A stylized graphic of two teal hands shaking, positioned diagonally across the lower half of the slide. The hands are rendered with a slight 3D effect and are set against a solid orange background.

Application of the GGE biplot to evaluate Genotype, Environment and GxE interaction on *P. radiata*: a case study

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GGE biplot Application

- ◆ GGE biplot analysis was developed by W. Yan (2000).
- ◆ Basic functions:
 - "which-won-where" pattern (specific genotypes recommended to specific environments).
 - Interrelationship between the trials
 - genotype evaluation (the mean performance and stability)
 - ranking G and E

Mathematic model

- ◆ The model based on singular value decomposition (SVD) of first two principal components is:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \varepsilon_{ij}$$

where is Y_{ij} the measured mean (DBH) of genotype i in environment j , μ is the grand mean, is the main effect of environment j , β_j being the mean yield across all genotypes in environment j , λ_1 and λ_2 are the singular values (SV) for the first and second principal components (PC1 and PC2), respectively, and ξ_{i2} are eigenvectors of genotype i for PC1 and ξ_{i1} PC2, respectively, η_{1j} and η_{2j} are eigenvectors of environment j for PC1 and PC2, respectively, ε_{ij} is the residual associated with genotype i in environment j .

Model

$$Y_{ij} - u - \beta_j = g_{i1}e_{1j} + g_{i2}e_{2j} + \varepsilon_{ij}$$

$$g_{il} = \lambda_l^{f_l} \xi_{il}$$

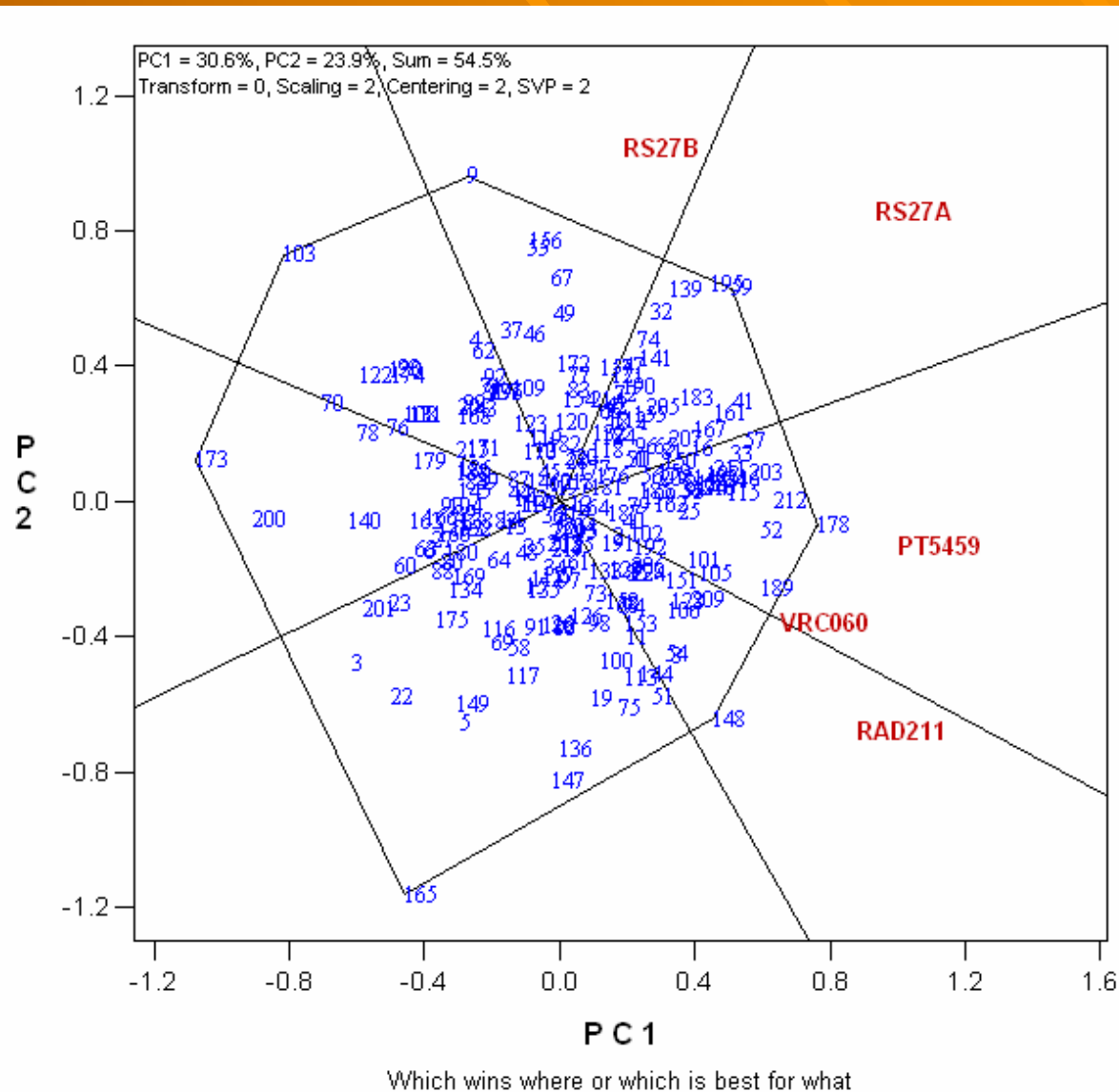
$$e_{lj} = \lambda_l^{1-f_l} \eta_{lj}$$

g_{il} and e_{lj} are PC scores for genotype i and environment j , respectively.

where f_l is the partition factor for **PC1**.

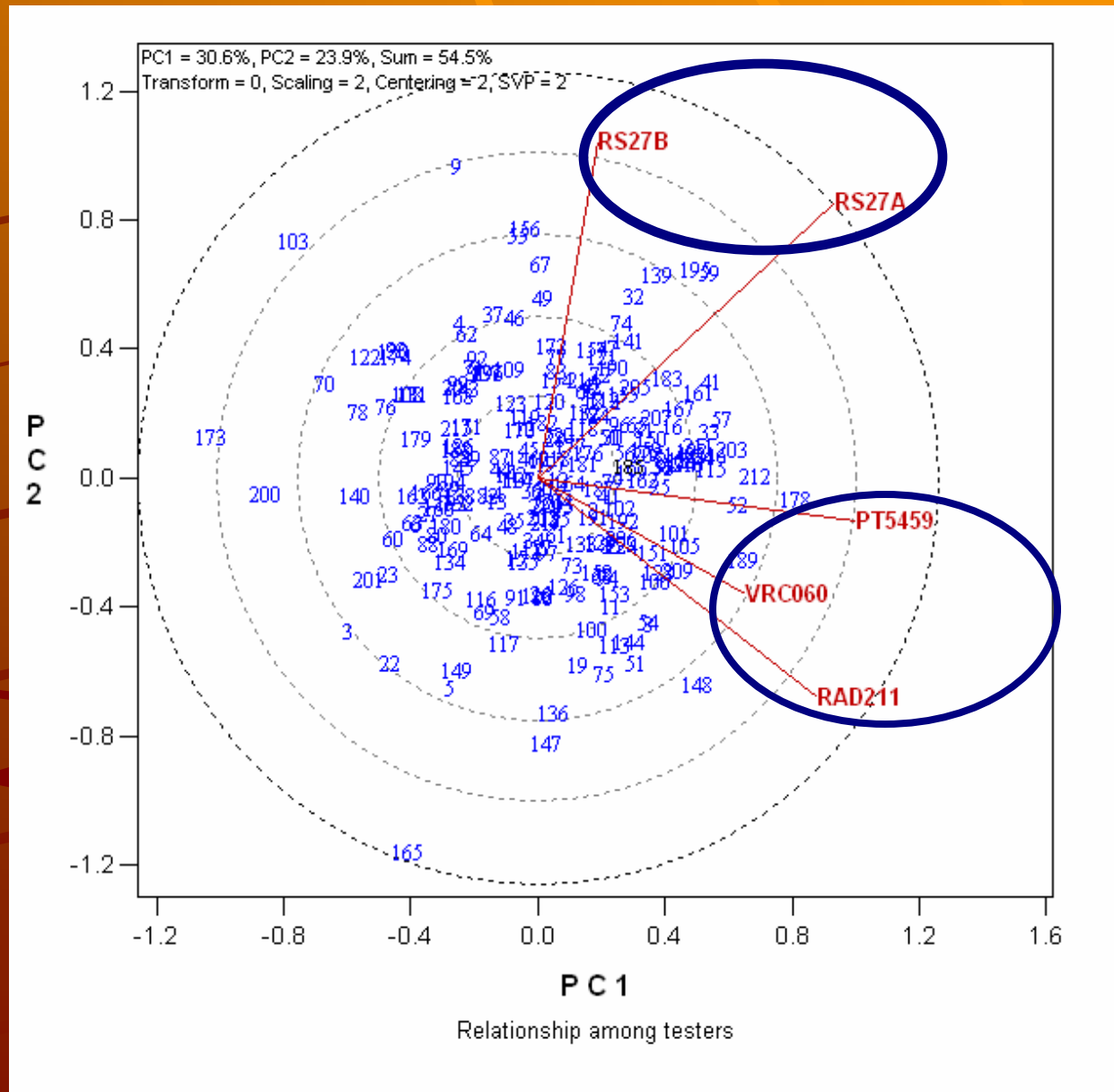
Theoretically, f_l can be a value between 0 and 1, but 0.5 is most commonly used.

Results “which-won-where”

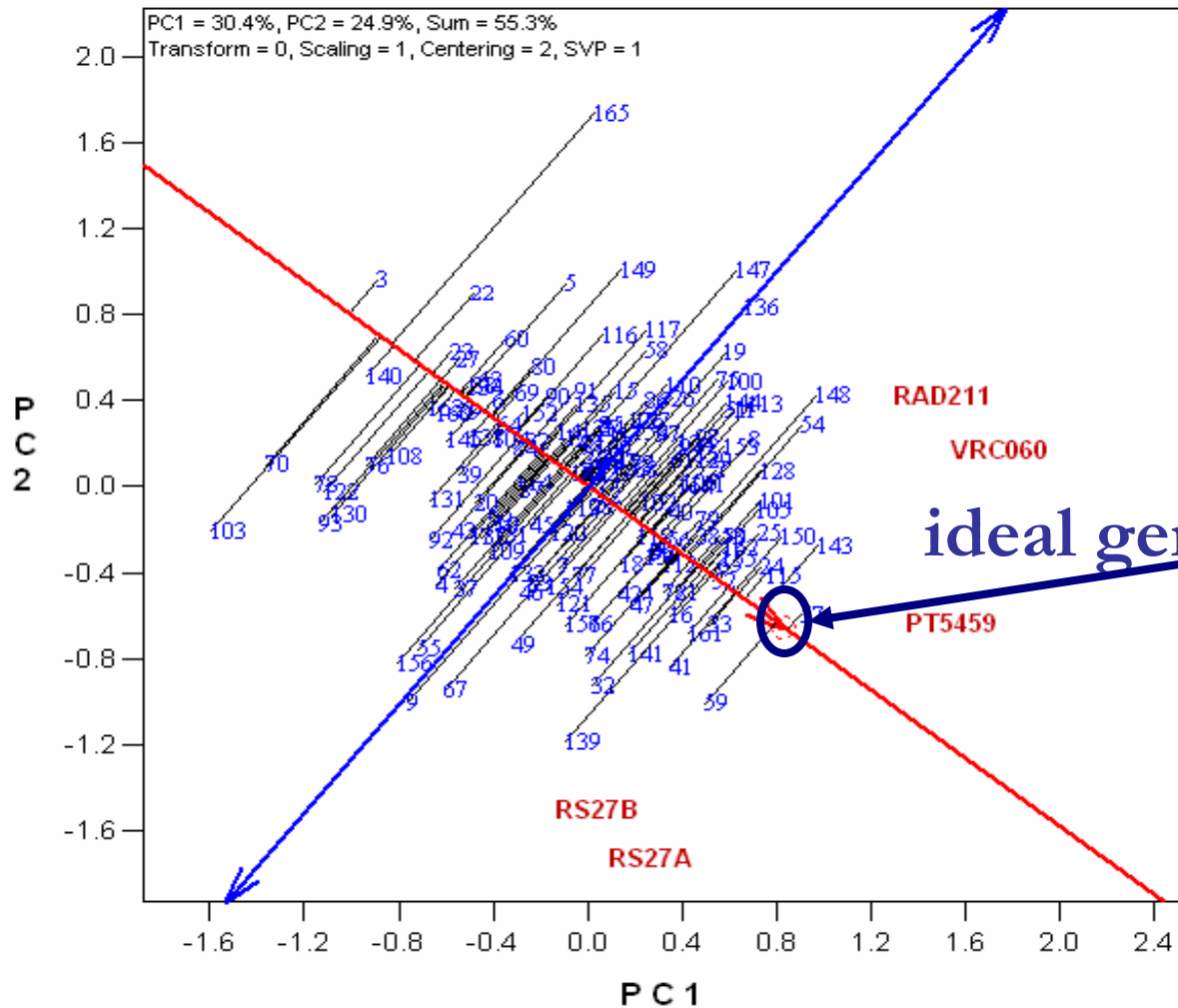


The first two
PCs explain
54.5% :
PC1=30.4%
PC2=24.9%

Relationship among environments

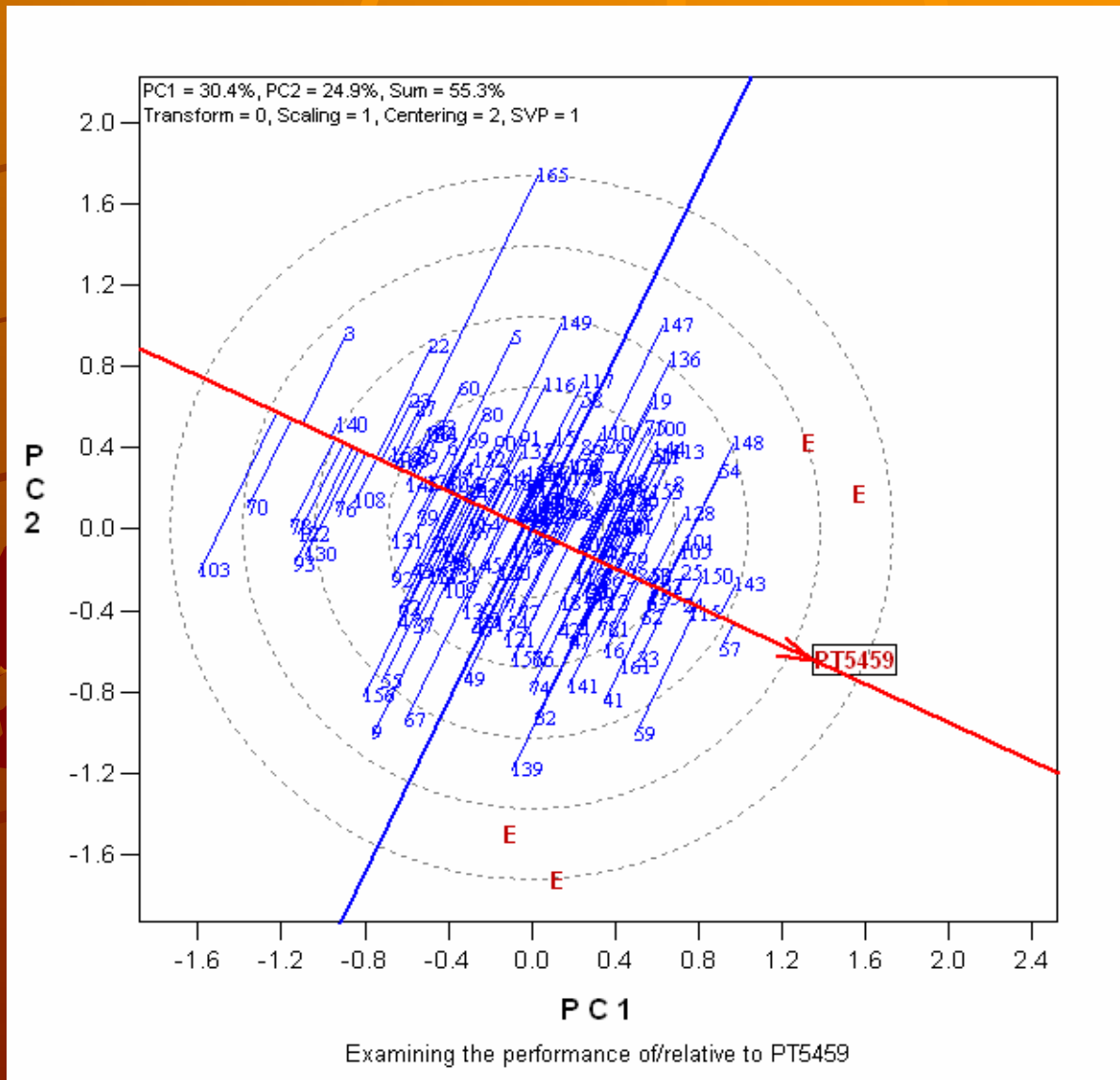


Family performance and stability

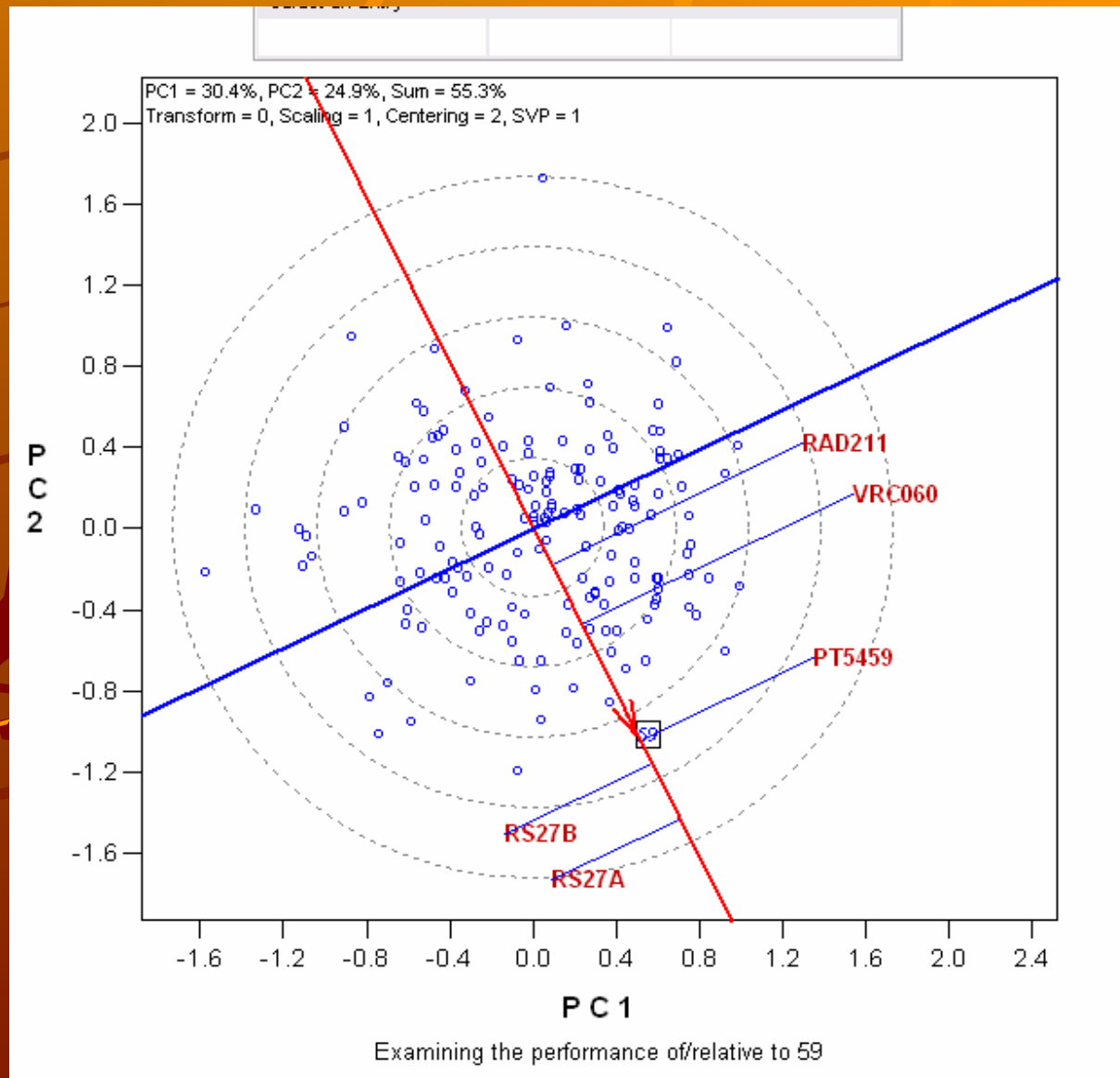


The Average Tester Coordination view

Examine genotypes



Examine environment



Discussion and conclusions

- ◆ Jointly use the function of classical GxE interaction methods.
- ◆ Visually reveal the patterns of GxE interaction.
- ◆ Superior to additive main effects and multiplicative interaction (AMMI), there are more visual interpretations.
- ◆ Superior to joint regression, not only show the mean performance and stability, but also show the genotype group's favourite environments.
- ◆ Visually show the interrelationship between the trials.

Discussion and conclusions

- ◆ GGE biplot analysis may explain only a small part of total GGE, PC1 and PC2 may be insufficient to explain the GGE.
- ◆ Does not have a serious statistical test.
- ◆ Advocate being backed by formal statistical analysis with integrating the elegant approach.

Thank you

