

SESSION III

BASES GÉNÉTIQUES DE L'HÉTÉROSI

The genetic basis of heterosis

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Formulae are derived for predicting the performance of crosses among populations in terms of effects defined in the F₂ populations of single loci and interaction effects among two or more loci. The difference between the F₁ and mid-parent mean includes dominance (D) additive \times additive (AA) and dominance \times dominance (DD) effects, that between the F₁ and F₂ only D and DD effects, and that between the F₂ and first backcross mean only AA effects. This parametrization is compared with that in terms of recombination loss, and it is argued that the latter is of limited value in prediction or interpretation of crossbred data.

Physiological explanations of heterosis

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The traditional explanations of heterosis (dominance, overdominance, epistasis) agree with genetic models referring to qualitative and quantitative modes of enzyme activity caused by allelic differences. The proposed models are illustrated in three figures.

Components of heterosis

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Heterosis has been defined for various two-way crossbred animal populations in terms of genetic components. Complementarity has been analyzed and for non-linearity and position effects general formulas have been derived.