Effect of phytobiotic blends on digestive microbiota of broiler chickens reared in two stocking densities

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Objectives

Investigating the effect of **phytobiotics** (PHY) on the **growth performance** and digestive **microbiota** of **chicken** according to **stocking densities**

Materials & Methods

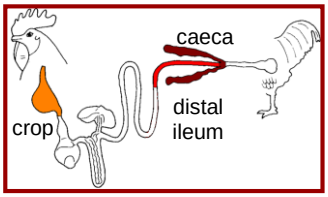
Animals: PM3 Ross broilers chickens

Housing conditions: 3 m² floor pens / 6 repeats per treatment

Stocking density: (EU 2010) 12 birds/m² ("low" density) ; 17 birds/m² ("high" density)

Dietary treatments: **Control:** Basic diet **Exp1:** PHYa d22-42; **Exp2:** PHYb d1-10 and PHYa d10-42

PHYa : anti-bacterial properties PHYb : anti-oxydative properties



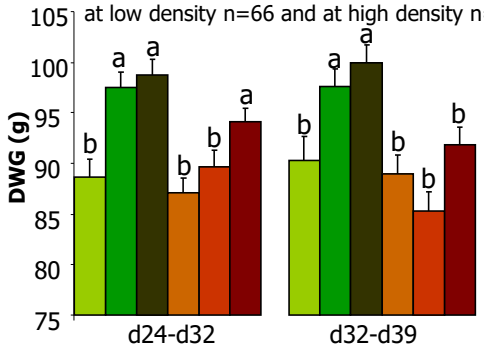
Microbiota analyses: **Samples:** Digestive content (crop, ileum, caeca) of d22 and d42 birds

TTGE (*all bacteria* primers) **Data analysis:** Analysis of similarity based on Pearson distance matrix

qPCR (*all bacteria, Enterobacteriaceae, Lactobacillus, Bacteroides, Clostridium leptum and C.coccoides group* primers)

Results

Daily Weight Gain (DWG) d24-d39



	d24-d32	d32-d39
Treatment (T)	<0.001	<0.0001
Density (D)	<0.0001	<0.01
T x D	NS	0.01

Degree of proximity (R) of TTGE profiles

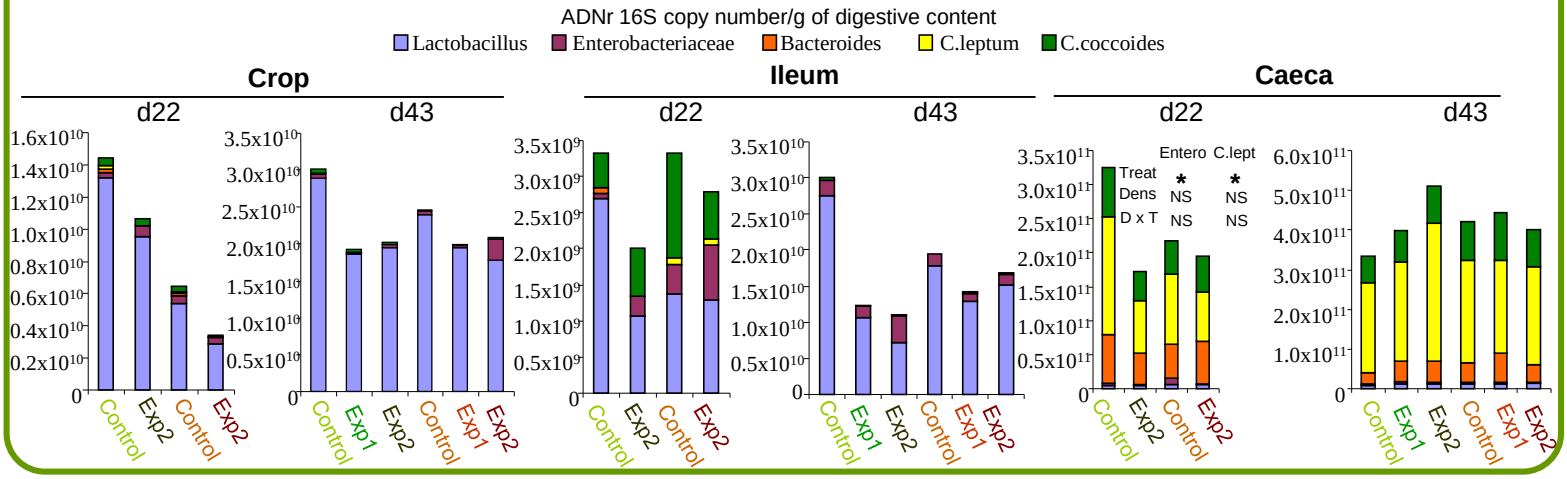
		Low density		High density	
		Exp1 vs control	Exp2 vs control	Exp1 vs control	Exp2 vs control
d22	**Crop**	-	NS	-	NS
	Ileum	-	NS	-	NS
	Caeca	-	NS	-	0.257
d42	**Crop**	NS	**0.615**	NS	NS
	Ileum	NS	NS	**0.552**	**1.000**
	Caeca	**0.677**	**0.750**	**0.917**	**0.896**

R>0.75 well-separated groups

0.50<R<0.75 separated but overlapping groups

0.25<R<0.50 separated but strongly overlapping groups

Real-time PCR quantification



Conclusion

Low density

Exp1 improved d24 to d32 and d32 to d39 DWG and led to a modification of microbiota at d42.

Exp2 improved d24 to d32 and d32 to d39 DWG, decreased the abundance of bacterial groups at d22 (Enterobacteriaceae and *Clostridium leptum*) and led to a modification of microbiota at d42.

High density

Exp1 led to a modification of microbiota at d42 but didn't improve DWG.

Exp2 improved d24 to d32 DWG, led to a modification of microbiota at d22 and d42 and decreased the abundance of bacterial groups at d22 (Enterobacteriaceae and *Clostridium leptum*).

Changes in microbiota were weak and not parallel with modifications of growth performance.

→ **Other factors** were involved in the **growth promoting effect** of these **phytobiotics**.

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