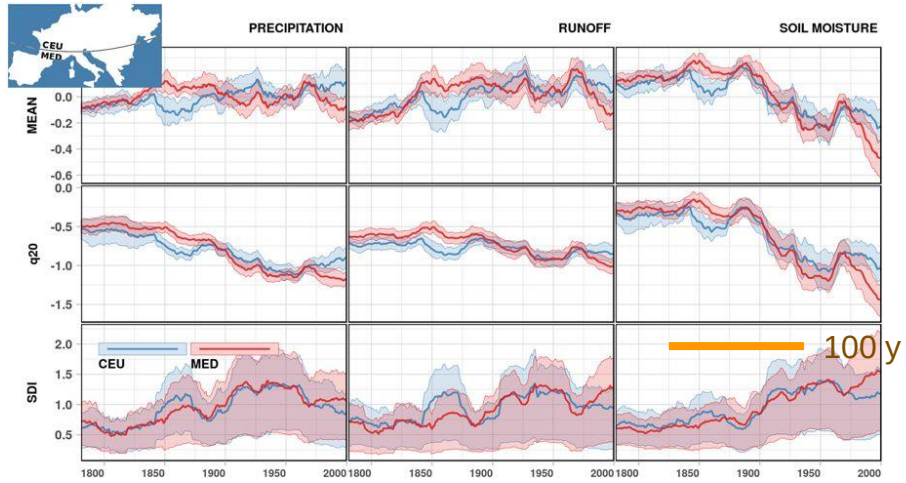
Can phenotypic marker-assisted selection for drought tolerance replace stress-trials in potato?

Haas, Manuela; Sprenger, Heike; Aneley, Gedif; Rudack, Katharina; Zuther; Ellen, Peters, Rolf ; Seddig, Sylvia; Walther, Dirk; Kopka, Joachim; Hincha, Dirk K.; Köhl, Karin I.

Potato, 2011, NW Germany

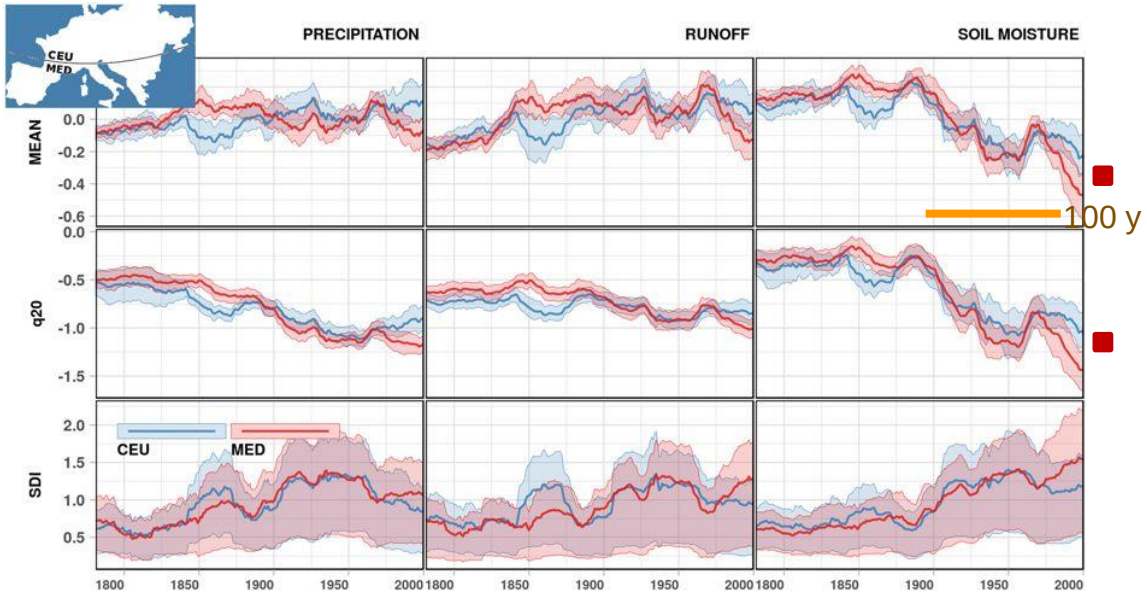
Corn, 1.7.18, NE Germany



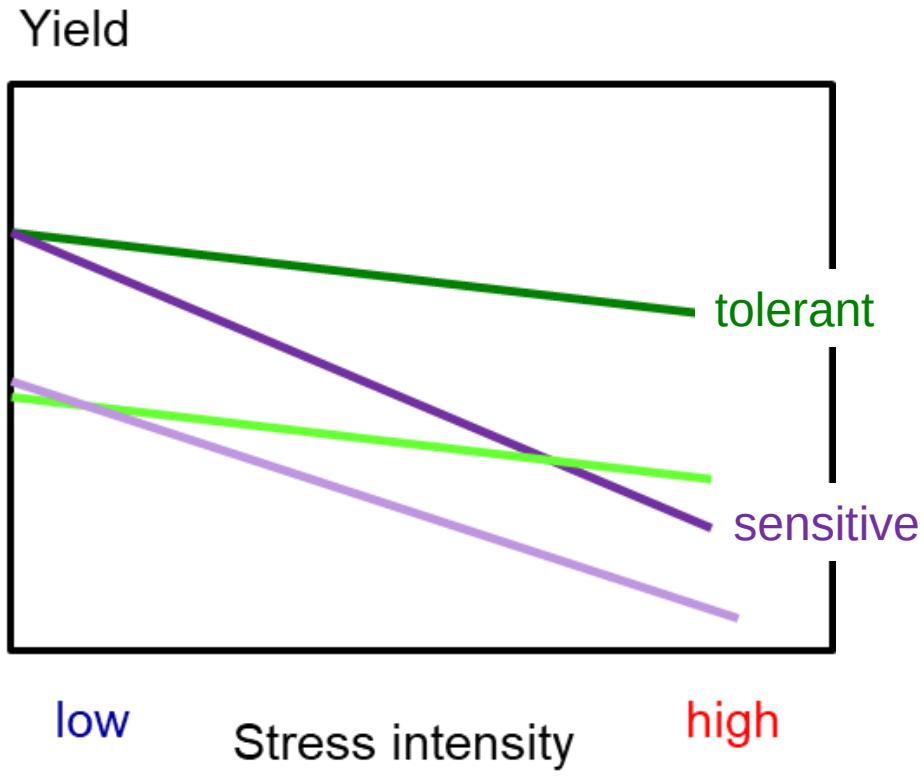
Hanel et al. 2018, Scientific reports

The challenge: yield stability at reduced water supply

- Prediction: increased likelihood of seasonal droughts will decrease yield
- Central Europe less precipitation during spring/summer
- Drought tolerant cultivars: increased yield stability

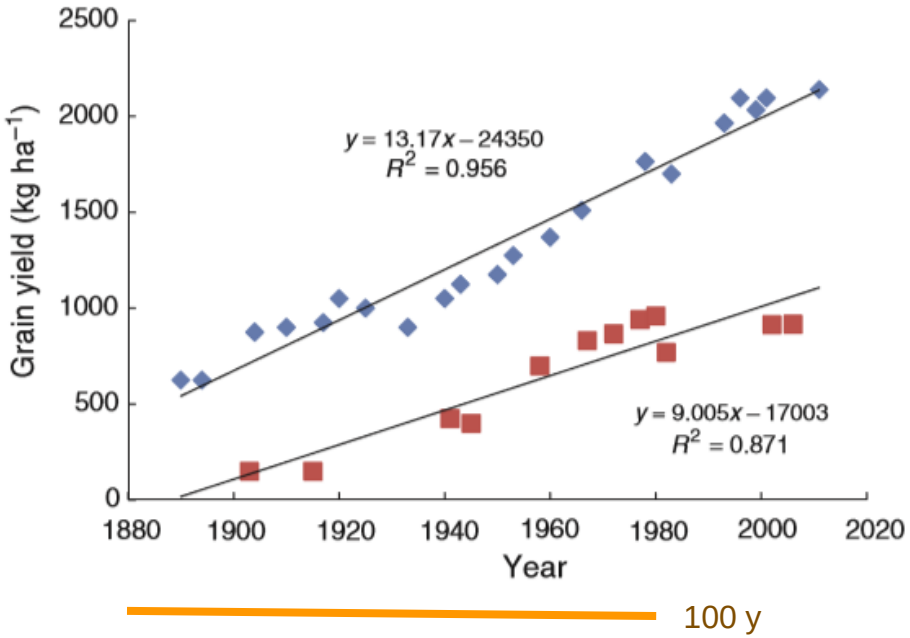


Temporal dynamic of precipitation and soil moisture (Hanel et al 2018)



The approach: marker assisted selection

- Classic tolerance breeding: selection on yield in arid environments successful but slow
- Marker assisted selection (MAS) may save years
- Approach: test ‚phenotypic' markers

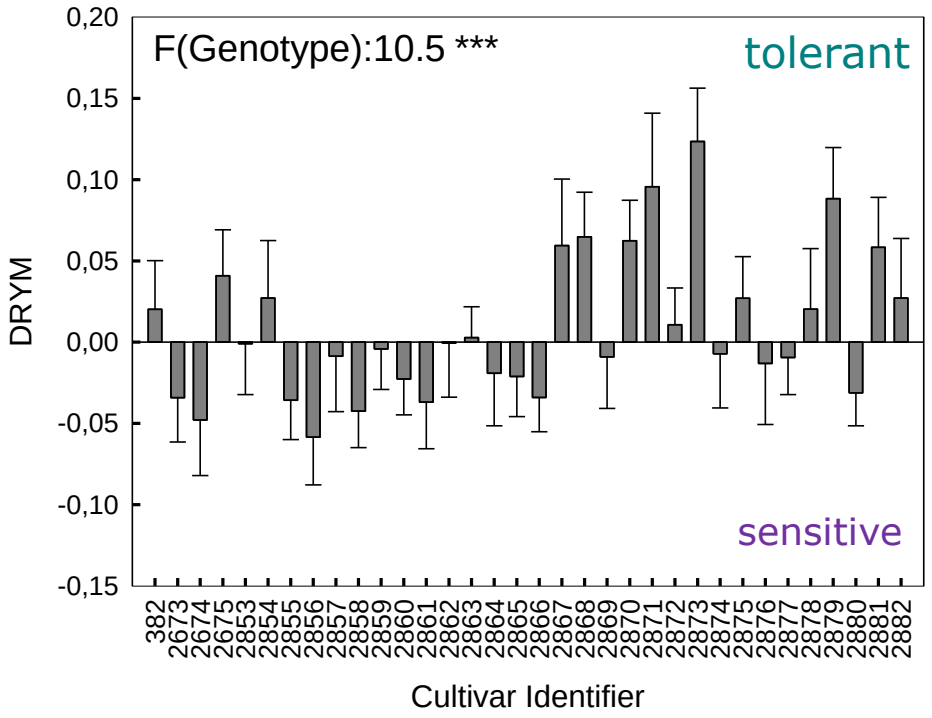


Australian wheat yield in favorable and dry years (Richards *et al* 2014)

Identification of metabolite/transcript markers for drought tolerance (TROST)

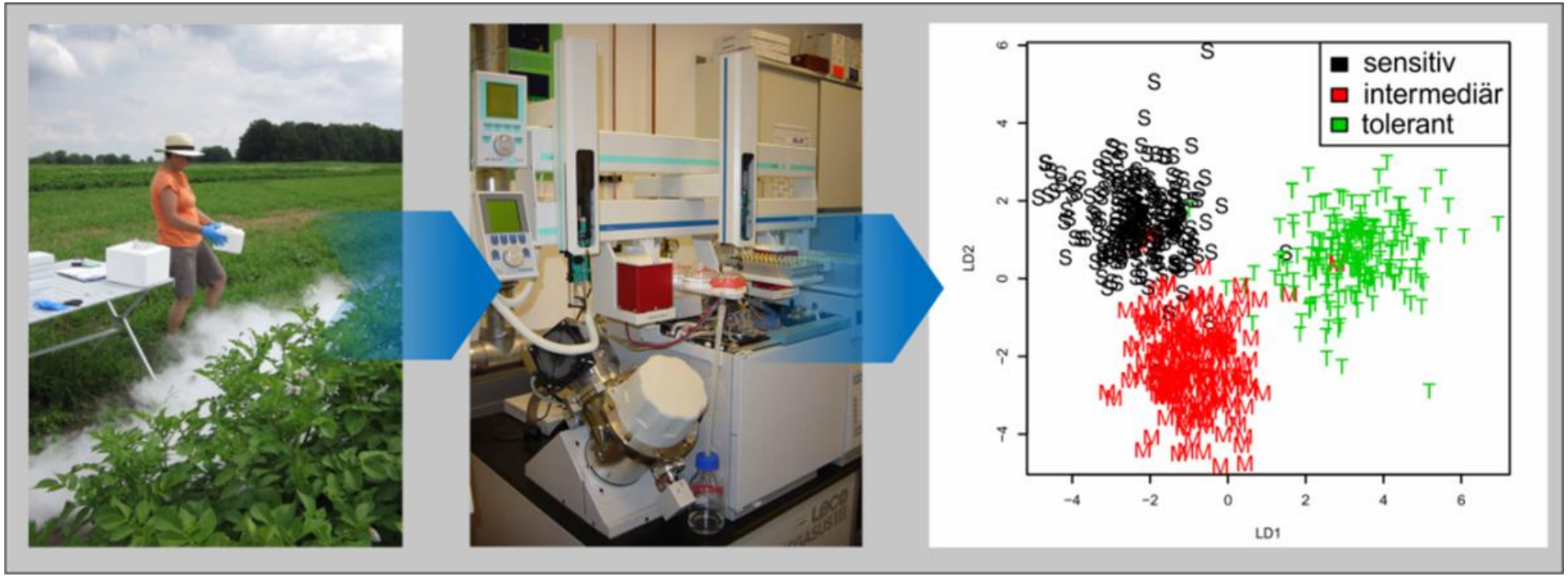
- 8 field and 6 pot trials with optimal and reduced water supply on 34 *Solanum tuberosum ssp tuberosum (4n)* cultivars
  - Data management pipeline for metadata, phenotyping, sampling and analytical data (DOI 10.1071/FP120)
  - Significant variation in drought tolerance based on **tuber** starch yield (DOI:10.1071/FP15013)

Drought tolerance in managed trials



Identification of metabolite/transcript markers for drought tolerance (TROST)

- Leaf sampling in field and pot trials at BBCH 50 - 59
- Metabolite (GC-MS) and transcript (NGS/qPCR) measurements (DOI: /10.1111/pce.12780)
- Development of a random forest prediction model for drought tolerance (DOI: 10.1111/pbi.12840)



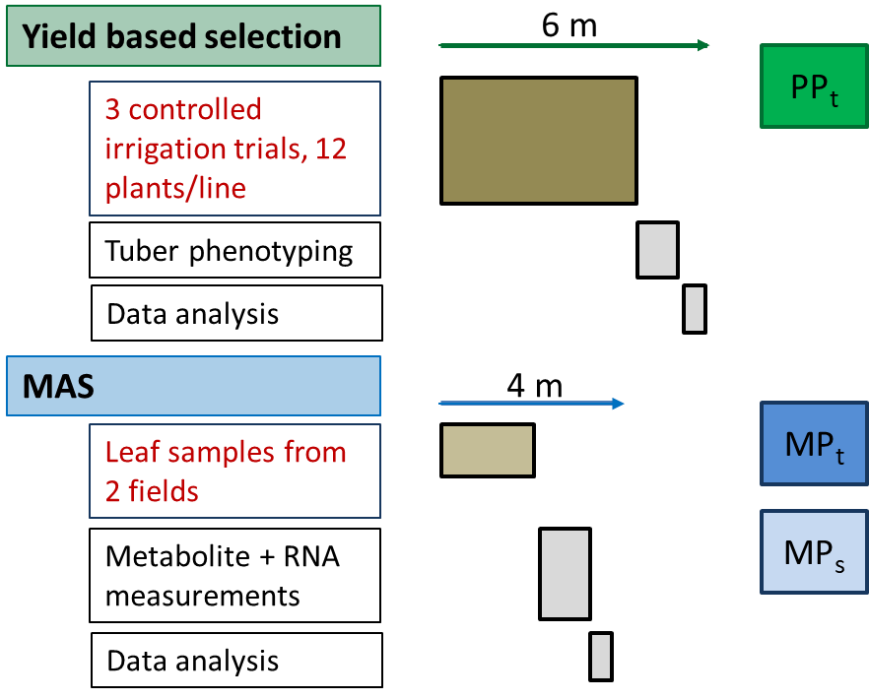
Cross-validation of metabolite/transcript marker model

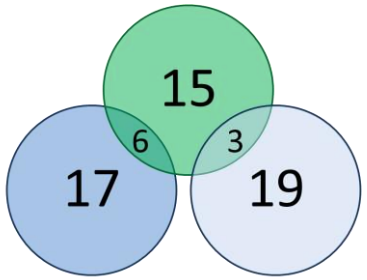
- Cross-validation of tolerance prediction on ~ 1000 samples from 8 independent field sites, 2 years
- Same 34 cultivars as in managed sites
- Prediction accuracy > 90 %
- Independent of agro-environment (DOI: 10.1111/pbi.12840)

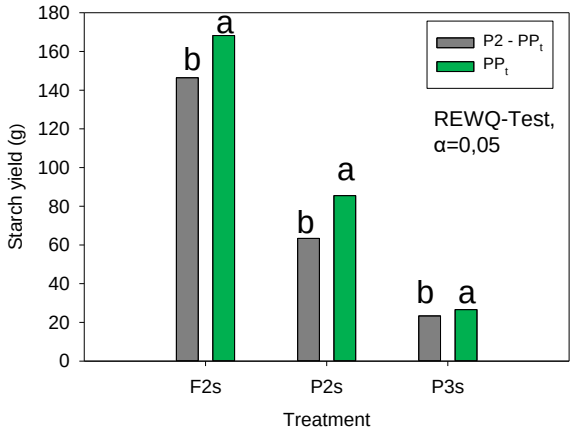
Field model		Predicted			Total	Classification error
		High	Mid	Low		
Observed	High	274	13	5	292	0.062
	Mid	10	295	11	316	0.066
	Low	1	16	286	303	0.056

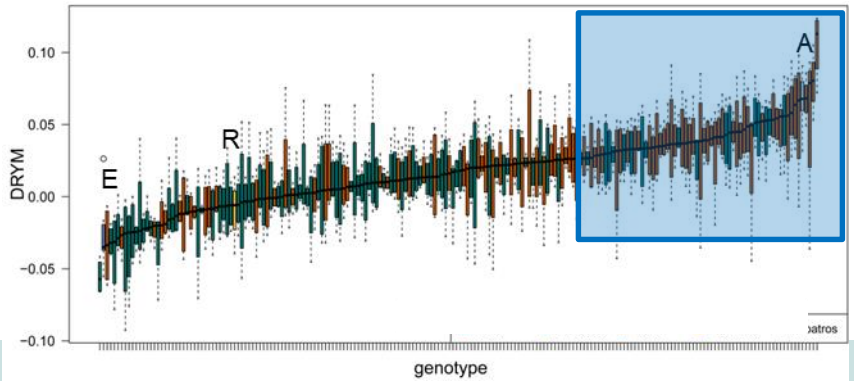
Selection experiment: classic phenotypic selection vs. MAS (VALDIS)

1. Generation of segregating population by cross of tolerant and sensitive cultivars (600 lines)
   - Selection against low yielding lines: 200 lines
   - Genotyping Renate Horn (U Rostock)
2. Drought stress trials and selection for high tolerance estimated from
   - **Tuber** starch yield: selection of phenotypic population PP_t
   - **Leaf** metabolite and transcript concentration, prediction model: selection of marker population MP_t





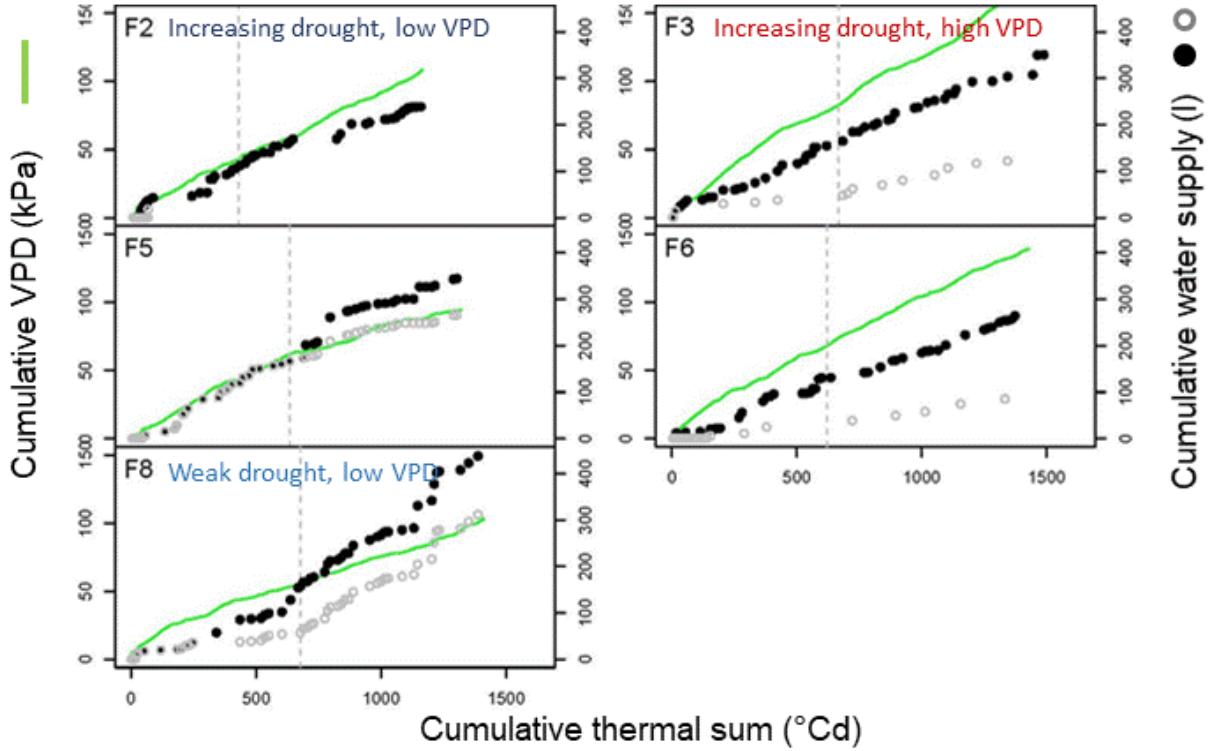




Test of 60 selected genotypes under fluctuating climate conditions

- Test system: 3 pot, 3 big-bag, 7 field trials with optimal (c) or reduced (s) water supply
- Characterization of variable experimental conditions by cumulative vapor pressure deficit (VPD), thermal sums and volume of water supply

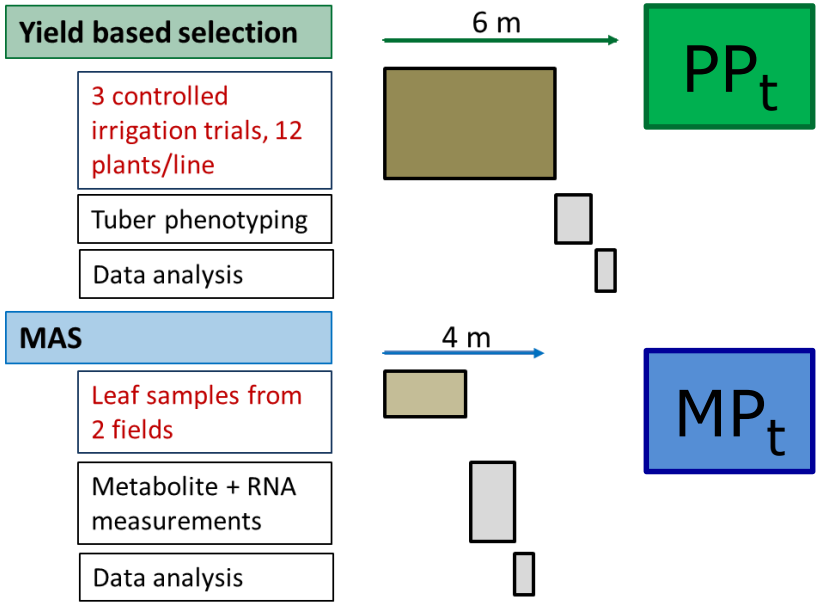
Typical Central European drought scenarios represented

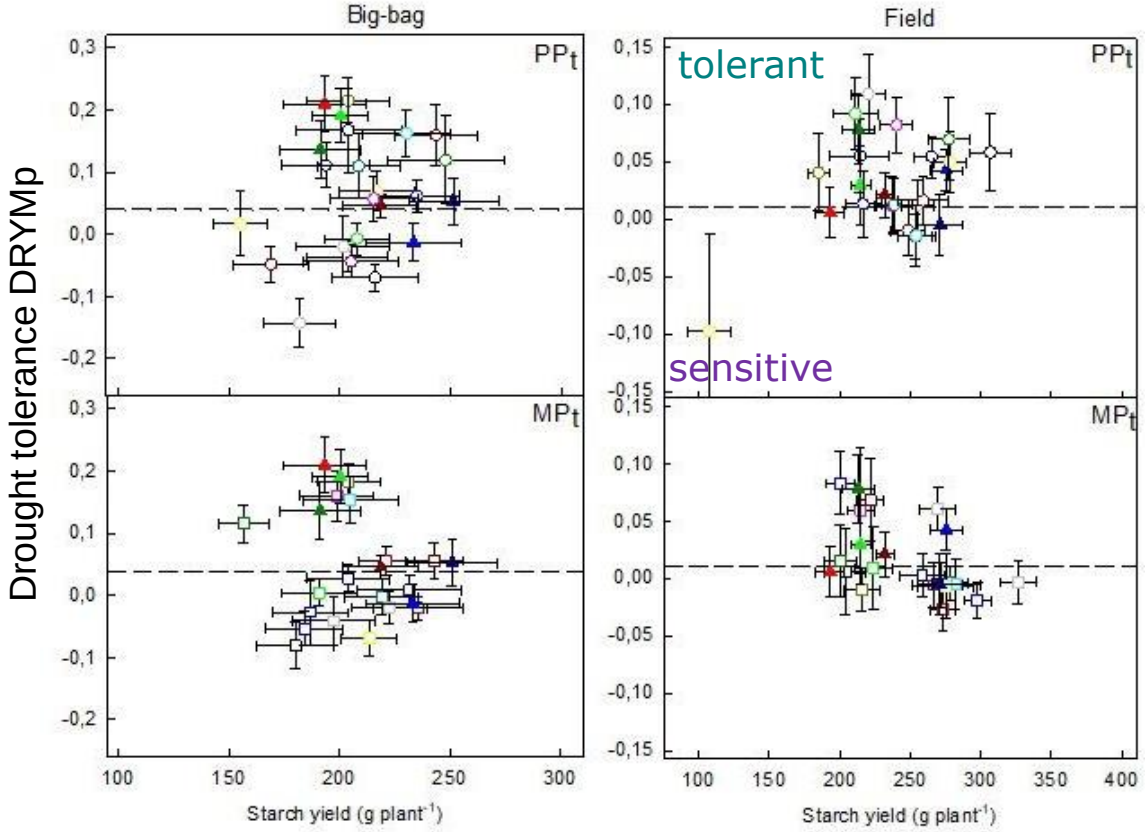


Performance of selection: drought tolerance and yield potential

Identification of lines with superior tolerance compared to mid-parent median:

- No yield penalty
- Marker-assisted selection based on metabolite/transcript marker model finds fewer tolerant lines than phenotypic selection based on yield data from small trial number BUT **faster**

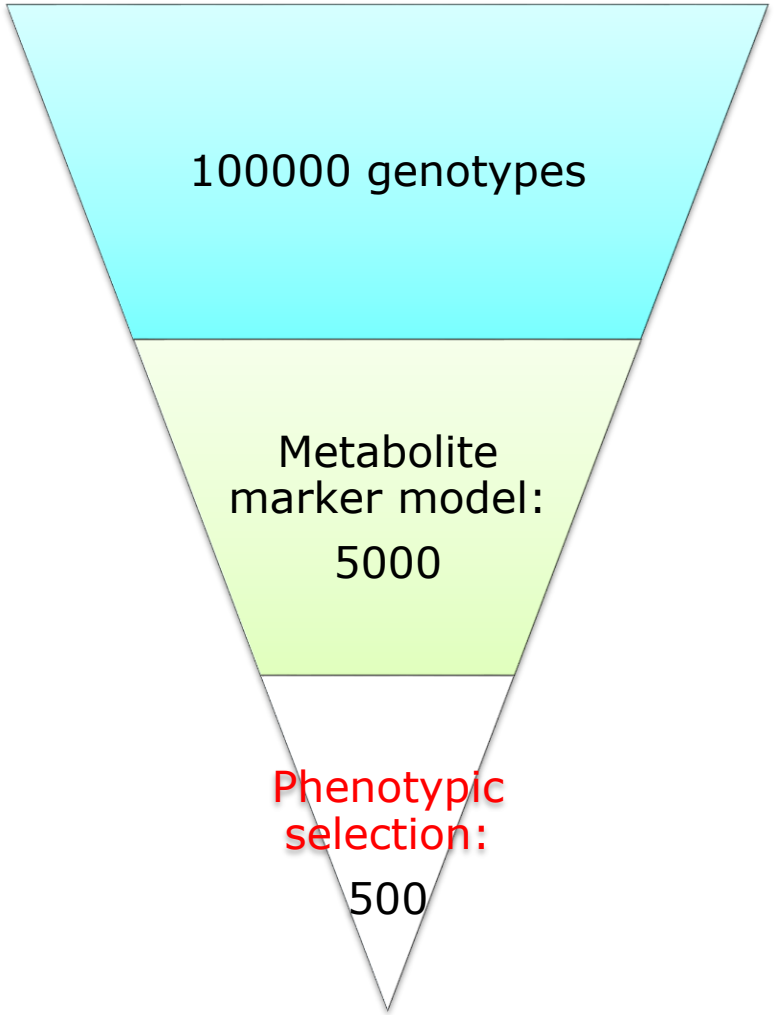




Second layer of selection

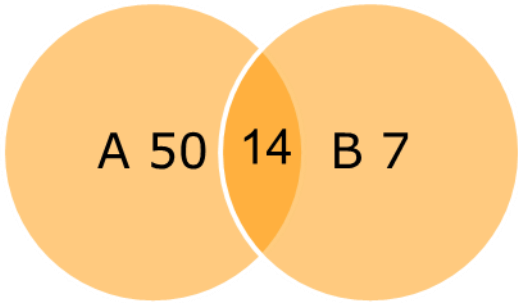
Generally low performance of MAS for polygenic traits (tolerance, yield)

- Idea: subsequent use of different selection systems
- Second selection system: automatic phenotyping systems
  - Remote measurements
  - Sensors on drones or automobile devices



Identification of phenotypic markers

- Drought stress trials in big-bags in variable environmental conditions
- 2015, 2016: population A 64 genotypes, population B 2017 – 2019: 21 genotypes
- Methods: Laser scanner and IR thermometry on automobile Fieldscan system
  - 8 laser scans per day and plant
  - 64 IR scans per day and plant



Conclusions

- Genetic variability for drought tolerance in European potato genepool
- Prediction-model based on metabolites/transcripts independent of agro-environment
- Selection based on marker model less successful but faster than phenotypic selection
- **Outlook**: potential drought tolerance marker derived from automatic phenotyping

Thanks to all partners, especially the German potato breeders