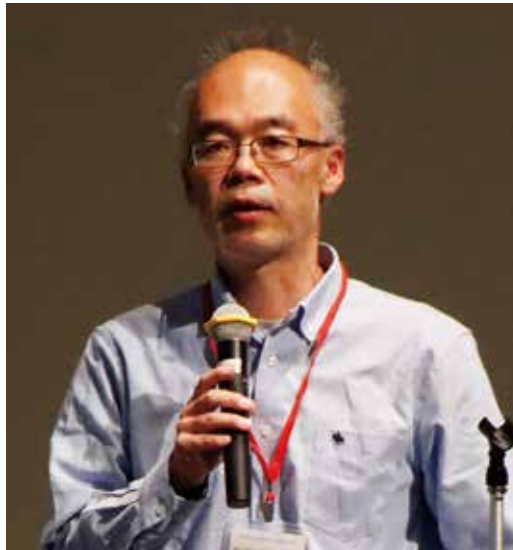


Diving into Genetic Diversity in Wild Wheats: A Case Study on *Aegilops tauschii* Coss.

Yoshihiro Matsuoka

Professor, Graduate School of Agricultural Science, Kobe University, Japan



Dr. Yoshihiro Matsuoka is a Professor at the Graduate School of Agricultural Science at Kobe University, Japan. Dr. Matsuoka uses wheat and its relatives as a model system to study the mechanisms for polyploid species formation. His current research interests include understanding how wild wheat populations are structured, investigating the adaptive mechanisms in wild wheats, exploring the genetic and ecological nature of the origins of common wheat, and finding ways to better utilize wheat genetic resources in breeding. To address questions related to these interests, he conducts cross-experiments and applies evolutionary and quantitative genetic analyses.

Abstracts

Climate change may have a significant impact on wheat production, which around one-third of the world's population relies on for subsistence. Wild wheats provide valuable genetic resources to help develop improved varieties that can adapt to harsh environments. *Aegilops tauschii* Coss. (formerly known as *Aegilops squarrosa* L.) is a wild diploid species native to the central part of Eurasia, from the Middle East and Caucasus to southwest and central Asia and central China. As the D genome progenitor of bread wheat, it serves as a valuable source of the “left-in-the-wild” alleles that can be used in breeding. Such alleles may have the potential to express useful phenotypes when transferred to bread wheat (*Triticum aestivum* L. subsp. *aestivum*). Within its vast geographic range, *Ae. tauschii* populations adapt to diverse local environments and exhibit high degrees of phenotypic variability. Understanding the species' natural trait variation patterns provides the basis for studies on the genetic mechanisms that underlie adaptation and, ultimately, is essential for enhancing the agronomic utilization of the species.

Ae. tauschii comprises two major lineages (TauL1 and TauL2) and one smaller (TauL3) lineage, which are defined by the similarity of accessions in nuclear and chloroplast molecular marker genotypes. Each lineage may correspond to an intraspecific group of accessions sharing a common ancestor that existed at some point in the past. These lineages differ in their patterns of geographic distribution: TauL1 exhibits a wide distribution across the species' range, whereas TauL2 is restricted to the western part of the range. TauL3 has been found in Georgia.

We examined the natural variation patterns in relation to these lineages for agronomic traits, including salt tolerance during germination and seedling growth, crossability with durum wheat, using a set of approximately 200 accessions (130 accessions for TauL1, 65 for TauL2, and five for TauL3) representing the entire species' range. Our findings include: (1) relative to TauL1, TauL2 and TauL3 showed sensitivity to salt at the germination and seedling stages, (2) some TauL2 accessions from the southern Caspian region showed a high potential for hybridization with durum wheat in terms of anther size and crossability. Overall, we conclude that the lineages provide a useful viewpoint to explore the natural variation patterns in agronomic traits in *Ae. tauschii*.

To facilitate the search for *Ae. tauschii* genes responsible for the expression of agronomic trait phenotypes, we assembled an enlarged set of non-redundant accessions (> 500 accessions). A population structure analysis revealed a small number of previously unknown TauL3 accessions from Azerbaijan and northern Iran.

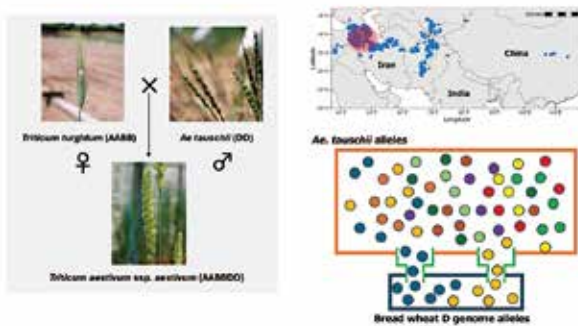
A downside of the lineages is that they are difficult to distinguish based on morphology; we need to genotype an *Ae. tauschii* accession to determine which lineage it belongs to. To address this issue, we adopted a machine learning approach, feeding thousands of spike photos into the model to enable it to classify the images according to the lineages used as labels. I will briefly report on the progress made with the approach.

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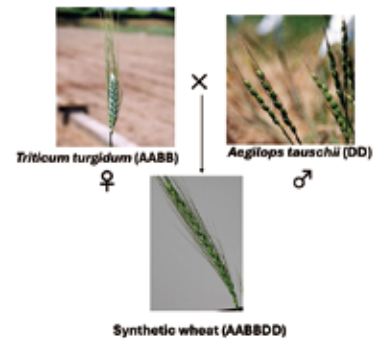
Yoshihiro Matsuoka
Kobe University



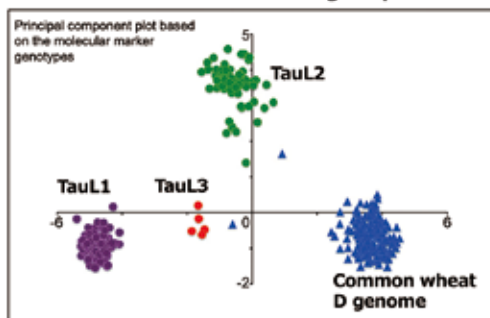
***Ae. tauschii* is a reservoir of unused alleles**



***Ae. tauschii* allele transfer via synthetic wheat**

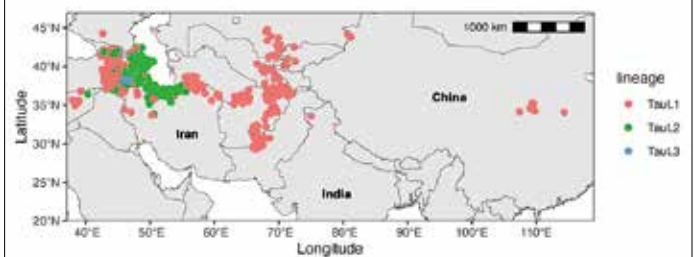


Structure of *Ae. tauschii* germplasm

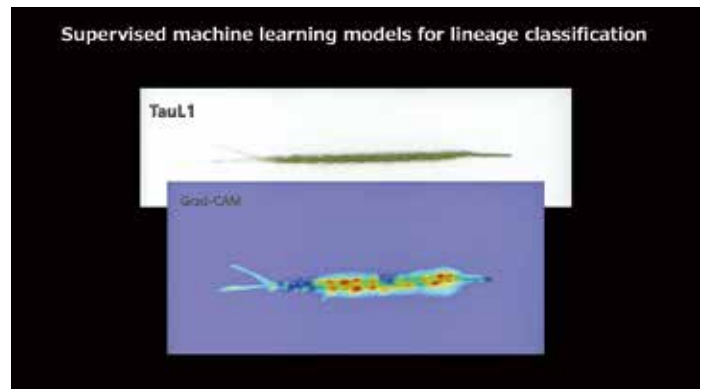
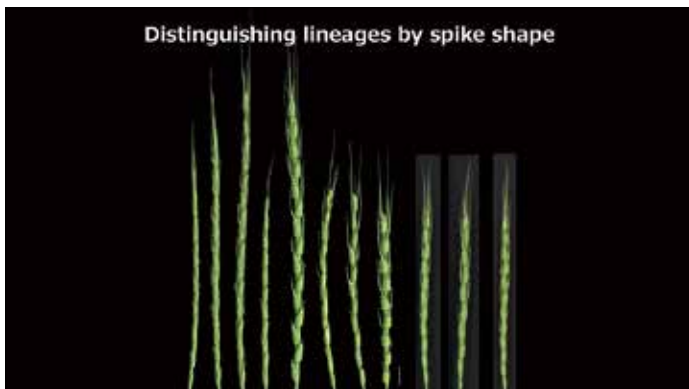
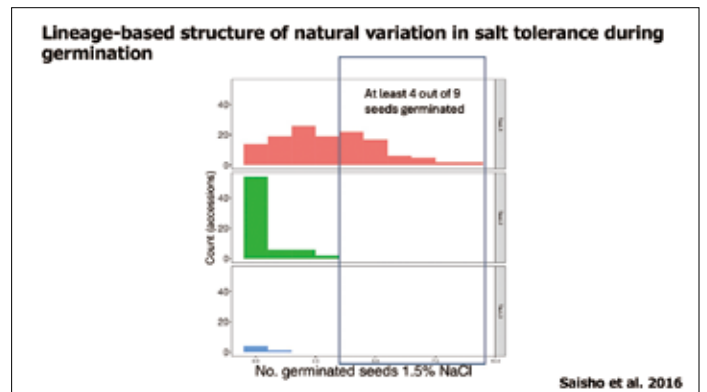
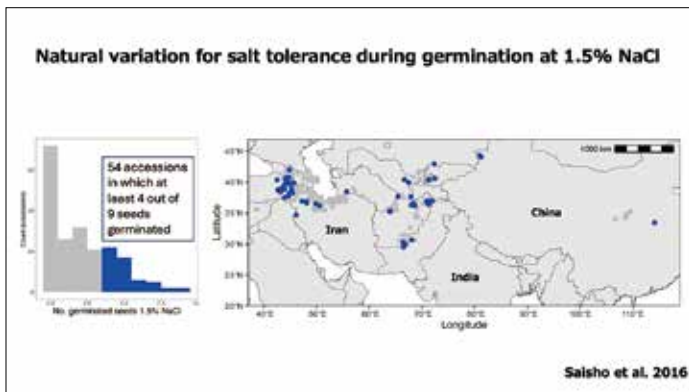
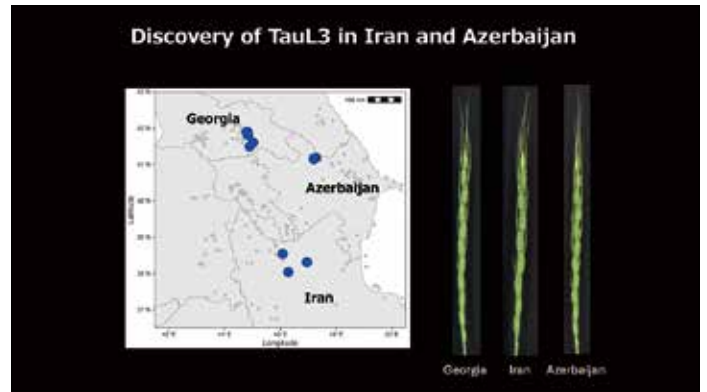
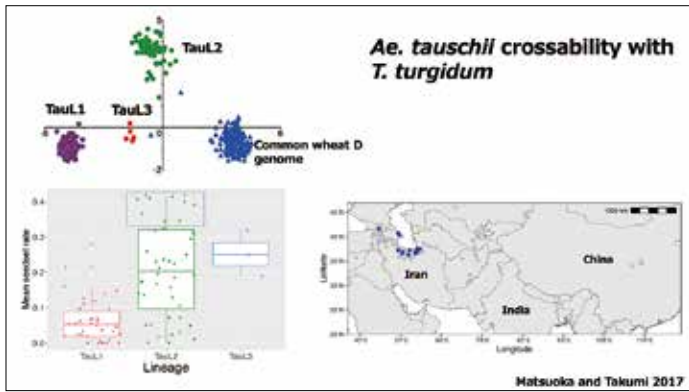


Matsuoka et al. 2013

TauL1 drove the species range expansion



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Conclusion

The lineages are useful in exploring the *Ae. tauschii* germplasm.

TauL1 is an important genetic resource for improving bread wheat



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