MANAGEMENT

Beef Logic

► by **R.A. "Bob" Long**

Are breeds a thing of the past?

The demise of beef cattle breeds, as we know them, was predicted repeatedly at the recent Beef Improvement Federation (BIF) annual meeting. One statement was, "We all know breeds are a thing of the past." Another speaker predicted far fewer breed associations, with those remaining recording several breeds and evolving into "biological type associations" of which there could be less than five.

WAIT! Before you schedule a herd dispersal, try to understand the origin of these prognostications.

Definitions

The BIF was formed in 1968 as "a means to standardize programs and methodology and to create greater awareness, acceptance and usage of beef cattle performance concepts." The federation neither makes nor enforces rules or laws — it only discusses and recommends. Member organizations include state beef cattle improvement associations (BCIAs), national breed associations, the National Cattlemen's Beef Association (NCBA), the Cooperative Extension Service and the Agricultural Research Service (ARS) of the U.S. Department of Agriculture (USDA).

The leaders of BIF are well-educated, bright, able and — for the most part — trained as population geneticists. They have contributed greatly to our industry through advances in performance-selection techniques that have made possible the use of expected progeny differences (EPDs) and other breed improvement tools. However, many of these leaders feel obligated to be progressive, and they sometimes convince themselves that a change in terminology means progress.

The definition of "breed" (which these gentlemen have declared obsolete) is simply "a group of related animals possessing uniform, identifying characteristics." These prophets support the replacement of "breeds" with either "biological types" or "composites."

Biological types

A biological type is a group of related animals possessing uniform, identifying characteristics. The cattle industry is accustomed to identifying breeds by color — black Angus, Red Angus, white-faced Hereford, white Charolais and black-and-white Holstein. However, groups can be identified by other characteristics, such as degree of muscling, maternal traits, meat quality or milk production.

The BIF predictors probably were referring to cattle homozygous for the double-muscled gene, such as Belgian Blue and Piedmontese, as one biological type (no details were given). Another type might be beef cattle of intermediate muscling and superior in maternal traits. A third could be light-muscled types superior in milk production. Finally, there are *Bos indicus* (such as Brahman) cattle. No more come to mind.

Regardless, the implication for the use of these biological types in beef production involves crossbreeding. The crossing of maternal strains with terminal-cross sires is an established procedure and is hardly new. The level of production depends on the excellence of the individuals in the cross, so continued improvement of available breeds is still needed.

Composites

A typical composite might be constructed by combining four breeds, with each breed contributing equally. For example, an F_1 generation is established by crossing breeds A and B. Another F_1 group is created by crossing breeds C and D. Finally, these two F_1 groups are crossed, which results in the F_2 generation and the foundation herd for this composite, with each breed contributing 25%. This foundation herd is then "closed." All future replacements — both male and female — come from within the herd.

The basis for such composites is Sewell Wright's work with guinea pigs back in 1922. His work was confirmed by Dickerson using cattle and swine in the late 1960s. These gentlemen offered the formula $(n\text{-}1)\div n$, which states that retention of the initial heterosis of the composite foundation with random mating within the herd is proportional to the number of breeds that made up the composite.

In the case of a four-breed composite, 25% of the heterosis is lost between the F_1 and F_2 generations, and no further loss takes place as long as no inbreeding occurs. Therefore, a breeder can maintain a composite herd indefinitely without further loss of heterosis provided all matings are random and the herd is large enough to prevent inbreeding.

Note particularly that the production level of the composite remains static. There are two ways to improve performance in composites. A new composite can be made using breeds superior to those used originally. Obviously, this requires the availability of superior breeds. The second method is to begin selection in the original composite. However, selection in the composite increases relationship and inbreeding, and the result is a group of related animals with uniform identifying characteristics — a new breed with no heterosis.

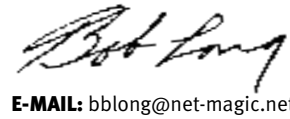
Here to stay

The development of a new breed superior in performance and predictability requires a great deal of time and numbers, and established breeds with similar programs will have continued to improve in productivity during that period. Extensive databanks and large numbers make established breeds difficult to surpass. It would appear that the current breeds with sound selection programs are here to stay.

If breeds are a thing of the past, why are there more Angus cattle registered than the rest of the beef breeds combined, and why do feedlot managers and packer buyers hunt for black hides and naturally polled heads?

Of course, the industry will experience change, and new technology will be used. But it will *not* come from changes in terminology.

Perhaps the brightest spot in the BIF meeting was the comment by Mark Thallman of the USDA Meat Animal Research Center (MARC) at Clay Center, Neb.: "Breeding decisions will be based on National Cattle Evaluation (NCE) rather than individual DNA tests, but NCE will be enhanced to accommodate DNA technology. For the foreseeable future, DNA information will only account for some of the genetics of any one trait. We will still need EPDs. DNA testing will not make phenotypic information unnecessary. Single-gene selection will be much worse than single-trait selection."



E-MAIL: bblong@net-magic.net