#### SESSION III

## BASES GÉNÉTIQUES DE L'HÉTÉROSIS

#### The genetic basis of heterosis

## W.G. HILL

#### Institute of Animal Genetics, West Mains Road, Edinburgh EH9 3JN, Scotland

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

# E. ANDRESEN and K. CHRISTENSEN

Department of Animal Genetics, Royal Veterinary and Agricultural University Bülowsvej 13, DK-1870 Copenhagen V, Denmark

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**

### V. JAKUBEC

Research Institute of Animal Production, Praha 10, Uhríneves, Czechoslovakia

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.