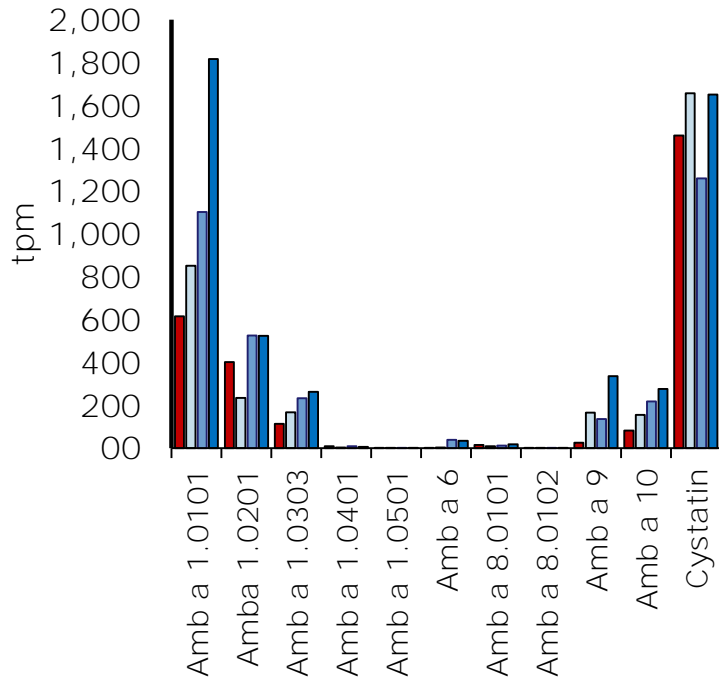
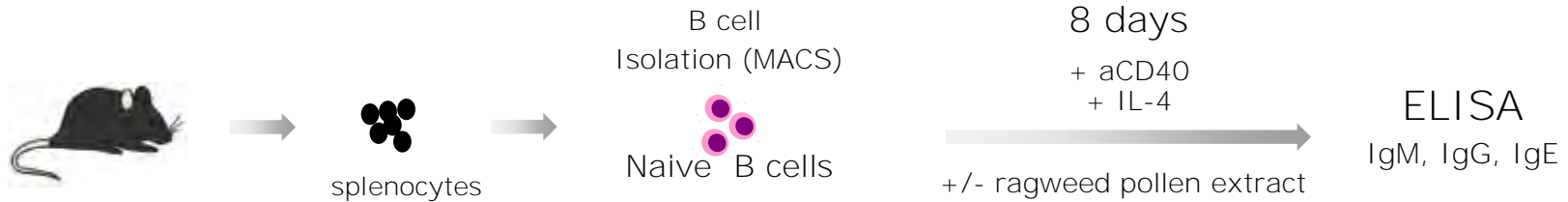
$$RPKM = \frac{C}{LN}$$

C: Number of mappable reads on a e.g. transcript

L: Length of transcript (kb)

N: Total number of mappable reads (million)

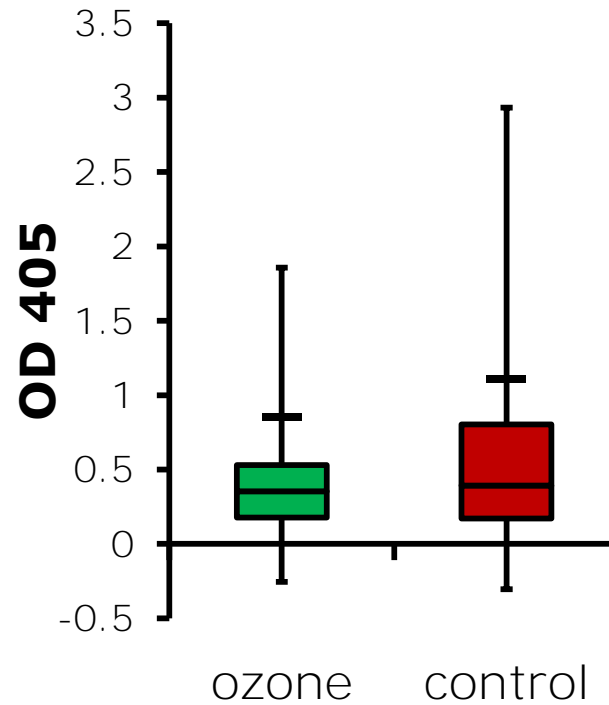
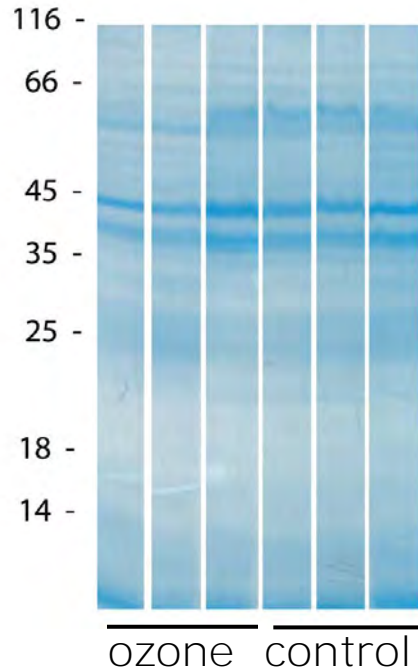
CO₂ and drought increase the IgE-enhancing potential of ragweed pollen



Öder S. et al. in preparation

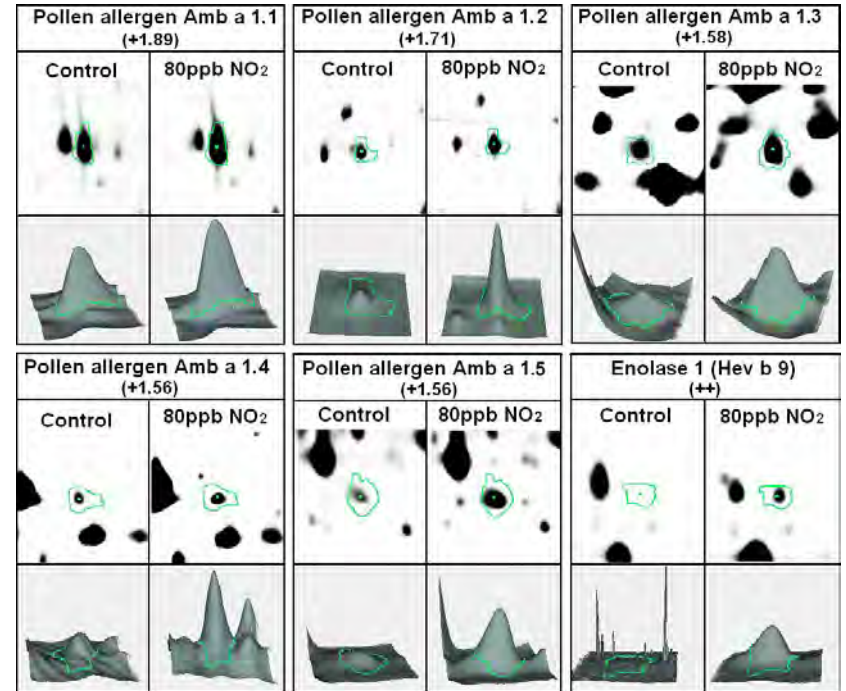
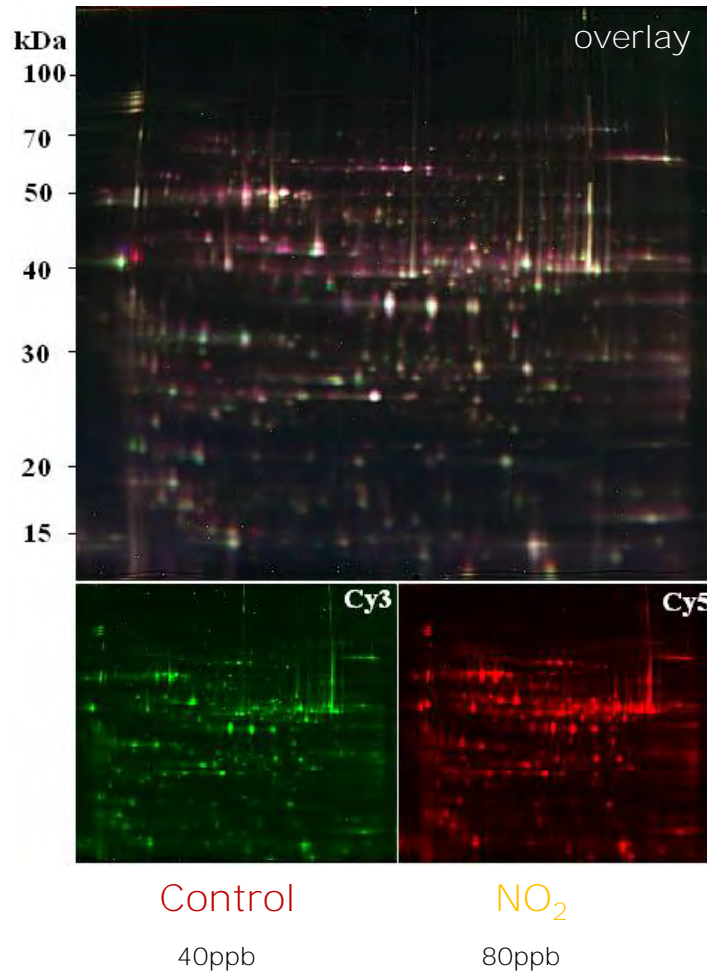
PROTEOMIC DATA

Ozone treatment does not increase the amount of the major allergen Amb a 1 on the protein level (ELISA)



Kanter et al. PLoS ONE 8:e61518, 2013

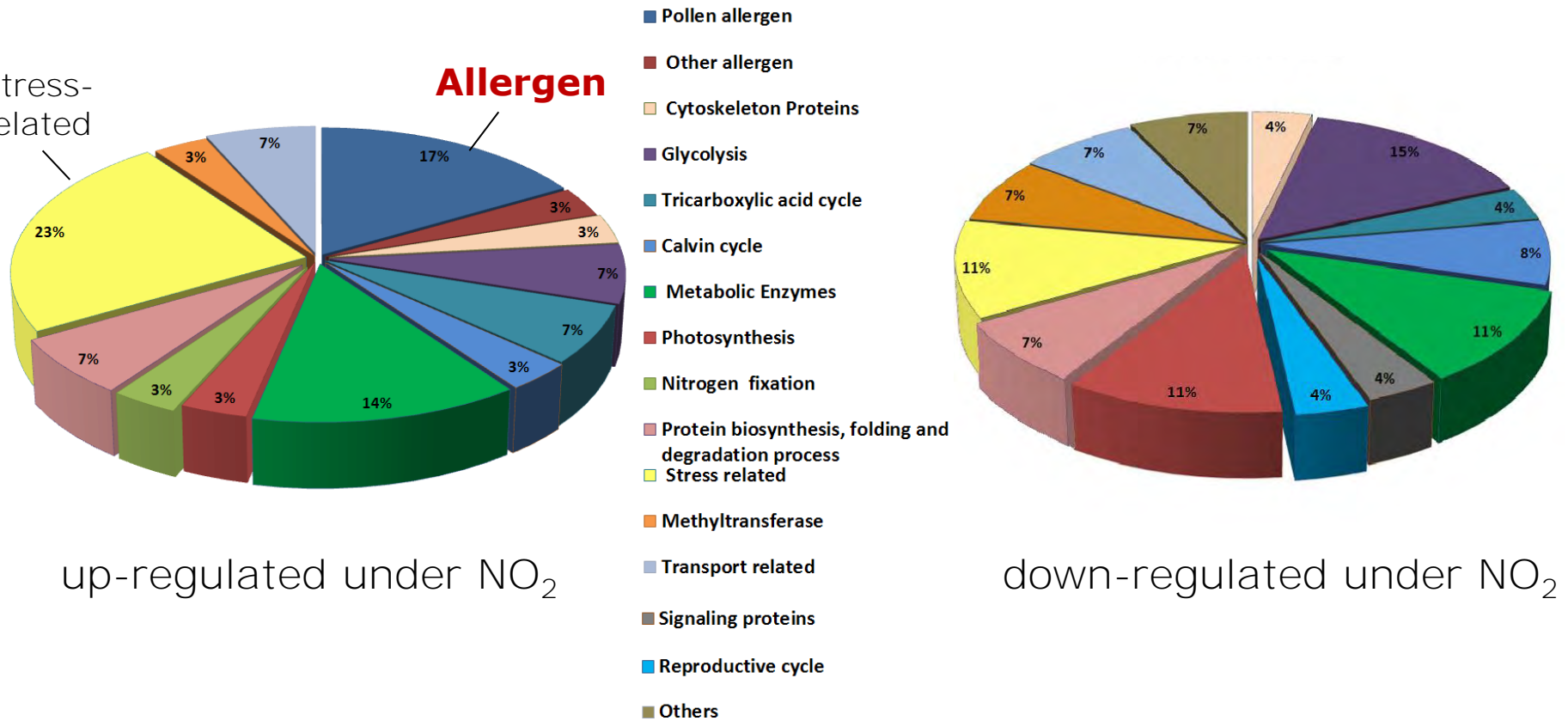
NO₂ treatment induces Amb a 1 isoforms and stress relevant proteins (2D-DIGE)



Proteins were identified by LC-MS/MS

(Zhao et al., PCE 2015)

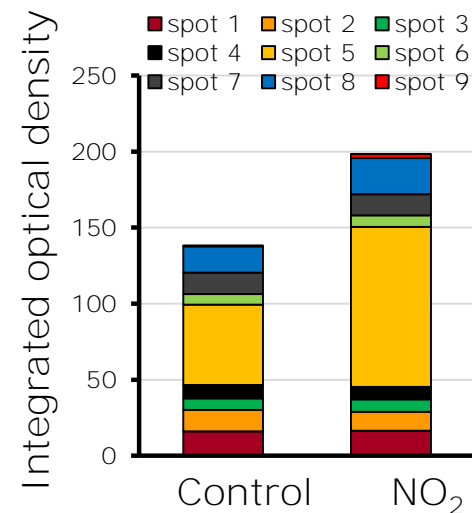
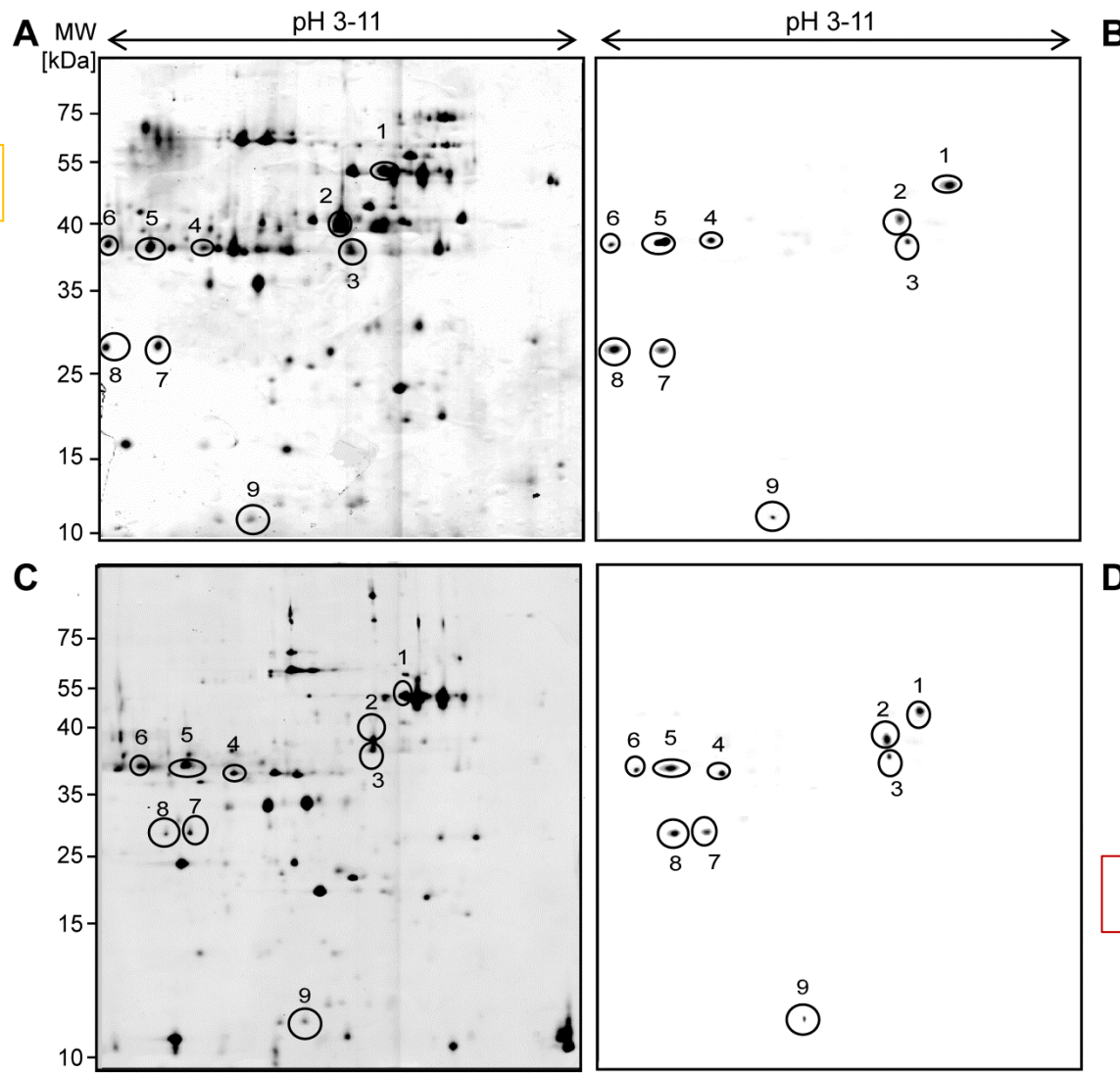
NO₂ treatment induces **Amb a 1** isoforms and **stress relevant** proteins (2D-DIGE; LC-MS/MS)



(Zhao et al., PCE 2015)

NO₂ treatment results in higher allergen recognition (2DWestern-Blot with sera from atopic patients)

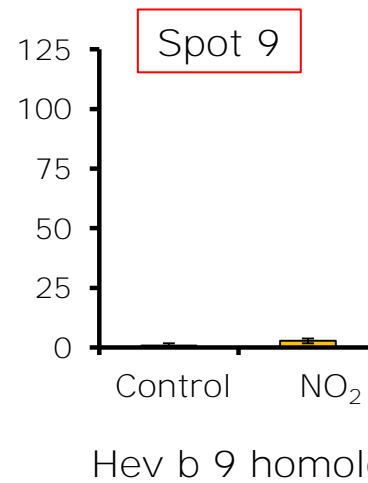
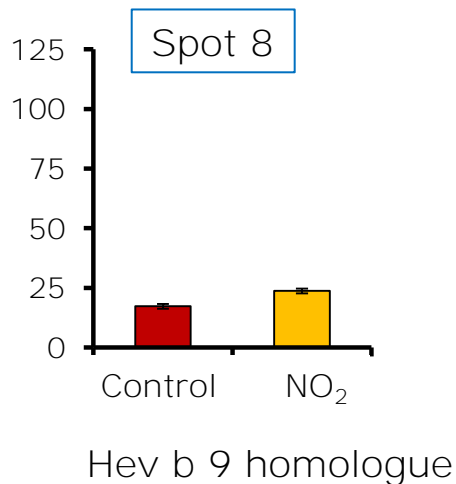
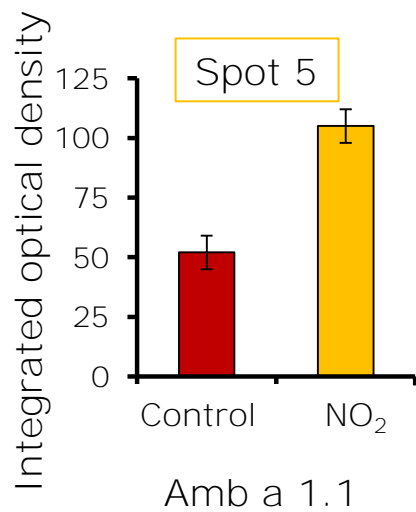
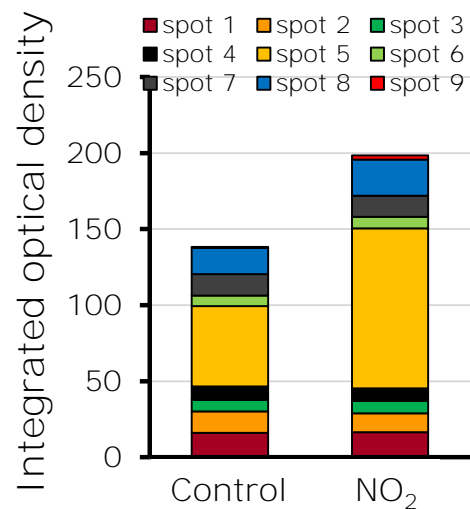
NO₂



Control

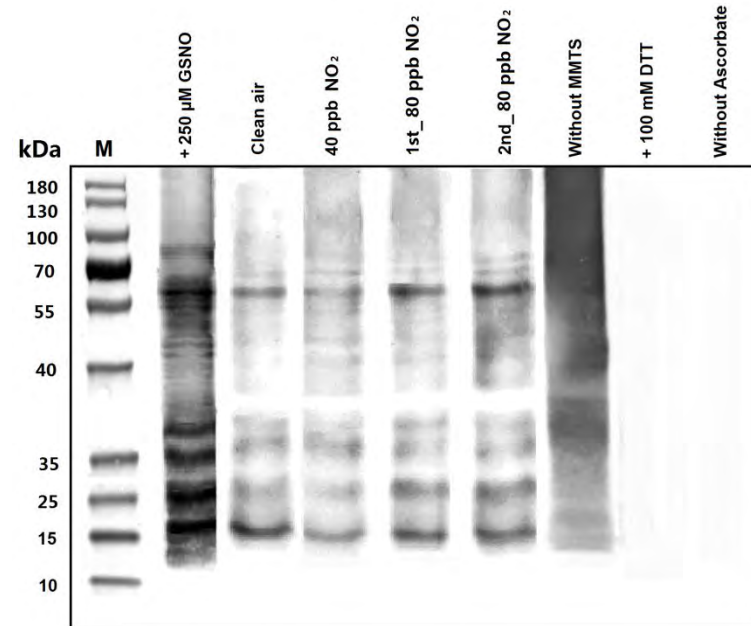
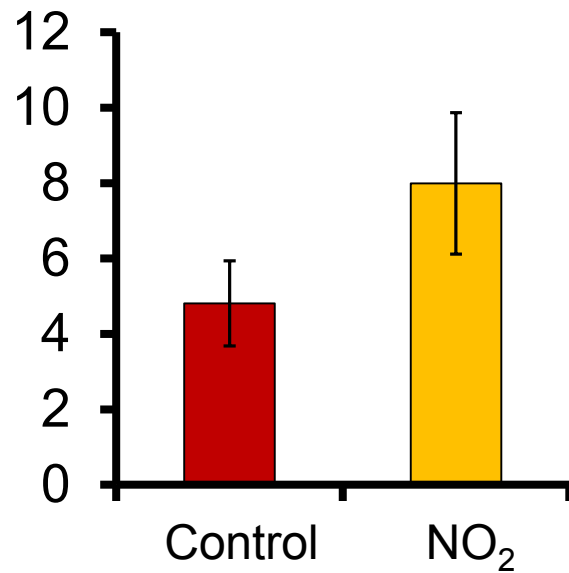
(Zhao et al., PCE 2015)

NO₂ treatment results in higher allergen recognition (2DWestern-Blot with sera from atopic patients)



(Zhao et al., PCE 2015)

NO₂ treatment induces nitrosylation of ragweed pollen proteins (biotin-switch; LC-MS/MS)



- Isoforms of major allergen **Amb a 1** can be **nitrosylated**

(Zhao et al., PCE 2015)

Future plans

- analysis of the influence of different environmental conditions on pollen allergenicity
 - detect new allergens and further characterization of them
 - analysis of pollen from different outside stands
-
- We are interested in new cooperation

People involved in the project:

Helmholtz Zentrum München
Institute of Biochemical Plant Pathology:

Ulrike Frank
Amr El Kelish
Feng Zhao
Karin Pritsch
Dieter Ernst
Jörg Durner

Research Unit for Environmental Engineering:

J. Barbro Winkler

ZAUM – Center for Allergy & Environment (ZAUM)/TUM
Institute for Allergy Research (IAF), Helmholtz Zentrum München

Maria Kamml
Sebastian Öder
Heidrun Behrendt
Jan Gutermuth

Research Unit Environmental Genomics:

Marion Engel

Institute of Bioinformatics and Systems Biology:

Matthias Pfeifer
Klaus Mayer

Core Facility Proteomics:

Christine von Törne
Stefanie Hauck

Technical University München; Institute of Environmental
Medicine, UNIKA-T

Claudia Traidl-Hoffmann
Steffi Gilles

University for Applied Science, Department of Natural
Sciences and Mechatronics

Paula Braun

LMU München; Clinic and Polyclinic for Dermatology and Allergology,
Faculty of Medicine

Franziska **Ruëff**

University of Innsbruck, Institute of Botany:

Andreas Holzinger

University of Salzburg, Department of Molecular Biology:

Michael Hauser
Fatima Ferreira