Advancing Whitetail Deer Breeding: Genetic Insights from Over 110,000 Samples

In the world of whitetail deer breeding, data-driven decisions are transforming how breeders build healthier, more resilient herds. A recent milestone from the North American Deer Registry (NADR) and Dr. Chris Seabury highlights this progress: analysis of over 110,000 whitetail deer DNA samples has revealed key insights into genetic health, diversity, and breeding strategies. This comprehensive dataset not only underscores the industry's overall strength but also equips breeders with tools to accelerate improvements in antler size, Chronic Wasting Disease (CWD) resistance, and overall herd vitality.

Beginning in late 2025, we will offer two new metrics produced from the NADR's database. The first of the two new deliverables made available will be the inbreeding coefficient ("F IBC". In general, the "F IBC" ranges from 0.00 to 1.00, where a value of 0.00 indicates no inbreeding and a value of 1.00 represents complete inbreeding. There could be occasions where the "F IBC" is negative in some instances. These tools will soon integrate with Game Management Solutions (GMS) for subscribers, potentially reshaping animal valuations. While technical, they promise to speed up breeding programs, protect herd health and enable the creation of "dream deer" beyond mere numerical chases.

A Strong Foundation: Industry-Wide Genetic Health

The NADR database paints an encouraging picture of the whitetail breeding industry's genetic landscape. On average, the inbreeding coefficient (IBC) stands at a remarkably low 0.037, indicating minimal inbreeding risks across the board. This low IBC helps dodge common pitfalls associated with inbreeding depression, such as weakened immune systems, reduced fertility, smaller antlers, and poor fawn survival rates.

Complementing this is an average observed heterozygosity of 40%, a robust measure of genetic diversity. Heterozygosity reflects the variety of alleles (gene variants) in the population, providing the raw material for selective breeding. This diversity has fueled significant advancements, including enhanced CWD resistance over recent years, all while maintaining a broad gene pool. As the NADR team notes, this is a "win worth protecting," ensuring the industry can continue pushing for genetic gains without compromising long-term sustainability.

The Hidden Dangers: Outliers and Inbreeding Risks

While averages are promising, they can mask problematic outliers. Some deer in the database exhibit extreme inbreeding, with IBC values as high as 0.89 - nearly fully inbred. These animals often pair with poor Genomic Estimated Breeding Values (GEBV), where lower or negative scores indicate better CWD resistance. In one worst-case example, a deer with a GEBV of +0.37 and heterozygosity about 10 times below average represents a "progress killer."

Breeding with such individuals introduces double copies of undesirable alleles across the genome, leading to stalled genetic improvements, wasted resources, and increased risks over generations. The advice is clear: high IBC combined with low diversity acts as a genetic bottleneck.

Elite Performers: Balancing Excellence and Diversity

On the flip side, many top-tier deer—those with strong negative GEBV scores for superior CWD resistance—also boast low IBC and high heterozygosity. These "outcross goldmines" allow breeders to stack elite traits safely, avoiding inbreeding traps and accelerating herd improvements. By prioritizing these animals, especially for widespread semen use, breeders can maintain momentum in genetic progress while safeguarding diversity.

This balance is crucial in an era where focus on individual alleles and GEBV has yielded results, but without diversity monitoring, risks like shrinking gene pools or accidentally fixing bad traits loom large. Metrics like IBC and heterozygosity serve as essential guardrails, helping answer key questions: Is a 96SS sire (a desirable PRNP genotype for CWD resistance) a diversity booster or a hidden risk? Can outcrossing preserve progress? Which bucks offer the fastest, safest gains?

Practical Guidance: Why It Matters and How to Act

Genetic diversity isn't just an abstract concept—it's nature's insurance against diseases and environmental challenges. Loss of diversity through bottlenecks, inbreeding, or line breeding heightens susceptibility to emerging threats like new infectious diseases. The new metrics empower breeders to improve GEBVs thoughtfully, select semen sires wisely, and identify true outcrosses.

Actionable Steps for Breeders

1. **Integrate Diversity into Decisions**: Don't rely solely on GEBV—use diversity as a multiplier for gains.
2. **Test Key Animals**: Assess sires for Inbreeding Coefficients and Heterozygosity to inform choices.
3. **Prioritize Balanced Bucks**: Favor low Inbreeding Coefficients, high Heterozygosity, especially for broad use.
4. **Cull Risks Proactively**: Remove high-inbreeding animals, regardless of superficial GEBV appeal.

Stay Updated: Monitor GMS for incoming diversity tools to refine your program.

Looking Forward: Sustainable Progress in Whitetail Breeding

The future of whitetail deer breeding extends beyond bigger antlers to encompass healthier, more adaptable herds. With tools like the NADR database, GMS, GEBV's, Inbreeding Coefficients, and Heterozygosity, breeders now have the data to make smarter, safer decisions. By embracing these insights, the industry can protect its genetic foundation, mitigate risks, and continue innovating. As the NADR team emphasizes, we've got the tools—let's use them to breed not just for today, but for generations to come.

Q1: How do I use this new information? What is the point?

A1: This information is designed to help breeders thoughtfully improve their GEBVs without excessive inbreeding or line breeding. Semen sires can also be selected with this in mind. True outcrosses can be guided or identified using this information.

Q2: Why should I care about inbreeding or line breeding?

A2: Genetic diversity is mother nature's insurance policy for ensuring the perpetuation of any species, at the population level. Loss of genetic diversity via population bottleneck and/or inbreeding or line breeding can render individuals more susceptible to new emerging infectious diseases, or even common diseases that exist today. Adaptability requires genetic diversity.

Q3: Are there any recommendations or "guardrails" for these values? Where should we aim?

A3: The national averages of these values as of 2025 provide one valuable benchmark for which to compare your herd (i.e., herd average), or to compare with your individual deer. The national average for "**F_IBC**" = 0.037111 at the time of writing this FAQ (11/01/2025). The national average for "**Obs_HET**" = 0.400557 at the time of writing this FAQ (11/01/2025). If your herd or individual deer are producing values for "**F_IBC**" that are much larger than the national average (i.e., like equal to or greater than 0.15), then you need to take some corrective action in the next breeding season to implement some degree of outcrossing.

Q4: Do you have any real working examples to highlight to show the value of this information?

A4: Yes, if you have a deer with positive GEBVs for CWD (GEBV = 0.322223) that is also a *PRNP* 96GG, and the "**F_IBC**" = 0.80, with "**Obs_HET**" = 0.10, this would mean the deer in question is highly inbred on top of a highly susceptible genetic background. It would also indicate that the deer has two copies of an undesirable CWD susceptibility allele at many different locations throughout the genome. Therefore, it would cost an inordinate amount of time and money to even attempt to "dilute" the CWD susceptibility alleles out of this lineage; all while increasing risk for CWD across generational time. Wouldn't you rather know this up front; and perhaps take an alternative approach that makes more economic sense while also reducing long term risk for CWD?

Another working example would be as follows: Many of the deer that have tested in the elite GEBV classes

(i.e., like less than say -0.35) but also are 96GS or 96SS have high levels of diversity, as estimated by the "**Obs_HET**", and low estimates for the inbreeding coefficient known as "**F_IBC**". For example, in one such elite deer the "**Obs_HET**" is greater than the national average at the time of writing (0.400557); with an inbreeding coefficient "**F_IBC**" that is less than the national average at the time of writing (0.037111), which should give the breeder confidence regarding concerns about the "overtightening" of lineages. Therefore, this new information can help guide better breeding decisions for progress related to CWD GEBVs; especially given the prioritization of *PRNP* 96S. Essentially you can monitor your genetic progress in real time annually and then adapt or strategize accordingly. You will no longer be limited to only what you can see in the pedigree to inform your outcrosses, or to determine when you need an outcross.

Q5: Outside of GEBVs for CWD, why would I need this new information?

A5: Breeding animals too tight causes the "unmasking" of negative recessive alleles. What this means is that inbreeding increases homozygosity; thereby producing genotypes comprised of two negative recessive alleles. Herein, I use the words "negative recessive allele" to denote that having two copies of this recessive allele causes negative consequences such as: congenital defects, general immune suppression or dysfunction, subfertility, reduced fawn survivability, reduced adult longevity, and/or enhanced susceptibility to common infectious diseases.