Recently, there was a reinvigoration of the concept of “gut health.” Field practitioners often correlate bad production outcomes, including diminished health and reduced growth efficiency, with poor gut architecture, as well as gut microbiota proliferation. This interference in production by the gut environment is surprising because the gut has long been considered a poorly refined organ solely equipped for the digestion and absorption of nutrients, with more noble functions, including homeostasis, resistance to disease, and growth efficacy, being performed by other internal organs. Interestingly, other biological disciplines have made quantum leaps in this field and have shown that the gut acts as an intelligent sensory organ in permanent communication with its continuously changing environment and that the gut is capable of substantial adaptation in response to changes in its internal environment. This begets the question of how we can make progress in the field of animal production and nutrition if we do not understand the molecular mechanisms driving the response of the gut to the diet, which seems to govern, more than we previously realized, the productive response of the animal in terms of growth, efficiency, and health.

Comparative physiology is an interesting approach to extrapolate findings from 1 species and apply it to another, especially at the molecular and cellular levels and even more in the postgenomic era. To help facilitate this process, the goal of the first Comparative Gut Physiology Symposium at the 2014 Joint Annual Meeting in Kansas City, MO, was to expose animal nutritionists to the current molecular and cellular discoveries that have been made in gut biology across animal species. The talks explored 2 methods of triggering an improvement in the productive response of farm animals using both 1) the gut epithelium as a specialized translator of messages coming from the lumen and 2) the interplay between the diet, the gut microbial ecosystem, and the immune response.

Furness et al. (2015) presented the specialized gut epithelial cells (i.e., enteroeendocrine cells), which translate the complex gut luminal messages directly or indirectly in response to the diet into a language that the body can understand. These cells are functionally connected by networks that magnify the messages and trigger a local response or activate the response of a distal organ. Additionally, they pointed out the plasticity of the gut and, particularly, its adaptability in relation to the diet with, for example, the induction of enzymes and transporters and growth of the mucosa. This knowledge was gained through studies in humans and rodents, thus allowing the authors to emphasize an interesting viewpoint. Although the appearance of the buildings may be different at the level of the organization of the digestive system (e.g., among ruminants, nonruminant mammals, birds, and fish), the individual building blocks (e.g., at a tissue component, cellular, or molecular level) are most often shared across species. What’s more, when different species are exposed to the same compound, their physiological responses are very comparable. This result opens the possibility of extrapolating insights from heavily investigated animal models to those species for which the research is scarce. Then, the question of whether a certain physiological response is converted to an improvement in production could be investigated in the target animal. At the very least, this comparative approach could help in the design of new and innovative feeding practices.

Interestingly, Connor et al. (2015) exemplified the comparative physiology approach by presenting