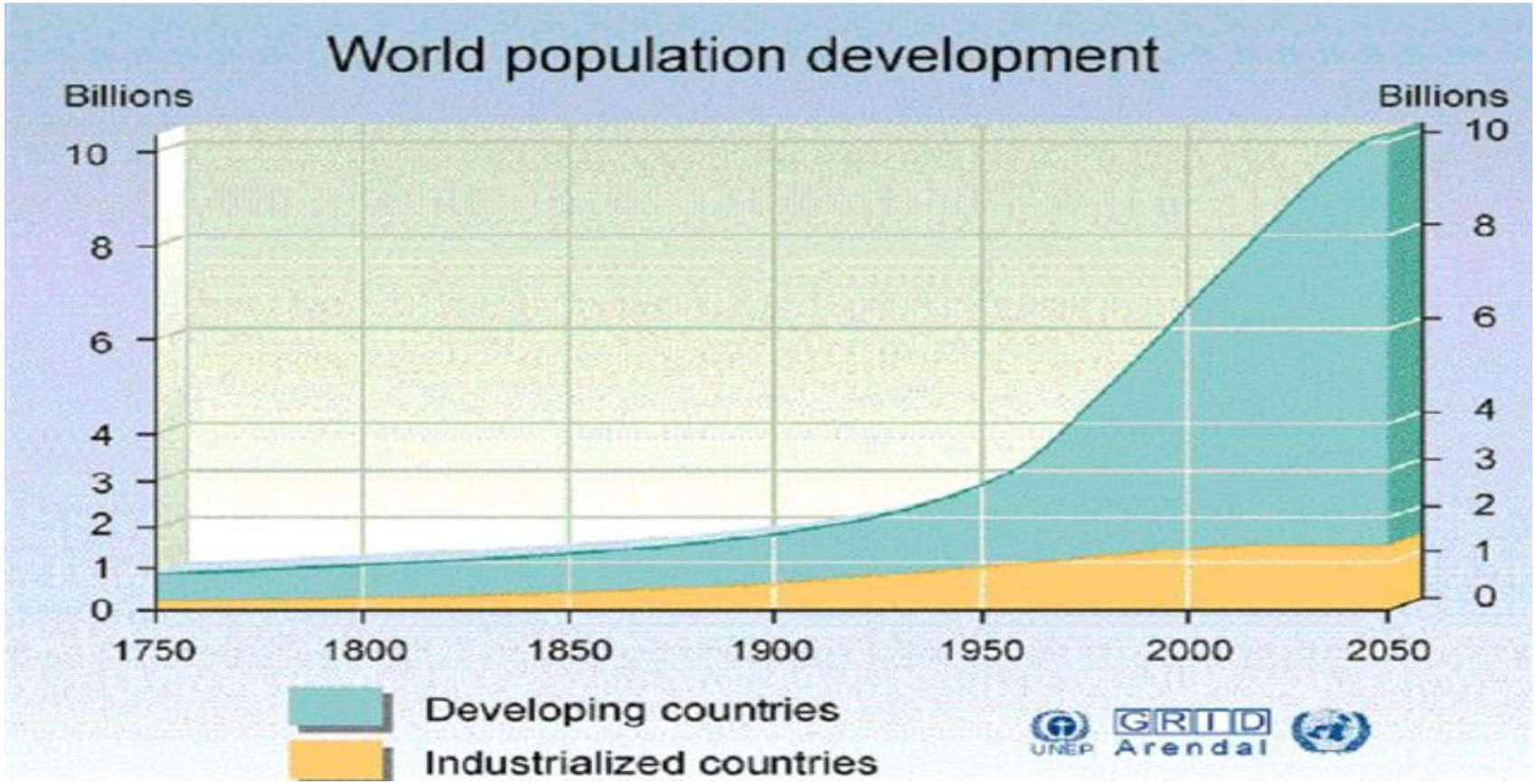
Statistical Analysis of Milk Yield by AMMI Analysis of Genotype-Environment Interaction

Hamrouni. A and M. Djemali

Animal Genetic and Feed Resources Research Lab.
National Institute of Agriculture of Tunisia (INAT)

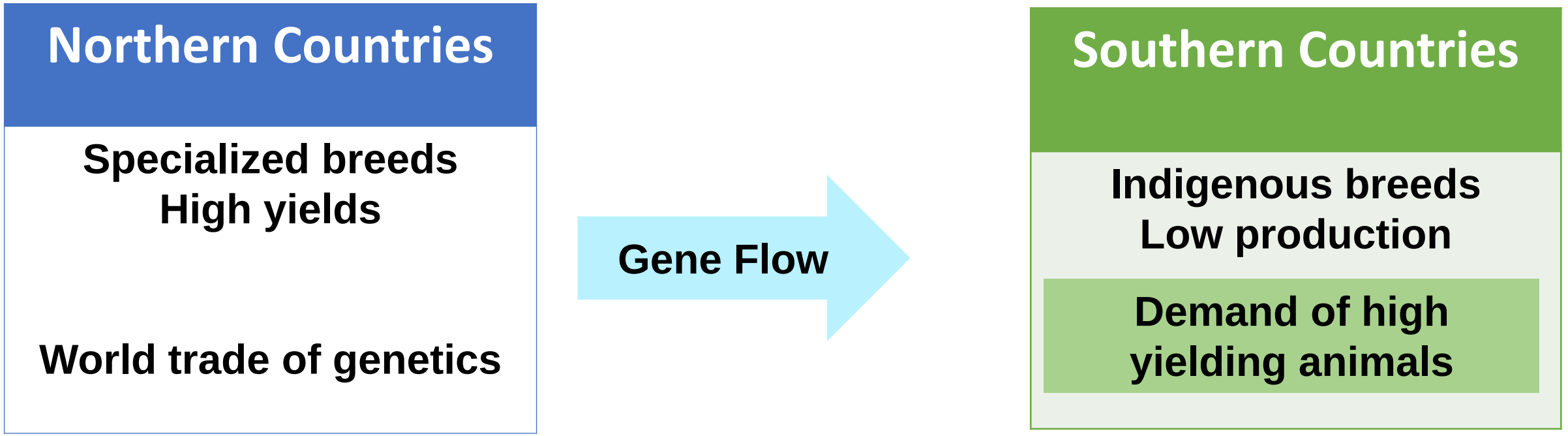
Justifications

1. **The world's population is expected to reach 9.1 billion by 2050.**



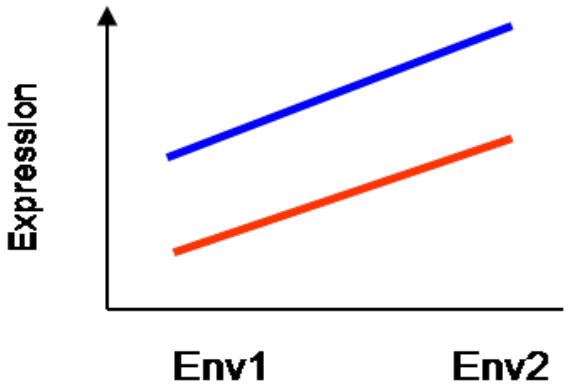
Justifications

2. Population growth led to a massive increase in demand for products of animal origin.

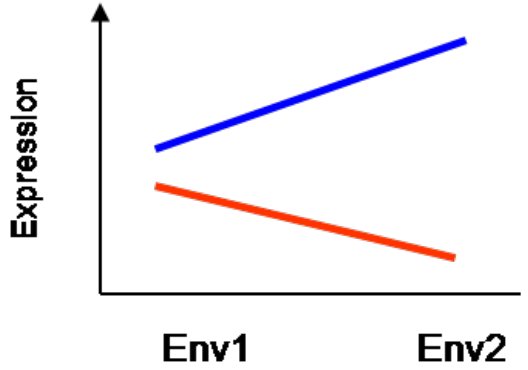


Justifications

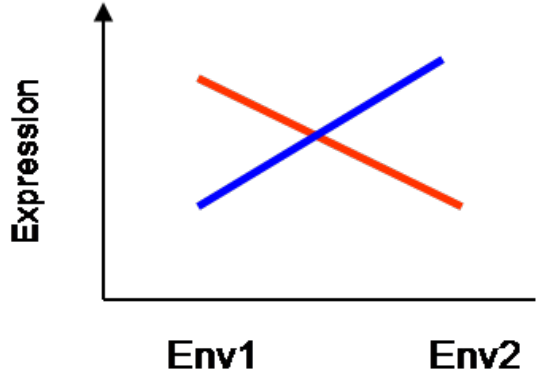
3. A diversity of situations translating G and E



1) No G×E interaction



2) Interaction G×E
(Scaling effect)



3) Interaction G×E
(Re-ranking) of individuals

Genetic Correlations for Production Traits

Regions	Genetic correlations	Authors
US-Latin America	**0.78-0.90**	Stanton et al. 1991
US-Spain	**0.82**	Carabano et al. 1989
Canada-New Zealand	**0.25-0.29**	Charagu et al. 1998
Kenya -UK	**0.49**	Ojango et al. 2002
European countries	**0.75-0.84**	Rekya et al. 2001

Objectives

1) Evaluate genetic parameters of milk yield in 3 different regions as separate traits

2) Apply the AMMI model to evaluate the GxE interaction in milk yield

Material and Methods

Data provided by the National Milk Recording Program (OEP)

North

Centre

South

Material and Methods

Means and variation of 305-days milk yield by region

Region	Northern	Central	Southern
Test-day records	54289	6335	2945
Number of cows	5760	677	475
Number of sires	519	70	159
$Milk_{305}$ (Kg)	**6125 ±1798**	**5664 ±1574**	**5946 ±1632**
Fat_{305} (Kg)	207 œ63	194 œ57	203 œ62
$Protein_{305}$ (Kg)	191 œ56	176 œ48	189 œ54

Material and Methods

Number of sires by region

North	Centre	South
519	70	159

Common Sires by region

North- South	North-Centre	South-Centre	North-Centre-South
63	**45**	**26**	**26**

Model 1 : Additive by Region

Milk yield305

=

Overall mean

+

Herd-Year + Season + Age of Dam + Lactation Number + Sire + MGS

+

Residual Error

Model 2. Additive Main Effects and Multiplicative Interaction model (AMMi)

$$Y_{ij}=\mu+G_i+E_j+\sum i_n U_{ni} V_{nj} + e_{ij}$$

Y_{ij} =Milk yield

G_i = The effect of the i^{th} genotype;

E_j = The effect of the j^{th} environment;

i_n = Value of the n^{th}interaction principal component analysis (IPCA), (n = 1, 2, ... P), where p is the maximum number of estimable main components);

U_{ni} = Value for the i^{th} genotype in the n^{th} IPCA;

V_{nj} = Value of the j^{th}environment in the n^{th} IPCA;

e_{ij} = Residual error.

AMMI Model

$$Y_{ijk} = \mu + g_i + e_j + ge_{ij} + E_{ijk}$$

$$Y_{ijk} - \mu - g_i - e_j - E_{ijk} = ge_{ij}$$

$$\begin{matrix} ge_{11} & ge_{12} & ge_{13} & \ldots\ldots & ge_{1n} \\ ge_{21} & ge_{22} & ge_{23} & \ldots\ldots & ge_{2n} \\ . & . & . & \ldots\ldots & . \\ ge_{i1} & ge_{i2} & ge_{i3} & \ldots\ldots & ge_{in} \\ . & . & . & \ldots\ldots & . \\ ge_{k1} & ge_{k2} & ge_{k3} & \ldots\ldots & ge_{kn} \end{matrix}$$

Results

Rank correlations for the 26 top sires (below diagonal), estimated 305-days heritabilities (on diagonals) and 305-days genetic correlations (above diagonal) by production region

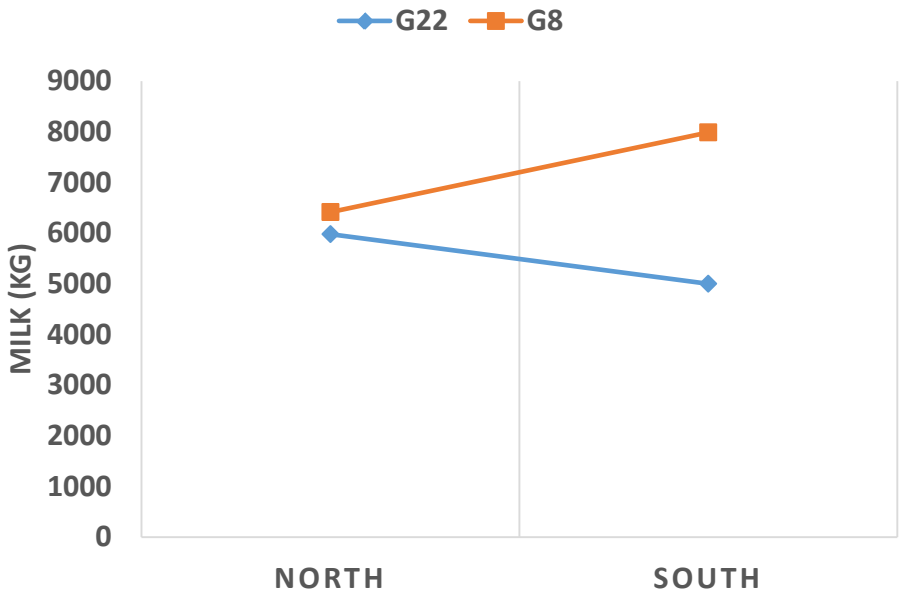
		Region		
		Northern	**Central**	**Southern**
	Nord	**0,18 ± 0,06**	**0,55**	**0,48**
Milk$_{305}$	**Centre**	0,20	**0,11 ± 0,04**	**0,37**
	Sud	0,24	0,41	**0,39 ± 0,13**
	Nord	**0,09 ± 0,02**	**0,59**	**0,37**
Fat$_{305}$	**Centre**	0,52	**0,14 ± 0,05**	**0,31**
	Sud	0,46	0,41	**0,32 ± 0,11**
	Nord	**0,19 ± 0,07**	**0,56**	**0,46**
Protein$_{305}$	**Centre**	0,49	**0,12 ± 0,04**	**0,31**
	Sud	0,33	0,38	**0,30 ± 0,10**

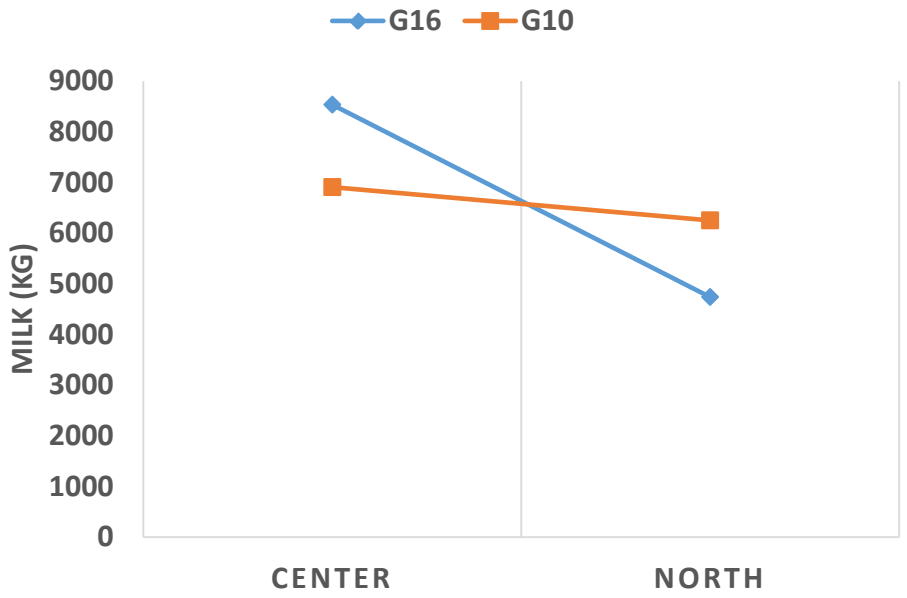
Ranking of Genotypes by Region

Rank	North	Center	South
1	G9	G19	G 8
2	G12	G8	G4
3	G14	G10	G10
4	G8	G12	G24
5	G5	G9	G13
6	G13	G7	G7
7	G10	G13	G6
8	G11	G6	G11
9	G7	G11	G23
10	G15	G5	G12
11	G1	G15	G1
12	G6	G22	G15
13	G22	G3	G18
14	G3	G24	G14
15	G26	G26	G16
16	G18	G4	G26
17	G2	G23	G19
18	G24	G2	G20
19	G20	G1	G22
20	G21	G18	G3
21	G4	G25	G17
22	G23	G20	G25
23	G17	G21	G5
24	G19	G16	G2
25	G16	G14	G9
26	G25	G17	G21

Results

Example of Interaction Genotype × Region



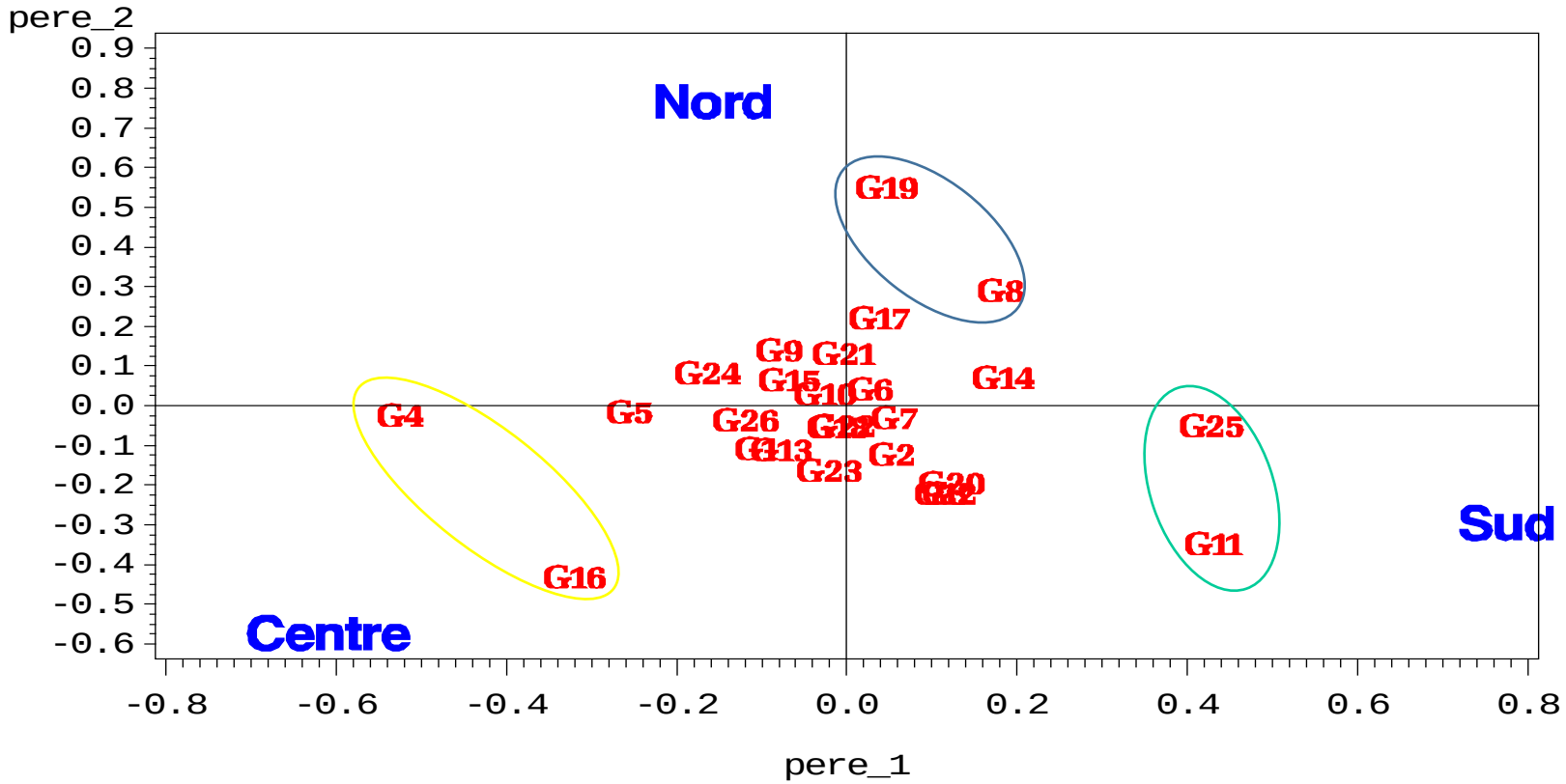


1) Interaction G×E
(Scaling effect)

2) Interaction G×E
(Re-ranking) of individuals

Results

AMMI Biplot showing the first two principal axes of interaction (IPCA1-IPCA2) for milk yield and 26 genotypes evaluated in 3 regions



Conclusions

- Obtained low genetic correlations among regions might indicate the existence of GxE.

- The AMMI method allowed for easy visual identification of superior genotypes for each set of environments.

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Acknowledgments

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