High throughput phenotyping of seeds from dry state to young seedlings

Wagner M.H.[1], Demilly D.[1], Ducournau S.[1], Belin E.[2-3], Léchappé J.[1], Dürr C.[2]

1 - GEVES, Station Nationale d'Essais de Semences, rue Georges Morel BP 90024, 49071 Beaucouzé, France
2 - INRA, UMR 1191, Unité Physiologie Moléculaire des Semences, 16 bd Lavoisier, 49045 Angers, France
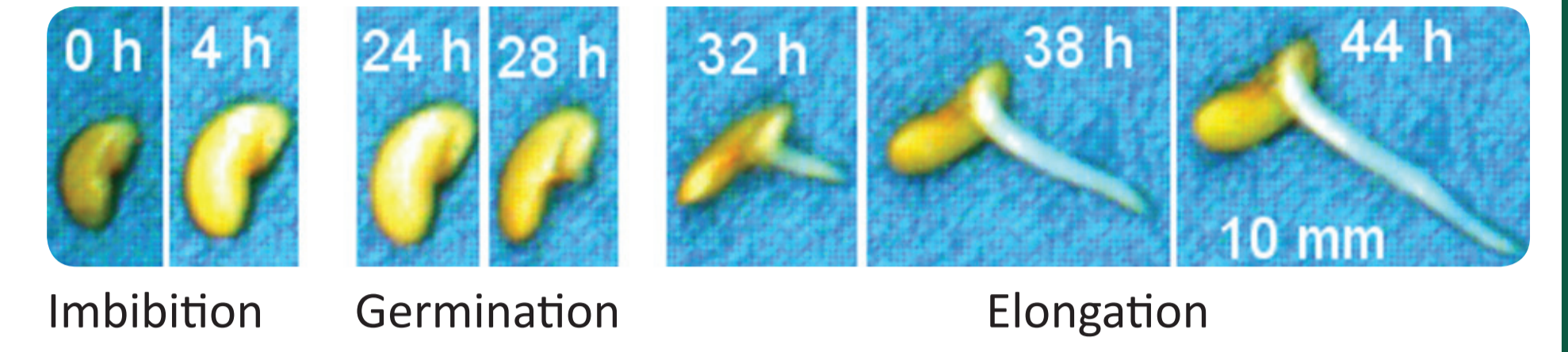3 - Université d'Angers, LISA Laboratoire d'Ingénierie des Systèmes Automatisés, 62 av. Notre-Dame du Lac, 49000 Angers, France
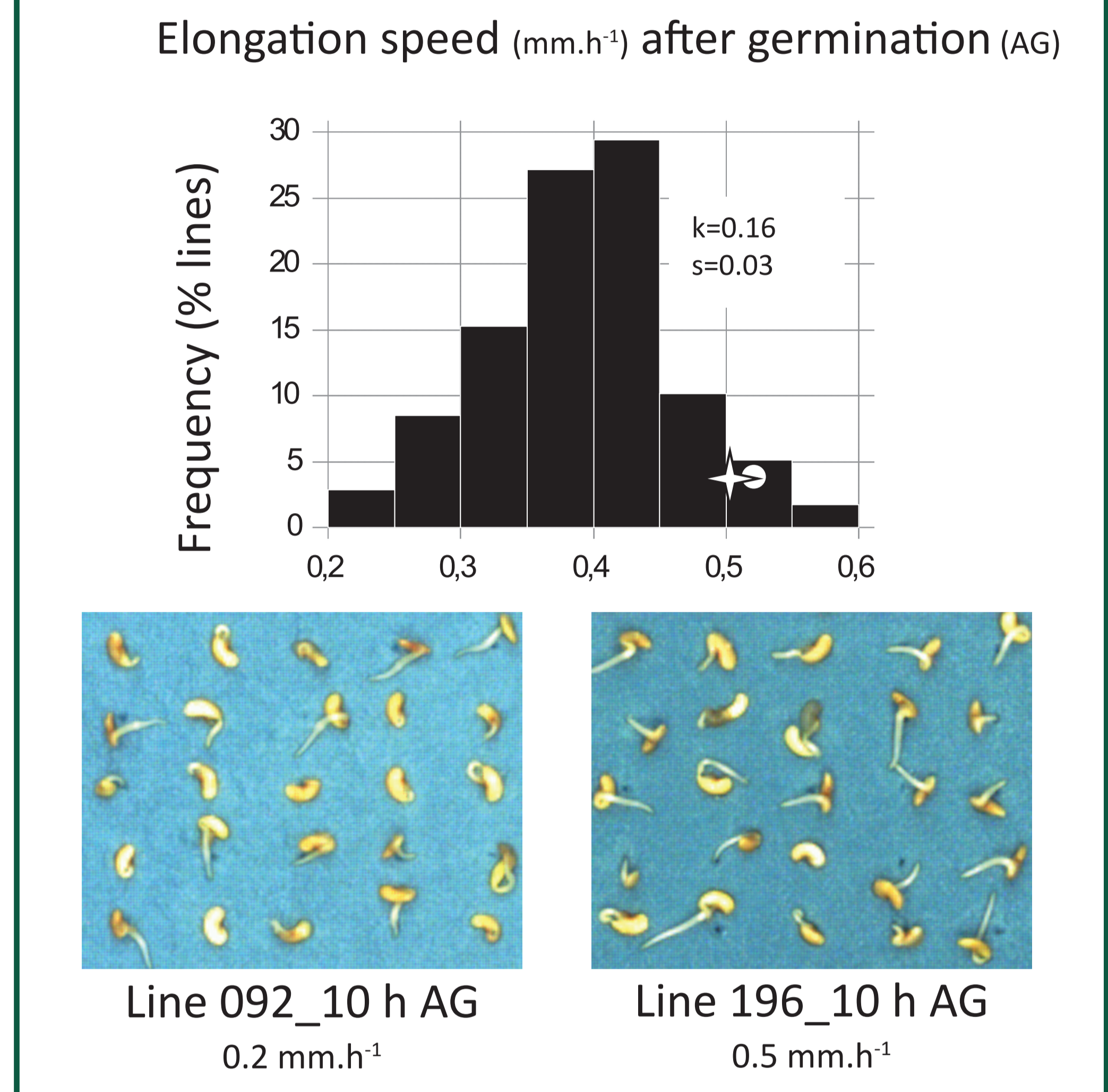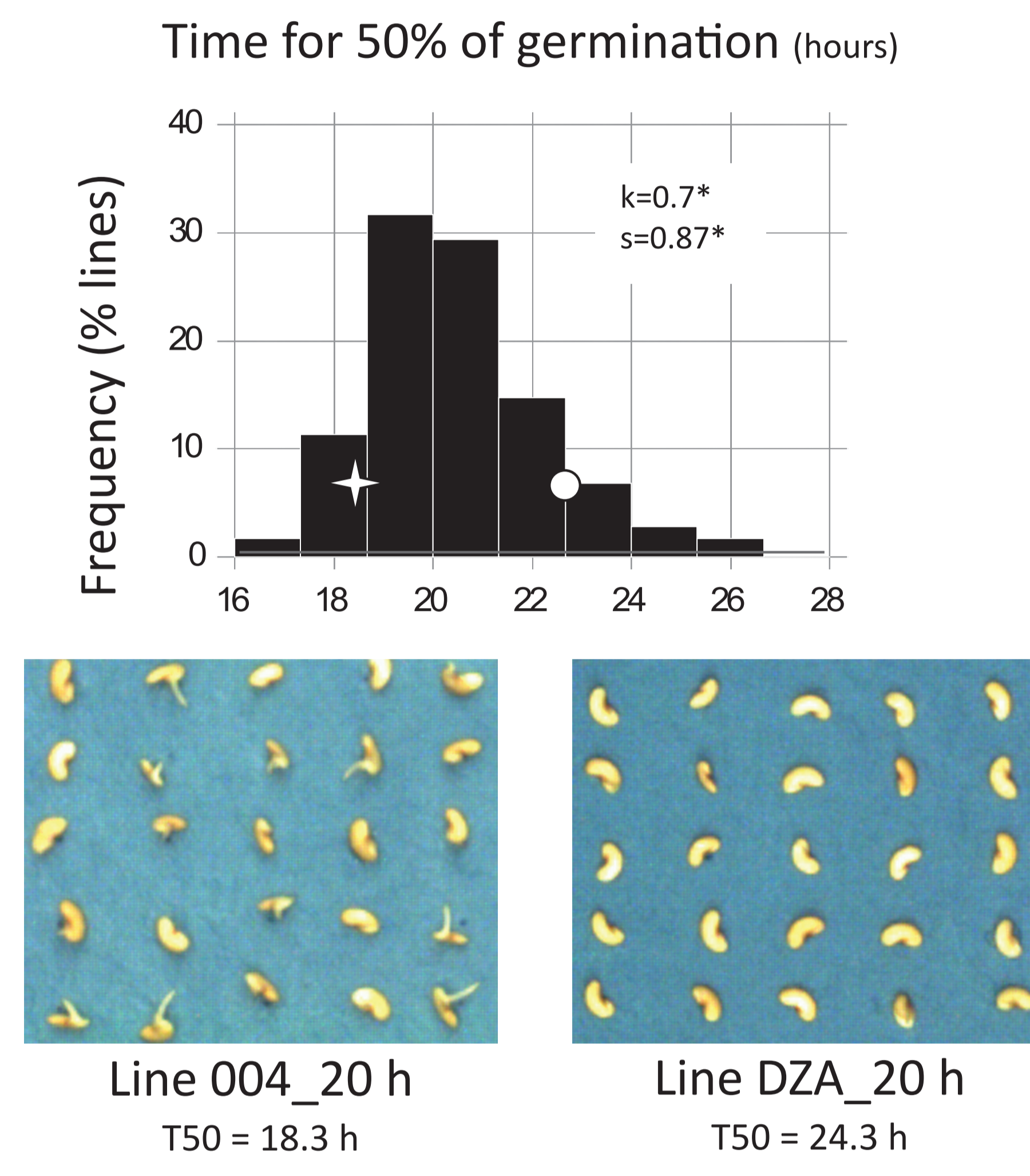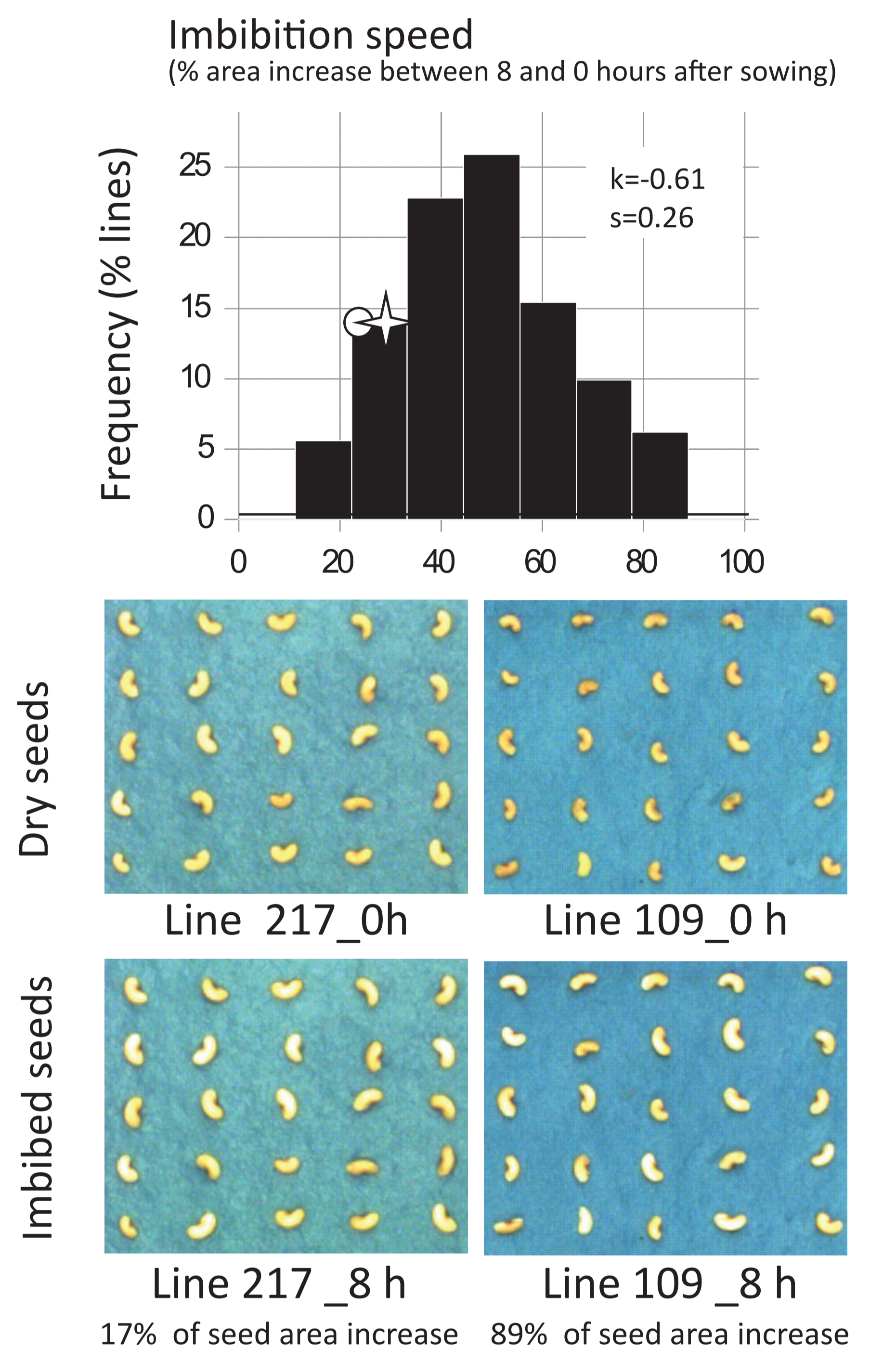
Germination monitoring by computer vision

Automated tools based on computer vision have been developed to provide accurate data related to seed germination which can be difficult and time-consuming. Image analyses allow clear separation of three steps : imbibition, radicle protusion and elongation. The vision machines are now routinely used on several species for research purposes or seed companies' requests.
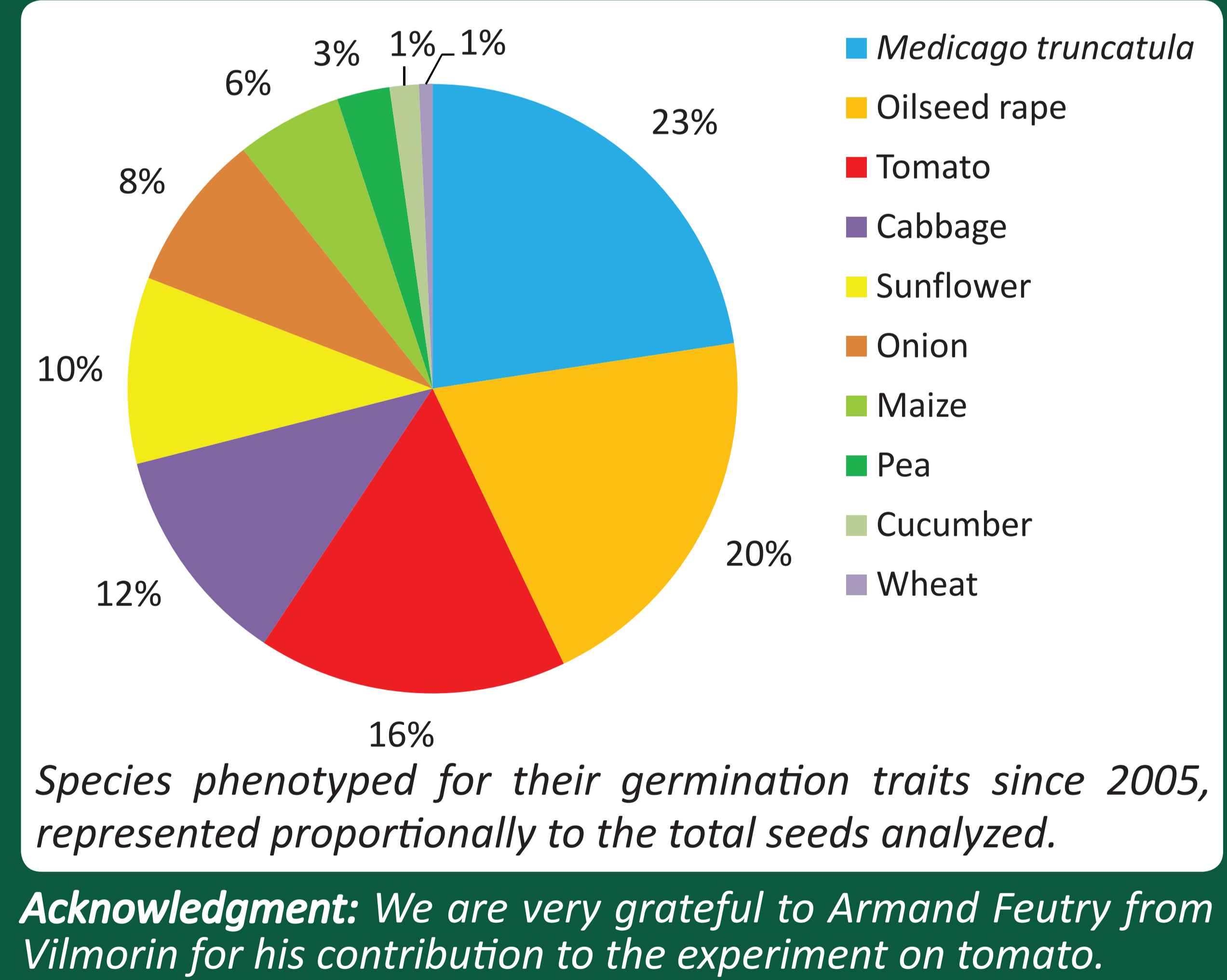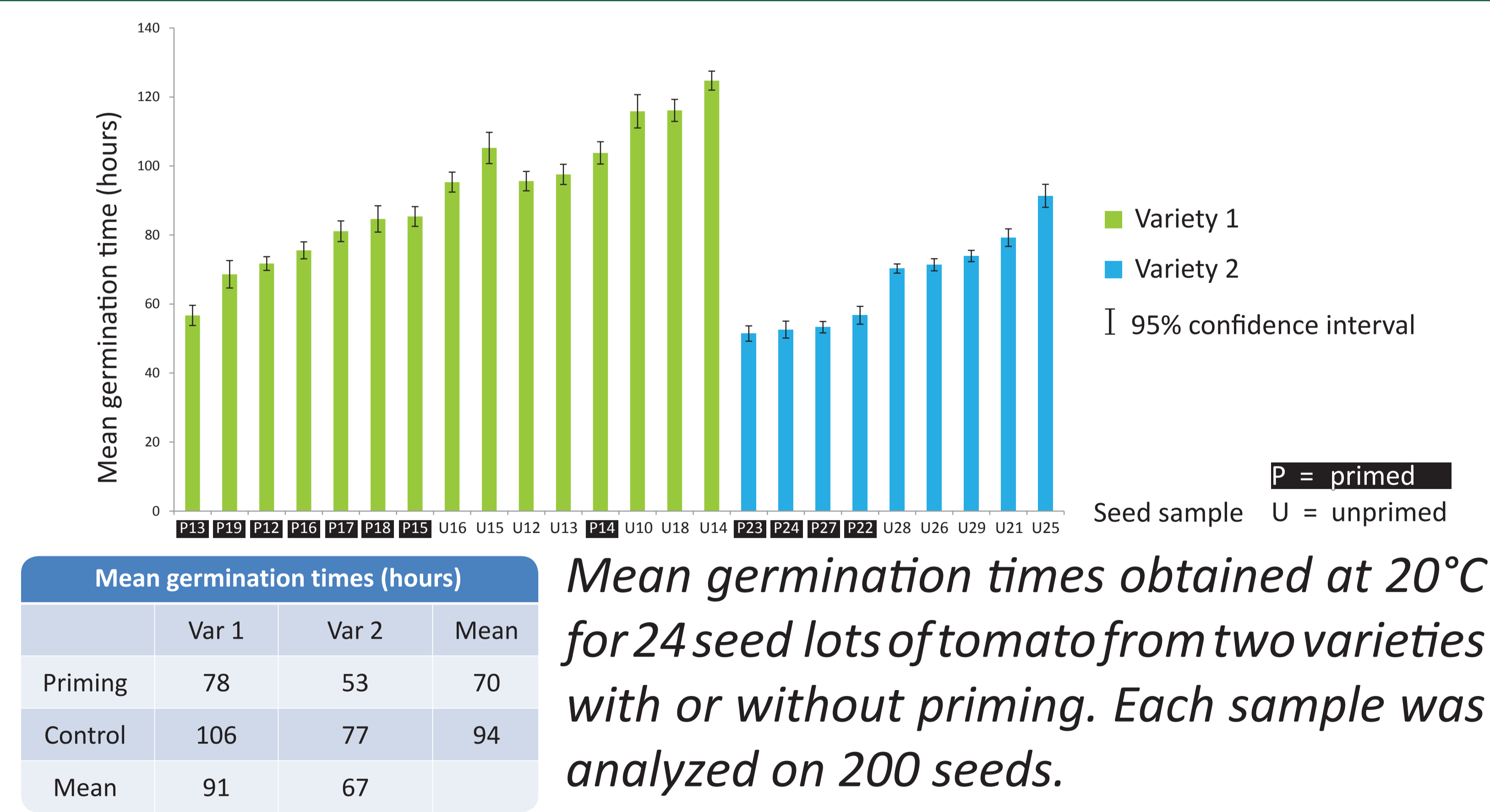

0 h   4 h   24 h   28 h   32 h   38 h   44 h   10 mm
Imbibition   Germination   Elongation

Phenotyping for seed science

Imbibition speed
(% area increase between 8 and 0 hours after sowing)
k=-0.61
s=0.26

Dry seeds
Line 217_0h   Line 109_0 h

Imbibed seeds
Line 217 _8 h   Line 109 _8 h
17% of seed area increase   89% of seed area increase

Time for 50% of germination (hours)
k=0.7*
s=0.87*

Line 004_20 h   Line DZA_20 h
T50 = 18.3 h   T50 = 24.3 h

Elongation speed (mm.h^{-1}) after germination (AG)
k=0.16
s=0.03

Line 092_10 h AG   Line 196_10 h AG
0.2 mm.h^{-1} 0.5 mm.h^{-1}

Distributions for imbibition, germination and elongation traits of 178 recombinant inbred lines from the population RIL4 (Jemalong A17 + x DZA 315.16 ○) of Medicago truncatula. Each RIL was analyzed on 4 x 25 seeds at 20°C. Phenotypic variability was observed for each trait even when parent lines were close. Two extreme lines are illustrated on the pictures under each distribution chart.

Menna Barreto Dias P, Brunel S, Dürr C, Huguet T, Demilly D, Wagner M-H, Teulat-Merah B. (2010). QTL analysis of seed germination and pre-emergence growth at extreme temperatures in Medicago truncatula. Theoretical and Applied Genetics, in press.

Vigour testing for seed technology

Variety 1
Variety 2
I 95% confidence interval

Seed sample   P = primed   U = unprimed

Mean germination times obtained at 20°C for 24 seed lots of tomato from two varieties with or without priming. Each sample was analyzed on 200 seeds.

Mean germination times (hours)			
	Var 1	Var 2	Mean
Priming	78	53	70
Control	106	77	94
Mean	91	67	

- Medicago truncatula — 23%
- Oilseed rape — 20%
- Tomato — 16%
- Cabbage — 12%
- Sunflower — 10%
- Onion — 8%
- Maize — 6%
- Pea — 3%
- Cucumber — 1%
- Wheat — 1%

Species phenotyped for their germination traits since 2005, represented proportionally to the total seeds analyzed.

Towards a seed phenotyping platform

According to the species, each automated germination device can analyze up to 1600 seeds simultaneously. Accurate and consistent data provided by image analysis can be used for modeling plant emergence, advancing seed knowledge and testing seed quality.

X-ray imaging, chlorophyll fluorescence sorting on dry seeds, seedling elongation measurements under darkness-like conditions and the tools presented here are all available on the new platform dedicated to seed phenotyping in Angers

GEVES - **G**roupe d'**É**tude et de contrôle des **V**ariétés **E**t des **S**emences
joel.lechappe@geves.fr

INRA - **I**nstitut **N**ational de la **R**echerche **A**gronomique
carolyne.durr@angers.inra.fr