Entwicklung eines ökonomisch ausgerichteten Zuchtprogramms für die bedrohte Schweinerasse „Bunte Bentheimer“

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vorgelegt von
ANNE DOROTHEA MARGARITA BIERMANN
geboren in Detmold

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1. Gutachter: Prof. Dr. Sven König
Fachgebiet Tierzucht
Fachbereich Ökologische Agrarwissenschaften
Universität Kassel

2. Gutachter: Prof. Dr. Horst Brandt
Institut für Tierzucht und Haustiergenetik
Justus-Liebig-Universität Gießen

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Zusammenfassung

Das Ziel dieser Arbeit war, ein ökonomisch ausgerichtetes Zuchtprogramm für die bedrohte Schweinerasse „Bunte Bentheimer“ zu entwickeln. Ein wesentlicher Bestandteil von Zuchtprogrammen für bedrohte Rassen ist der Erhalt der genetischen Diversität durch Vermeidung von weiterer Inzucht und Reduzierung des Inzuchtzuwachses. In **Kapitel 2** wurde die Population der Bunten Bentheimer unter Berücksichtigung der gesamten zur Verfügung stehenden Abstammungsinformationen in Bezug auf genetische Diversität, Inzucht und verwandtschaftlicher Verhältnisse analysiert. Der aktuelle durchschnittliche Inzuchtkoeffizient lag mit 12% auf einem relativ hohen Niveau. Die durchschnittliche Inzuchtzunahme lag bei 1,66% pro Generation. Effektive Maßnahmen zur Inzuchtkontrolle sind daher unerlässlich und müssen im Zuchtprogramm integriert werden. Durch die Bestimmung optimaler Einsatzfrequenzen selektierter Tiere ist es möglich, Inzucht zu kontrollieren aber gleichzeitig auch Zuchtfortschritt zu generieren. Das konnte am Beispiel von Zuchtwerten für Fruchtbarkeitsmerkmale gezeigt werden. Basierend auf den optimalen Einsatzfrequenzen der selektierten Elterntiere wurden zur weiteren Reduzierung der Inzucht in der Folgegeneration konkrete Anpaarungspläne erstellt. Die Anpaarungen wurden unter Berücksichtigung der Natursprungproblematik durch Festlegung von Zuchtgebieten konzipiert. Die Umsetzung dieser wurde allerdings erschwert durch die eingeschränkte Verfügbarkeit der Eber. Schließt man die künstliche Besamung als mögliche Alternative aus, müssten die Zuchtgebiete so optimiert werden, dass die vorgeschlagenen Anpaarungen auch in die Praxis umgesetzt werden können.

Die Gestaltung eines Zuchtprogramms erfordert zudem die Verfügbarkeit populationsgenetischer Parameter. Für die Fruchtbarkeitsmerkmale „Anzahl lebend geborener Ferkel“ (NBA) und „abgesetzter Ferkel“ (NW) lagen die Heritabilitäten bei jeweils 12%. Auch die genetischen Varianzen lagen in einem guten Bereich, so dass für beide Merkmale Zuchtfortschritt durch Selektion möglich ist. In **Kapitel 3** wurden genetische Parameter für Fleischleistungs- und Fleischqualitätsmerkmale geschätzt. Als Grundlage dafür dienten sowohl *in vivo* Ultraschallmessungen, die direkt am lebenden Tier durchgeführt wurden, als auch Messungen, die am Schlachtkörper bzw. an einer Fleischprobe erfolgten. Zucht-, Mast- und auch Schlachttiere wurden am RYR1 Genort typisiert, um Allel-Substitutionseffekte zu schätzen. Die quantitativen- und molekulargenetischen Ansätze wurden genutzt, um darauf aufbauend zur Verbesserung der Fleischqualität Zuchtstrategien zu entwickeln. Für das Fleischqualitätsmerkmal intramuskulärer Fettgehalt (IMF) wurde die höchste Heritabilität von 0,78 bei einer ebenfalls hohen additiv-genetischen Varianz geschätzt. Dennoch ist die Erfassung dieses Merkmals mit einem relativ hohen Kostenaufwand verbunden. Ein mögliches Hilfsmerkmal ist die Rückenspeckdicke (BF_{iv}), die direkt am Selektionskandidaten erfasst werden kann. Die genetische Korrelation zwischen beiden Merkmale lag bei $r_g = 0,39$. Die Assoziationsstudie am RYR1 Genort zeigte, dass die Anwesenheit des ungewünschten Allels einen negativen Effekt auf IMF hatte, d.h. der IMF Gehalt wurde reduziert. Darauf aufbauend wurde eine Zuchtstrategie entwickelt, die Phänotyp (BF_{iv}) und Marker-Informationen am RYR1 Genort des Selektionskandidaten kombiniert. Durch die zusätzliche Berücksichtigung der Marker-Informationen konnten eine höhere Genauigkeit und ein höherer Zuchtfortschritt erzielt werden im Vergleich zu einer Strategie, die nur auf den phänotypischen Leistungen basiert. Die Ausnutzung dieser Allel-Substitutionseffekte setzt allerding voraus, dass entsprechende Allel-Frequenzen in der Population vorhanden sind. Intensive Sanierungsmaßnahmen, insbesondere in den letzten Jahren, lassen vermuten, dass die Frequenz des unerwünschten Allels mittlerweile deutlich geringer ist als zum Zeitpunkt der Studie mit $q = 0,13$. Dennoch könnte dieser Ansatz Modellcharakter für zukünftige genetische Marker haben.

In **Kapitel 4** wurde basierend auf einer Konsumentenbefragung mit integrierter Verkostung von Fleischproben indirekt die Zahlungsbereitschaft für unterschiedliche Fleischqualitäten erfasst. Alle Fleischproben wurden zusätzlich hinsichtlich der instrumental erfassbaren Fleischqualität untersucht und durch ein geschultes Panel im Sensorik Labor in Bezug auf die sensorische Qualität beurteilt. Außerdem wurde die direkte Zahlungsbereitschaft für unterschiedliche Qualitätsausprägungen der optischen Merkmale „Fleischfarbe“, „Fleischmarmorierung“ und „Fleischsaftverlust“ anhand von Fotografien erfasst. Die Ergebnisse dieser Befragung wurden genutzt, um ökonomischen Gewichte für Merkmale der Fleischqualität und sensorischen Qualität abzuleiten. Für IMF ergab sich ein hohes ökonomisches Gewicht von 57,52 € pro Merkmalseinheit bei dem aktuellen Populationsdurchschnitt von 1,57%. Mit steigendem Populationsmittel sinkt das ökonomische Ge-

wicht und nähert sich ab einem Mittelwert von 2% einem Wert von 0,00 €. Aus züchterischer Sicht wäre daher ein durchschnittlicher IMF Gehalt von mindestens 2% anzustreben. Für Fleischqualitätsmerkmale, die beim Verzehr nicht direkt erfassbar sind, wie die Farbhelligkeit oder der Tropfsaftverlust, ist die direkte Methode zur Erfassung der Zahlungsbereitschaft (basierend auf den Fotografien) der indirekten (basierend auf der Verkostung) vorzuziehen, um ökonomische Gewichte abzuleiten. Die geschätzten genetischen Parameter und abgeleiteten ökonomischen Gewichte wurden anschließend für Zuchtplanungsrechnungen verwendet. Im Zuchtziel wurde in erster Linie die Fruchtbarkeit (NBA) und Fleischqualität (IMF) berücksichtigt. Die Zuchtprogramme basierend auf einer Stationsleistungsprüfung waren trotz der relativ hohen Züchtungserträge nicht wirtschaftlich. Gründe dafür waren die hohen variablen Kosten der Leistungsprüfung. Zur Vermeidung der hoher Kosten und der besseren Anpassung an kleine Betriebsstrukturen wurde alternativ ein Zuchtprogramm modelliert, das auf *in vivo* Ultraschallmessungen für BF_{iv} basiert, direkt erfasst am Selektionskandidaten. Der Züchtungsgewinn für diese Zuchtstrategie lag bei 35,92 € pro Tier. Der Zuchtfortschritt für IMF war allerdings erwartungsgemäß geringer als bei direkter Selektion auf das Merkmal.

Basierend auf den Ergebnissen wurde in **Kapitel 5** ein Entwurf für ein Zuchtprogramm erstellt, das die notwendigen Maßnahmen zur Inzuchtkontrolle beinhaltet und Zuchtfortschritt für rassespezifische Merkmale zulässt. Zudem ist dieser Entwurf angepasst an die kleinen Betriebsstrukturen und die unterschiedlichen Vermarktungsstrategien, die sich bereits etabliert haben.

Summary

The main objective of this thesis was the development of an economically straightened breeding program for the endangered pig breed “Bunte Bentheimer”. One of the main constituents when modelling breeding schemes for endangered breeds is the maintenance of genetic diversity by decreasing the rate of inbreeding and avoidance of inbreeding in subsequent generations. In **chapter 2** the whole pedigree of the Bunte Bentheimer population was analyzed in consideration of genetic diversity, inbreeding and relationship. The current average inbreeding coefficient was relatively high (12%) as well as the average rate of inbreeding per generation (1.66%). Hence, effective strategies to control inbreeding and implementation in a breeding program are indispensable. Optimal genetic contributions of selected animals enable to control inbreeding and simultaneously achieve genetic gain. This was demonstrated based on estimated breeding values for fertility traits. Optimal genetic contributions of selected parents were used to design mating schemes and to reduce inbreeding even more in the subsequent generation. Mating designs were draft according to natural service that is predominately practice in this population. Only within specific regions, mating from candidates was allowed. However, feasibility was hindered, due to restricted availability of boars. To transfer suggestions into practice, specific regions have to be optimized.

The designing of breeding programs furthermore genetic parameters for traits of interest are requires. For the fertility traits “number of piglets born alive” (NBA) and “number of piglets weaned” (NW) estimated heritabilities were $h^2 = 0.12$. Additive genetic variances were relatively high, indicating the possibility of improvements through selection. Genetic parameters for production and meat quality traits were estimated in **chapter 3**. Estimates were based on records for *in vivo* traits, measured ultrasonically on living animals, on carcass measurements, and for meat quality on meat samples. Breeding, fattening and slaughtered animals were additionally genotyped at the RYR1 locus to estimate allele substitution effects. Breeding strategies on meat quality were designed by combining quantitative-genetic and molecular-genetic approaches. For intramuscular fat content the highest heritability was estimated ($h^2 = 0.78$) as well as high additive genetic variance.

However, recording of this trait is relatively expensive. To reduce costs for performance testing, backfat thickness measured directly on selection candidates (BF_{iv}) can be used as indicator trait for IMF. Genetic correlation between IMF and BF_{iv} was moderate (r_g = 0.39). Allele substitution effect at the RYR1 locus was negative on IMF, i.e. IMF decrease when the unfavorable allele is present. Based on these results a breeding strategy was modeled combining the phenotype (BF_{iv}) and genetic marker information at the RYR1 locus of the selection candidate. Accuracy and selection response increased when compared with a strategy without genetic marker information. Nevertheless, using genetic marker information and allele substitution effects, corresponding allele frequencies are required. In the recent years acute actions on reducing the frequency of the unfavorable allele were carried out. This lead to the assumption, that today allele frequency is much lower than q = 0.13 as estimated when analysis were done. However, this approach might be considered as a prototype for future important genetic marker.

In **chapter 4** consumers were asked for their willingness to pay for tasted meat samples to derive indirectly their willingness to pay for different quality classes. All samples were also analyzed regarding instrumental quality traits and sensorial quality traits. Latter was defined by a trained panel. Additionally, consumers were directly asked for their willingness to pay for different quality classes presented as photographs. The photographs included traits regarding the appearance of meat, being the brightness of the meat, the marbling, and the drip loss. Subsequently the results were used to derive economic values for meat quality and sensorial quality traits. For the meat quality trait IMF the derived economic value was very high (57.52 € per trait unit) at the current population mean of 1.57%. Increasing the population mean up to about 2% IMF, leads to a decrease of the economic value close to zero. Results indicate the economic advantage of breeding strategies on meat quality in particular when marketing strategies are focused on niche-markets. For traits that are not ascertainable by tasting (being the case for color and drip loss), determination of consumers' willingness to pay should be based on meat photographs, rather than on tasted meat samples, to derive economic values. Estimated genetic parameters and derived economic values were used for modelling breeding schemes and evaluation with respect to profitability (discounted profit) and annual genetic gain. The breeding goal primarily focused on improvements for fertility (NBA) and meat quality (IMF). Despite high discounted returns, breeding schemes based on an on-station test for full-sibs of selection candidates to directly record meat quality traits were not profitable. To avoid such high breeding costs for on-station tests, a breeding scheme was modeled adapted to small-scale and low-input production systems. Such a low cost variant is possible via *in vivo* measurements for backfat thickness. BF_{iv} applications allow recording of selection candidates without slaughtering, and were considered as an index trait to improve meat quality. Discounted profit for this breeding scheme was large and positive denoted with 35.92 € per animal. As expected, annual genetic gain for IMF was lower as obtained by direct selection on IMF.

Based on these results a breeding program was designed in **chapter 5** according to strategies to control inbreeding and generate genetic gain for breed specific traits. The breeding program was adapted to small-scale production systems and includes different already established marketing strategies.

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KAPITEL 1

Allgemeine Einleitung

Warum bedrohte Rassen erhalten?

Dieses Kapitel soll einen einleitenden Überblick geben zum Thema bedrohte Nutztierrassen und einige Besonderheiten für deren Zuchtarbeit darstellen. Der aktuelle Stand der Forschung in Bezug auf die einzelnen Themengebiete ist Bestandteil der jeweiligen Kapitel selbst.

Als Grundlage für die Zuchtarbeit bei bedrohten Rassen stellt sich zunächst die Frage: „Warum sollen wir bedrohte Rassen überhaupt erhalten?“. Diese Frage nach dem „Warum“ stellten sich Wissenschaftler bereits schon vor 40 Jahren (Ryder, 1976) und die Argumente dafür sind bis heute dieselben geblieben. Aus wissenschaftlicher Sicht bietet eine hohe Variation tiergenetischer Ressourcen die Möglichkeit „neue“ (bisher unbekannte und/oder züchterisch irrelevante) Merkmale zu erforschen. Betrachtet man den Wandel der Zuchtziele in den letzten Jahrzehnten, z.B. in der Schweinezucht, wird deutlich, dass immer mehr sehr unterschiedliche Merkmale die Zuchtziele prägen. Während in den 60er Jahren auf hohe Fleischleistung selektiert wurde, erfolgte ab den 70er Jahren eine zunehmende Gewichtung von Fleischbeschaffenheitsmerkmalen (Glodek, 1992). Anfang der 90er Jahre wurde durch intensive Selektion auf die Wurfgröße ein beachtlicher Zuchtfortschritt in diesem Merkmal erzielt, was allerdings mit erhöhten Ferkelverlusten einherging. Die Verbesserung der Aufzuchtleistung sollte unter anderem durch eine gute Mütterlichkeit der Zuchtsauen realisiert werden. Die gesetzlich vorgeschriebene Gruppenhaltung tragender Sauen ab 2013 ließ große Zuchtunternehmen in die Untersuchung einer Reihe von Verhaltensmerkmalen investieren (Tönepöhl, 2012). Die letzten Jahre waren zunehmend geprägt durch das Interesse an Gesundheitsmerkmalen, Langlebigkeit, aber auch Merkmalen der Fleischqualität, z.B. in Bezug auf den Ebergeruch (Haberland, 2014). Dieser Wandel ist auch bei anderen Spezies zu beobachten. Funktionale Merkmale (Kramer, 2013) oder die genetische Hornlosigkeit gewinnen in Zuchtprogrammen für Rinder an Bedeutung. Beim Hinterwälder Rind zeigte Rössler et al. (2013), im Rahmen einer Befragung der Züchter zu präferierten Selektionsmerkmalen, dass innerhalb der Population eine Verschiebung der Nutzungsrichtung zu verzeichnen ist. Die zunehmende Bedeutung der Mutterkuhhaltung lässt neue Merkmale wie z.B. Charaktereigenschaften der Tiere in den Vordergrund rücken. Die Veränderungen in den Selektionskriterien und Zuchtzielen in der Tierzucht werden maßgeblich durch die Öffentlichkeit und durch politische Entscheidungen und Maßnahmen geprägt. Die gesellschaftlichen und politischen Entwicklungen sind aber schwer vorauszusagen und somit auch die zukünftiger Zuchtziele in der Tierzucht. Dieser stetige Wandel macht die Bewahrung der tiergenetischen Variabilität so essentiell, denn ohne sie könnten mögliche unbekannte Merkmalsausprägungen verloren gehen. Aus agrarwirtschaftlicher und ökonomischer Sicht ist die Bewahrung tiergenetischer Ressourcen entscheidend, um auf zukünftige Marktanforderungen reagieren zu können.

Die Erhaltung bedrohter Rassen beinhaltet aber auch einen kulturellen und historischen Aspekt. Das Bunte Bentheimer Schwein zählt zu den wenigen verbliebenen alten deutschen Schweinerassen. Sein Ursprungsgebiet liegt in der Region um die Stadt Bad Bentheim, welcher diese lokale Rasse ihren Namen zu verdanken hat. Die meisten Zuchtbetriebe sind auch heute noch in dieser Region anzutreffen. Der kulturelle Wert des Bunten Bentheimer Schweines für diese Region ist daher unumstritten. Durch die Regionalität eröffnen sich Märkte, die im Bereich der Nischenproduktion ausgeschöpft werden können. Der Nutzen, der diesen Rassen dadurch zugeschrieben wird, sichert letztendlich deren Erhalt und die Bewahrung eines wertvollen Kulturgutes.

Von der bedrohten Rasse zurück zum Nutztier

Tiere, die zum Nutzen des Menschen geschaffen wurden, können ohne diesen Nutzen nicht bestehen. Die Blütezeit des Bunten Bentheimer Schweines lag in den 50er Jahren, als die Zuchtziele in der Schweinezucht geprägt wurden durch die Nachkriegszeit und dem Bedarf nach fettreichen, energieliefernden Lebensmitteln. Die in den darauffolgenden Jahren zunehmende Nachfrage nach Rassen mit der entgegengesetzten Veranlagung, nämlich einem hohen Fleischanteil, führte zur rapiden Abnahme des Bestandes. Solche Entwicklungen sind allerdings keine Erscheinung der vergangenen Jahre, sondern sind ebenso in den heutigen Tagen zu beobachten. Die in den 70er Jahren in der DDR entwickelte Rasse Leicoma gilt heute als die meist gefährdetste deutsche Schweinerasse. Der Bestand an Zuchttieren beschränkt sich auf nur noch einen Betrieb. Interessierte Züchter, Schweinehalter, Verarbeiter und Vermarkter werden aktuell zur Bildung einer Interessengemeinschaft gesucht, um die Rasse Leicoma z.B. im Rahmen eines Qualitätsfleischprogramms zu vermarkten und somit den Erhalt zu sichern (Bundesanstalt für Landwirtschaft und Ernährung, 2015a). Im Falle des Bunten Bentheimer Schweines kam es im Jahre 2003 zur Gründung des „Verein zur Erhaltung des Bunten Bentheimer Schweines e.V.“ und im gleichen Zuge wurde die Züchtervereinigung für alte Schweinerassen „Nordschwein e.V.“ ins Leben gerufen. Diese Entwicklung war entscheidend für den Aufbau eines bundesweiten Herdbuchs und die Erfassung der in Deutschland noch vorhandenen Bestände. Der Erfolg dieser Maßnahme spiegelt sich in der Entwicklung der Bestandszahlen wider. Zum Vergleich sind diese mit den einheimischen Rassen Leicoma und Schwäbisch-Hällisches Schwein in Abbildung 1 dargestellt, wobei für das Schwäbisch-Hällische Schwein für die Jahre 2008 und 2009 keinen Daten vorlagen.

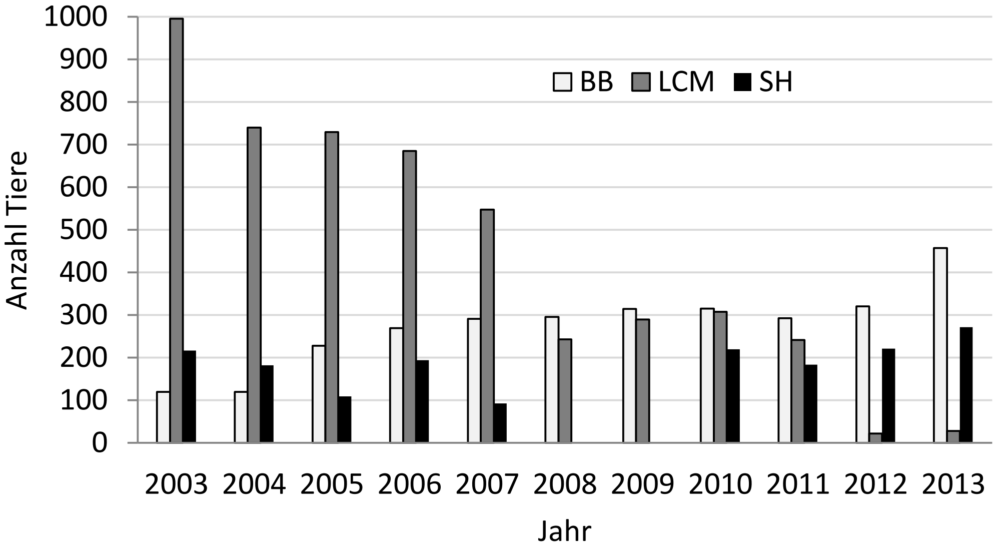

Abbildung 1: Entwicklung der Bestandszahlen der einheimischen Schweinerassen Bunte Bentheimer (BB), Leicoma (LCM) und Schwäbisch Hällisches Schwein (SH) nach Angabe der Zentralen Dokumentation Tiergenetischer Ressourcen in Deutschland (Bundesanstalt für Landwirtschaft und Ernährung, 2015b).

Die Implementierung eines Qualitätsfleischprogrammes zum Erhalt einer Rasse, setzt zunächst voraus, dass für die entsprechende Vermarktung die nötige Nachfrage durch den Endkonsumenten vorhanden ist. Aktuell ist im Lebensmitteleinzelhandel ein zunehmendes Angebot an Biolebensmitteln, regionalen, vegetarischen und veganen Produkten zu beobachten. Die Palette an möglichen Alternativen zu den konventionellen Lebensmitteln steigt also tendenziell. Öffentliche und politische Debatten in Bezug auf die Lebensmittelherstellung zeigen generell ein erhöhtes Interesse und Bewusstsein seitens des Konsumenten (Olynk, 2012). Für Alternativen zur konventionellen Lebensmittelerzeugung scheint also durchaus eine Nachfrage existent zu sein. Spiller und Schulze (2008) zeigten, dass unter den Fleischkonsumenten eine etwas kleinere Gruppe existiert, die eine höheren Preisbereitschaft zeigt und bei der besonders Qualitätsprodukte gefragt sind, z.B. gekennzeichnet durch eine besondere sensorische Qualität, regionale Tradition, ökologische Produktion oder verbesserte Haltungsformen. Allein die Existenz eines potentiellen Marktes macht ein Qualitätsprogramm allerdings nicht erfolgreich. Um gewissen Qualitätsstandards zu erfüllen bietet ein darauf angepasstes Zuchtprogramm die Möglichkeit gewünschte Zuchtzielmerkmale, z.B. der Fleischqualität, zu stärken und den wirtschaftlichen Erfolg zu gewährleisten.

Zuchtprogramme für bedrohte Nutztierrassen

Auf globaler Ebene sind die Maßnahmen zum Erhalt tiergenetischer Ressourcen von der FAO (2007) im „Global Plan of Action for Animal Genetic Resources“ festgehalten. Als Grundlage zur Umsetzung dieser Maßnahmen auf nationaler Ebene dient das "Nationale Fachprogramm zur Erhaltung und nachhaltigen Nutzung tiergenetischer Ressourcen" (2008) das vom Bundesministerium für Ernährung, Landwirtschaft und Verbraucherschutz herausgegeben wurde.

Ein wesentlicher Bestandteil von Erhaltungszuchtprogrammen ist die Bewahrung der genetischen Variabilität durch die Minimierung des Inzuchtzuwachses innerhalb einer Population. Maßnahmen zur Inzuchtkontrolle sind der Spezies, Rasse und Population anzupassen. Für bedrohte Hühnerrassen stellte Weigend (1999) am Beispiel der Rasse Vorwerkhühner ein Modell vor, bei dem durch Rotation der Hahnennachkommen innerhalb eines Züchterringes die Verpaarung eng verwandter Tiere verhindern wird. In der Rinderzucht ist generell die künstliche Besamung weit verbreitet, was mit einer guten Verfügbarkeit von Besamungsbullen einhergeht. Bei der einheimischen Rinderrasse „Rotes Höhenvieh“ kann bei der Auswahl eines geeigneten Besamungsbullen online direkt eine Anpaarungsplanung durchgeführt werden. Durch Angabe der Tiernummer wird der Inzuchtkoeffizient des Nachkommen berechnet und somit die verwandtschaftlichen Verhältnisse der Eltern aufgezeigt (Bundesarbeitsgemeinschaft Rotes Höhenvieh, 2015). Für einige lokale Rinderrassen stehen sogar aktuelle Zuchtwertlisten zur Verfügung. So werden z.B. für die Vorderwälder und Hinterwälder Rinder in Baden-Württemberg seit August 2014 Zuchtwerte geschätzt. Neben dem Erhalt der genetischen Diversität ist man bei diesen Rassen bereits bestrebt, Zuchtfortschritt in den entsprechenden Zuchtzielmerkmalen zu generieren (Landesamt für Geoinformation und Landentwicklung in Baden-Württemberg, 2015). In der Schweinzucht erfolgt das Inzuchtmanagement ebenso durch konkrete Anpaarungspläne. Bei den in Österreich einheimischen Schweinerassen Turopolje und Mangaliza beträgt der maximal zulässige Inzuchtkoeffizient der für die Anpaarung selektierten Elterntiere <= 13%. Das Zuchtziel dieser Zuchtprogramme ist definiert durch den Erhalt genetischer Vielfalt und der Konsolidierung des rassetypischen Phänotyps (ARCHE Austria, 2015). Eine züchterische Bearbeitung basierend auf einer Zuchtwertschätzung erfolgt nicht. Beim Bunten Bentheimer Schwein werden ebenfalls Anpaarungsplanungen durchgeführt, um Inzucht in den Folgegenerationen zu vermeiden. Im Gegensatz zu den österreichischen Rassen ist das Zuchtziel beim Bunten Bentheimer Schwein u.a. auf eine „exzellente Fleischqualität“ ausgelegt, bedingt durch viele bereits etablierte Vermarktungsstrategien im Nischen- und Premiumsegment. Eine züchterische Bearbeitung ist bisher allerdings nicht möglich, da generell keine Leistungsprüfung und Zuchtwertschätzung für Fleischqualität erfolgt.

Für die langfristige und nachhaltige Nutzung tiergenetischer Ressourcen ist eine Unterstützung durch öffentliche Mittel erforderlich (FAO, 2007). Durch die Förderung von Forschungsprojekten, z.B. in Kooperation mit wissenschaftlichen Institutionen, können grundlegende Erkenntnisse gewonnen werden, die zur Entwicklung von rassespezifischen Erhaltungszuchtprogrammen benötigt werden, aber auch Modellcharakter für andere Rassen und Spezies haben können. Darüber hinaus gibt eine kontinuierliche Förderung, z.B. durch die Auszahlung von Haltungsprämien, Anreiz zur Zucht und Haltung bedrohter Rassen. Neben der staatlichen Förderung ist eine gute Vermarktungsstrategie für den wirtschaftlichen Erfolg und damit der nachhaltigen Erhaltung einer Rasse entscheidend. Beispiele aus der Schweinezucht zeigen, dass die Vermarktung reingezüchteter Tiere, z.B. zur Herstellung spezieller Produkte wie beim Ibérico Schwein, durchaus möglich ist. Demgegenüber kann durch Anwendung systematischer Gebrauchskreuzungen die Marktfähigkeit von Schlachttieren und somit die Gesamtwirtschaftlichkeit verbessert werden (Brandt et al., 2010; Chainetr et al., 2002). Bei der Vermarktung vom Bunten Bentheimer Schwein zeichnet sich keine einheitliche Strategie ab, in der Regel werden aber nur Reinzuchttiere vermarktet.

Bei der Entwicklung eines Zuchtprogrammes spielt die Vermarktungsstrategie allerdings eine entscheidende Rolle, wenn Zuchtzielmerkmale und deren ökonomische Gewichtung im Gesamtindex festgelegt werden. Um den wirtschaftlichen Erfolg eines Zuchtprogramms abzuschätzen, können darauf aufbauend Zuchtplanungsrechnungen durchgeführt werden und ggf. Änderungen in den Merkmalen und deren Gewichtung vorgenommen werden.

Zielsetzung der Arbeit

Das allgemeine Ziel dieser Arbeit besteht in der Entwicklung eines ökonomisch ausgerichteten Zuchtprogramms für die Rasse Bunte Bentheimer. Dabei sollen durch geeignete Maßnahmen zur Inzuchtkontrolle und Aufrechterhaltung rassetypischer Eigenschaften sowohl Aspekte der Erhaltungszucht berücksichtigt werden, als auch züchterische und ökonomische Aspekte, indem Zuchtfortschritt für wirtschaftlich relevante Merkmale ermöglicht wird. Das Zuchtprogramm soll an die aktuellen Betriebsstrukturen angepasst und durch eine gute Anwendbarkeit und Umsetzbarkeit gekennzeichnet sein. Daraus ergeben sich die folgenden notwendigen Arbeitsschwerpunkte:

In **Kapitel 2** soll zunächst die Population der Bunten Bentheimer Schweine unter Berücksichtigung der gesamten zur Verfügung stehenden Abstammungsinformationen hinsichtlich ihrer genetischen Diversität und Inzucht analysiert werden. Basierend auf populationsgenetische Analysen für Merkmale der Fruchtbarkeit sollen Selektions-und Anpaarungsplanungen durchgeführt werden, die Zuchtfortschritt ermöglichen bei gleichzeitiger Inzuchtkontrolle.

In **Kapitel 3** sollen anschließend populationsgenetische Parameter für Merkmale der Fleischleistung- und Fleischqualität geschätzt werden um darauf aufbauend Zuchtstrategien zu modellieren, die zur Verbesserung der Fleischqualität beitragen. Diese sollen unter besonderer Berücksichtigung des RYR1 Gens und der Anwendung von *in vivo* Leistungsprüfungen evaluiert werden.

Die ökonomischen Gewichte für nicht-marktrelevante Merkmale wie die Fleischqualität werden in **Kapitel 4** abgeleitet, um anschließend Zuchtplanungsrechnungen zur Beurteilung der Wirtschaftlichkeit für unterschiedliche Zuchtstrategien zu evaluieren.

Die Bedeutung der gewonnenen Erkenntnisse zur Erstellung eines Zuchtprogramms für die Rasse Bunte Bentheimer werden in **Kapitel 5** diskutiert.

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KAPITEL 2

Implementation of genetic evaluation and mating designs for the endangered local pig breed 'Bunte Bentheimer'

A.D.M. Biermann, E.C.G. Pimentel, M. Tietze, T. Pinent and S. König

Department of Animal Breeding, University of Kassel
Nordbahnhofstraße 1a, 37213 Witzenhausen, Germany

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ABSTRACT

A pedigree including 1,538 individuals of the endangered pig breed 'Bunte Bentheimer' and 3,008 records with the fertility traits 'number of piglets born alive' (NBA) and 'number of piglets weaned' (NW) were used to i) characterize the population structure, ii) to estimate genetic (co)variance components and estimated breeding values (EBV), and iii) to use EBVs for the application of the concept of optimal genetic contributions. The average coefficient of inbreeding increased from F = 0.103 to F = 0.121 within the two recent cohorts. Average rate of inbreeding amounted 1.66%, which resulted in an effective population size of N_e = 30 animals in the recent cohort. Average generation interval was 3.07 years considering the whole pedigree, and in total only 612 sows and boars generated offspring. Estimated heritabilities for both traits NBA and NW were 0.12, and the estimated genetic correlation between both traits was 0.96. The variance component due to the service sire was higher than in commercial pig breeds, presumably due to the widespread use of natural service boars. The EBVs for NBA from 333 selection candidates (63 boars and 270 sows) were used to determine optimal genetic contributions. Based on selected animals and their optimal genetic contributions, specific mating designs were evaluated to minimize inbreeding in the next generation. Best results were achieved when using a simulated annealing algorithm, and allowing artificial insemination.

Keywords: Endangered pig breed, fertility, inbreeding, optimal genetic contributions

INTRODUCTION

The local origin of the pig breed 'Bunte Bentheimer' (**BB**) is the polder region in northwestern Germany. An extended overview of breeding activities which started in the middle of the 19th century is given by Kolk gen. Sundag et al. (2006), and by Voss (2012). In brief, an F1-cross of local Landrace sows with Berkshire boars from the UK was established in 1900 as a synthetic line, and only a limited percentage of migration from Cornwall boars from the UK, and Poland-China boars from the US, was allowed. Furthermore, some gene flow from Tamworth pigs at the end of the 19th century is assumed. Official herd book registration of the BB started in 1950. However, population size of the BB breed substantially decreased from the middle to the end of the 20th century due to the importance of lean meat percentage, which restricted the use of fatty pig breeds. In the past three decades, population size included less than 100 registered boars, and less than 250 registered sows per year (Kolk gen. Sundag, 2006).

Motivation of farmers for keeping endangered breeds imply external financial support, and several strategies for making decisions in livestock conservation programs exist (Simianer, 2005). An alternative and more promising strategy for conservation might be based on economic competitiveness. Chainetr et al. (2002) suggested the implementation of systematic regional crossbreeding schemes in certificated 'meat quality programs' by including endangered breeds, e.g. BB and Sattlebacks. However, when adopting the current payment system, BB progeny revealed economic inferiority compared to commercial controls. Nielsen et al. (2006) developed a concept for sustainable animal breeding objectives, which enables to include traits without direct market values, e.g. animal welfare, in overall breeding goals. Consequently, when applying this concept, the economic value of endangered breeds used for alternative objectives may increase. The BB are mainly used for organic pig production systems, and consequently, a strong focus aims on improvements on the trait components of behavior, female fertility, and meat quality (Biermann et al., 2012). But so far, also meat quality traits, e.g. intramuscular fat or marbling, are not considered in the current payment system for pork. In addition to economic weights, an overall breeding goal for BB implies the availability of genetic (co)variance component estimates for the traits of interest. A further challenge for sustainable breeding strategies in small and endangered populations is to maintain inbreeding and genetic relationships on an acceptable level (e.g. Luis et al., 2007). Combining both aspects of maximizing genetic gain and minimizing genetic relationships in the BB breed may be achieved with the application of the optimum genetic contribution (**OGC**) theory (Meuwissen, 1997).

The aim of the present study was to: i) evaluate the population structure of the BB breed, ii) estimate genetic parameters for traits which have been officially recorded in the BB breed in the past two decades, and iii) combine results of genetic evaluations and genetic relationships in the population to define a breeding strategy for the BB breed by applying the OGC-concept. Furthermore, detailed mating plans were developed based on a simulated annealing algorithm, and compared with alternative strategies for the restricted use of natural service sire boars.

MATERIALS AND METHODS

Data

The BB population as a small local pig breed is generally used for meat production in small-scale family farms. In most cases and according to the guidelines of organic pig production, pigs are reared and kept in extensive or in low input production systems. The distributions of registered sows and boars in Germany in the year 2012 are represented in the Supporting Information (Figure S1). Most of the farms were located in Lower Saxony and in North Rhine-Westphalia. The herd size ranged between 1 and 30 sows, and from 0 to 3 boars.

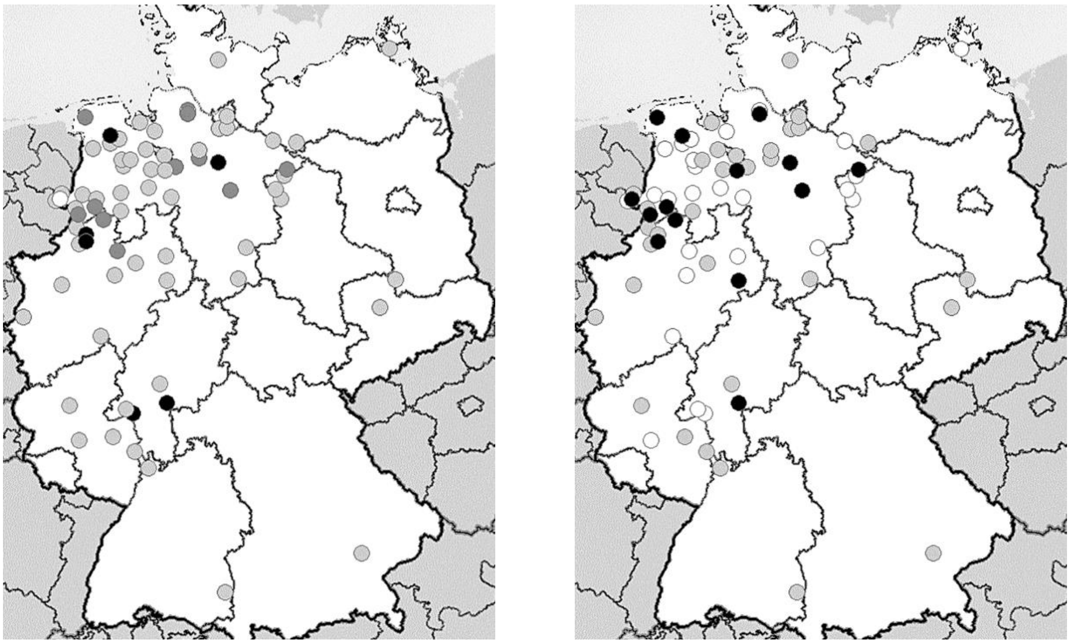

Figure S1. Distribution of registered BB sows (left) and registered BB boars (right) in Germany based on information in the utilized dataset. On the left: black points = 11-30 sows per farm, dark grey points = 5-10 sows per farm, light grey points = 1-4 sows per farm, and white points = 0 sows per farm. On the right: black points = 2 boars per farm, light grey points = 1 boar per farm, and white points = 0 boars per farm.

A total of 3,008 female reproduction records from 1985 until 2012 along with pedigrees were obtained from the breeding organization 'Nordschwein e.V.'. Reproduction traits were the 'number of piglets born alive' (NBA) and the 'number of piglets weaned' (NW) from in total 872 sows. The pedigree comprised 1,538 individuals from birth years 1977 to 2011. Due to a limited number of pigs in some years, cohorts of animals were defined. Animals born within a time period of 3 consecutive years were considered as a cohort (except the first cohort, which included 4 birth years) summing up in a total of 11 cohorts (Table 1). The active breeding stock, i.e. registered pigs (as of March 2012), comprised 333 animals. These animals were considered as potential selection candidates, i.e. possible parents of the next generation.

Table 1. Number of male and female parents, average generation interval (GI), averaged individual inbreeding rate ($\overline{\Delta F}$), and effective population size based on the rate of inbreeding (N_e)

Cohort	Birth years	No. of sires	No. of dams	GI	$\overline{\Delta F}$	N_e
1	77/78/80/81	2	1			
2	82/83/84	4	4			
3	85/86/87	7	18	3.20	7.40	7
4	88/89/90	26	59	2.37	5.74	9
5	91/92/93	36	58	2.93	3.58	14
6	94/95/96	28	36	3.63	3.80	13
7	97/98/99	33	45	3.53	3.11	16
8	00/01/02	39	68	3.03	2.59	19
9	03/04/05	66	130	2.97	2.11	24
10	06/07/08	98	162	2.87	1.63	31
11	09/10/11	84	131	3.20	1.66	30
Average whole Pedigree				3.07	2.38	21

Pedigree Analysis

Criteria for the pedigree completeness level were the percentage of animals with both known parents, the longest ancestral path, and the average number of discrete generation equivalents. These criteria were calculated using the software package CFC (Sargolzaei et al., 2006). Additionally, the average pedigree completeness index (**PCI**, MacCluer et al., 1983) within cohorts was computed using the software system POPREP (Groeneveld et al., 2009) for 6 generations deep.

Further pedigree analysis by applying POPREP included the calculation of generation intervals, and coefficients of inbreeding and of coancestry. Individual rates of inbreeding and parameters based on the probability of gene origin (effective number of founders, effective number of founder genomes, and effective number of non-founders) were computed using CFC.

Generation Interval

The generation interval (**GI**), defined as the average age of the parents at the birth of their selected offspring (Falconer and Mackay, 1996), was calculated by year of birth and were averaged within cohorts.

Coefficient of Inbreeding and of Coancestry

The average coefficients of inbreeding ($\boldsymbol{F}$) and of coancestry ($\boldsymbol{f}$) were computed by year of birth and were averaged within cohorts. The coefficient of coancestry between the parents of an individual, which is half of the relationship coefficient, is equal to the coefficient of inbreeding assuming random mating. Hence, the coefficient of coancestry is useful to predict the coefficient of inbreeding in the subsequent generation (Falconer and Mackay, 1996). Inbreeding and coancestry can also be used to estimate the deviation of non-random mating (**α**), using the formula described in Caballero and Toro (2000):

$$(1 - F) = (1 - f)(1 - \alpha).$$

A negative value of α indicates avoided matings between related individuals (Toro et al., 2000).

Effective Population Size

The individual rate of inbreeding (ΔF_i) was calculated using the formula by Gutiérrez et al. (2009):

$$\Delta F_i = 1 - \sqrt[t_i - 1]{1 - F_i}$$

where t_i is the discrete generation equivalent and F_i the inbreeding coefficient of the individual i. Individual rates of inbreeding were averaged within cohorts ($\overline{\boldsymbol{\Delta F}}$) and were used to calculate the effective population size ($\boldsymbol{N_e}$) using the following formula by Falconer and Mackay (1996):

$$N_e = \frac{1}{2\overline{\Delta F}}.$$

Effective Number of Founders

The effective number of founders ($\boldsymbol{N_{ef}}$) measures the founder contribution to the population under study (here: the active population). Founders were defined as animals with both parents unknown. N_{ef} is defined as the number of equally contributing founders, which would give the same level of genetic diversity as in the active population (Lacy, 1989).

Effective Number of Founder Genomes

The effective number of founder genomes ($\boldsymbol{N_{ge}}$) is defined as the number of equally contributing founders with no loss of founder alleles, which would give the same level of genetic diversity as in the active population and was calculated as in Caballero and Toro (2000).

Effective Number of Non-founders

The effective number of non-founders ($\boldsymbol{N_{enf}}$) accounts for the contribution of non-founders to the active population and therefore the effect of random genetic drift in the non-founders generations. N_{enf} was computed according to Caballero and Toro (2000).

Genetic Diversity

The three parameters N_{ef}, N_{ge}, and N_{enf} are related as follows:

$$\frac{1}{2N_{ge}} = \frac{1}{2N_{ef}} + \frac{1}{2N_{enf}}.$$

Parameters were used to measure the amount of genetic diversity accounting for loss of diversity due to genetic drift and unequal founder contribution ($\boldsymbol{GD}$) (Lacy, 1995):

$$GD = 1 - \frac{1}{2N_{ge}}$$

and accounting for loss of diversity due to unequal founder contribution ($\boldsymbol{GD}^*$) (Lacy, 1995):

$$GD^* = 1 - \frac{1}{2N_{ef}}.$$

Estimation of Variance Components and Breeding Values

Genetic parameters and breeding values (EBV) for NBA and NW were estimated in a bivariate animal model applying the DMU program package (Madsen and Jensen, 2000), and using AI-REML. The statistical model for both traits was defined as follows:

$$\begin{bmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}_1 & 0 \\ 0 & \mathbf{X}_2 \end{bmatrix} \begin{bmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_1 & 0 \\ 0 & \mathbf{Z}_2 \end{bmatrix} \begin{bmatrix} \mathbf{u}_1 + \mathbf{p}_1 \\ \mathbf{u}_2 + \mathbf{p}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{W}_1 & 0 \\ 0 & \mathbf{W}_2 \end{bmatrix} \begin{bmatrix} \mathbf{s}_1 \\ \mathbf{s}_2 \end{bmatrix} + \begin{bmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{bmatrix}$$

where: subscript 1 represents NBA and subscript 2 represents NW; **y** is a vector of observations; **b** is a vector of fixed effects; **u** is a vector of random additive genetic effects; **p** is a vector of random permanent environmental effects; **s** is a vector of random sire effects; **e** is a vector of random residual effects; and **X**, **Z** and **W** are incidence matrices. Fixed effects included an overall mean, parity number, herd, year and a regression on the age of the sow. The assumed (co)variance structures of random effects were as follows:

$$\mathbf{V}\begin{bmatrix}\mathbf{u}_1\\ \mathbf{u}_2\\ \mathbf{p}_1\\ \mathbf{p}_2\\ \mathbf{s}_1\\ \mathbf{s}_2\\ \mathbf{e}_1\\ \mathbf{e}_2\end{bmatrix}=\begin{bmatrix}\begin{bmatrix}\sigma^2_{\mathbf{a}1} & \sigma_{\mathbf{a}12}\\ \sigma_{\mathbf{a}12} & \sigma^2_{\mathbf{a}2}\end{bmatrix}\otimes\mathbf{A} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix}\\ \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{bmatrix}\sigma^2_{\mathbf{p}1} & \sigma_{\mathbf{p}12}\\ \sigma_{\mathbf{p}12} & \sigma^2_{\mathbf{p}2}\end{bmatrix}\otimes\mathbf{I} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix}\\ \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{bmatrix}\sigma^2_{\mathbf{s}1} & \sigma_{\mathbf{s}12}\\ \sigma_{\mathbf{s}12} & \sigma^2_{\mathbf{s}2}\end{bmatrix}\otimes\mathbf{I} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix}\\ \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{matrix}0 & 0\\ 0 & 0\end{matrix} & \begin{bmatrix}\sigma^2_{\mathbf{e}1} & \sigma_{\mathbf{e}12}\\ \sigma_{\mathbf{e}12} & \sigma^2_{\mathbf{e}2}\end{bmatrix}\otimes\mathbf{I}\end{bmatrix}$$

where **I** is an identity matrix of appropriate order, and **A** is the numerator relationship matrix, σ_a^2 is the additive genetic variance, σ_p^2 is the permanent environmental variance, σ_s^2 is the service sire variance, and σ_e^2 is the residual variance. EBVs of both traits NBA and NW were standardized to a mean of 100 and standard deviation of 20, where EBV > 100 indicates genetic superiority.

Optimum Genetic Contributions and Specific Mating Designs

The OGC algorithm as implemented in the GENCONT program (Meuwissen, 2002) was used to select boars and sows with their optimal mating frequencies in order to maximize NBA while constraining additive genetic relationships. The vector of contributions of each selected animal is defined as **c**, the estimated breeding values of selection candidates for NBA are included in vector $\mathbf{u_s}$, and $\mathbf{A_s}$ is the genetic relationship matrix among selection candidates. Maximizing genetic gain in NBA implies to maximize $\mathbf{c'u_s}$, while the average genetic relationships, $\mathbf{c'A_sc}$, were constrained. Potential selection candidates comprised 63 boars and 270 sows. Following the request of the breeding organization, 30 sows with equal genetic contributions to the next generation were selected. Each selected boar was mated with at least 1 sow, and with at most 3 sows. According to the current level of inbreeding in the BB population, additive genetic relationships were constrained in the range from 0.23 to 0.27. The OGC algorithm determines optimal genetic contributions of selection candidates by considering a long term perspective in inbreeding management, but without specifying mating designs among selected sows and boars for the next round of matings.

For minimizing the average inbreeding coefficient in offspring in the next generation, Sonesson and Meuwissen (2000) developed a so-called 'simulated annealing algorithm (**SAA**)'. This algorithm uses GENCONT-output, i.e. suggested global mating frequencies of selected candidates. All combinations of matings between sows and boars are tested (changing of mating partners in consecutive runs). The design resulting in the lowest average genetic relationships between selected sows and boars is to be considered the optimal one. Essential steps of the algorithm are summarized by König et al. (2010).

In theory, SAA implies availability of selected sows and boars for specified matings. Feasibility is ensured via artificial insemination. Therefore, the mating design was named AI-Mate. However, in the BB population, a high percentage of pig producers prefer natural service boars. Exchange of boars is only possible within short distances, e.g. local regions. Hence, we developed an own mating design (NSB-Mate) covering the features of SAA, i.e. testing all combinations between selected sows and boars with the ultimate goal of reducing inbreeding in the next generation, but only allowing matings from candidates kept in the same region. For a first application, regions were defined to be the federal states of Germany.

RESULTS AND DISCUSSION

Pedigree Structure and Demographic Parameters

The whole pedigree of the BB population comprised 1,538 individuals. The percentage of animals with both known parents amounts 95.84%. The depth of the pedigree is represented by the longest ancestral path and the average number of discrete generation equivalents and were 16 and 6.71, respectively. The average PCI for 6 generation deep was above 95% since the year 2006 (Cohort 10), and indicates a fairly good pedigree completeness (Supporting Information, Figure S2).

The average GI in the BB breed comprised 3.07 years considering the whole pedigree, but GI slightly differed between cohorts (Table 1). Melka and Schenkel (2010) found much lower average GI for the breeds Duroc (1.60), Hampshire (2.07), Lacombe (1.73), and Landrace (1.65) in Canada. Bühler and Postler (2004) found an average GI of 1.49 years within the endangered German pig breed Schwäbisch-Hällisches. The considerably high GI in the BB population probably results from the small-scale production systems along with a limited use of artificial insemination and a restricted availability of boars. Same boars were used over a long period. Furthermore, the BB breed does not have an organized reproduction cycle based on a strict fertility management as prevalent in modern pig breeds. In some cases, sows only have one or even no litter per year, probably because pig producers voluntarily extend the interval from farrowing to first insemination.

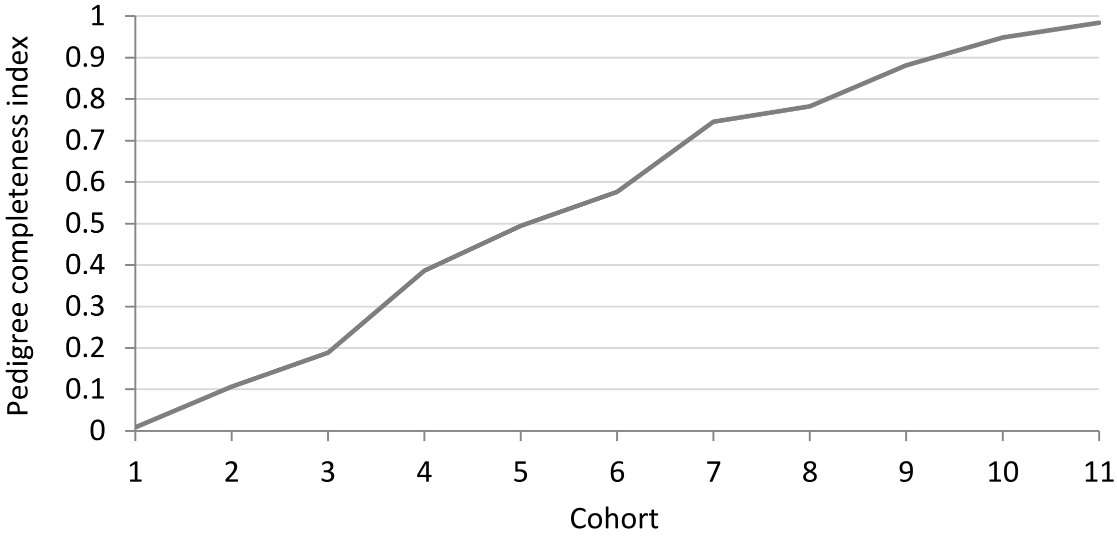

Figure S2. Pedigree completeness index by cohort.

Distl et al. (2006) demonstrated that only half of the breeding pigs were used to generate the next generation. This result is in accordance to the fact that only 612 animals in the whole pedigree and 64 animals in the active population generated progeny. This unused genetic potential probably indicates reduced genetic diversity in the BB breed (Distl et al., 2006).

Inbreeding and Genetic Diversity

Average inbreeding coefficients and average coefficient of coancestry fluctuated over the time (Figure 1). Since 2004 (cohort 9) the deviation of non-random mating was negative. This was in consequence due to the mating strategy initiated by the breeding organization, where matings between highly-related individuals were avoided. However, considering changes between the two recent cohorts, average inbreeding increased from F = 0.103 (cohort 10) to F = 0.121 (cohort 11). Similar level of inbreeding was found in the endangered French pig breeds Basque and Gascon with average inbreeding coefficients of F = 0.141 and F = 0.089*,* respectively (Mercat, 2007). However, inbreeding coefficients are affected by depth and completeness of pedigrees, which should be kept in mind when making comparisons of inbreeding coefficients across breeds or populations.

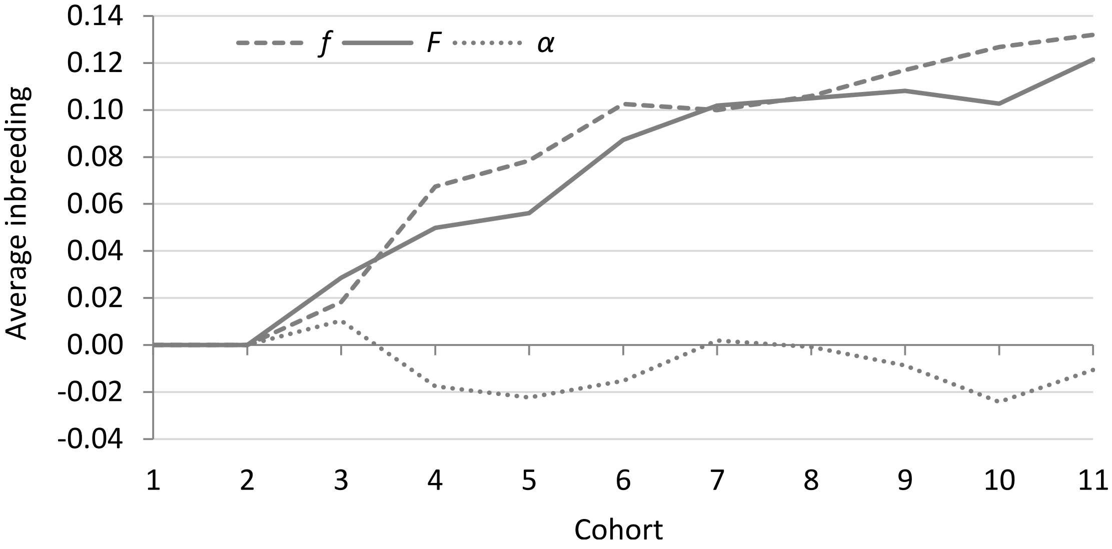

Figure 1. Average coefficient of inbreeding (F), average coefficient of coancestry (f) and deviation of non-random mating (α).

In conservation programs, the rate of inbreeding is an important parameter to measure genetic diversity. Here, the ultimate goal is to keep the rate of inbreeding per generation below 1%, with a corresponding effective population size of at least N_e= 50 (FAO, 2003). We observed decreasing rates of inbreeding in the BB population over the time (Table 1), probably as the consequence of the mating management, as mentioned above. However, in the most recent cohort (animals born between 2009 and 2011) average inbreeding rate slightly increased compared to the previous cohort, exceeded the 'critical value' and resulted in an effective population size of N_e = 30 animals. Increasing inbreeding and increasing deviation of non-random mating in the most recent cohort probably indicate that the applied mating management was efficient in the short-term. However, in long-term perspective, the effect seems to be oppositional (Caballero and Toro, 2000).

Parameters based on the probability of gene origin estimated for the active population were N_{ef}= 11.09, N_{ge}= 3.88, and N_{enf}= 5.96. The total number of founders was N_f = 35. N_{ef} was used to measure the contribution of founders to the active population. Low ratios between N_{ef} and N_f indicate an unequal contribution of founders due to high selection intensity and frequent use of particular animals (Melka and Schenkel, 2010). In the BB breed, this ratio was N_{ef}/N_f = 0.32. Figure 2 shows the decline of genetic diversity due to unequal contribution of founders. During the last decade, the loss of genetic diversity due to unequal founder contribution was 0.71%.

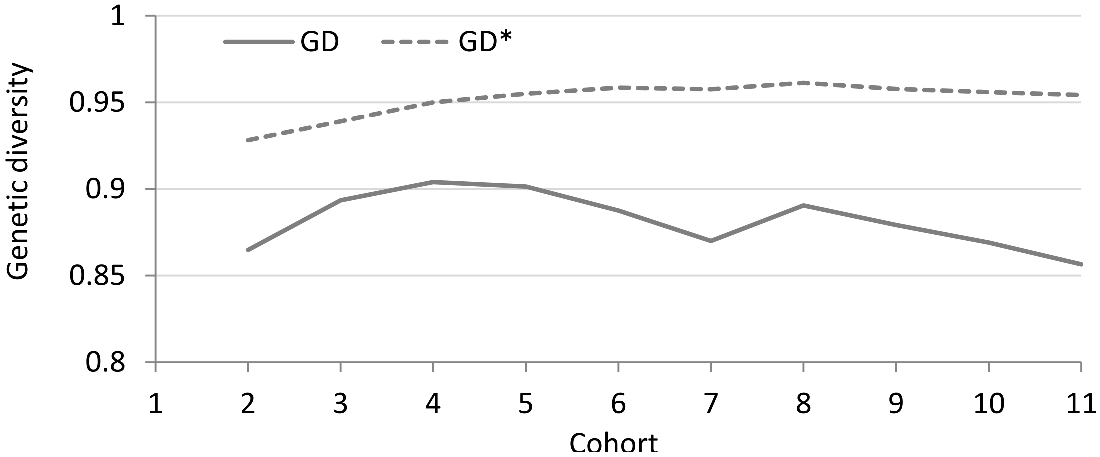

Figure 2. Genetic diversity accounting for loss of diversity due to genetic drift and unequal founder contribution (GD) and accounting for loss of diversity due to unequal founder contribution (GD^*).

Especially in small populations like the BB, the decline of genetic diversity can be the consequence of random genetic drift. N_{ge} accounts for both loss of genetic diversity due to unequal founder contribution and genetic drift. The ratio between N_{ge} and N_{ef} measures the impact of genetic drift, whereas a low ratio indicate a high impact (Melka and Schenkel, 2010). This ratio was N_{ge}/N_{ef} = 0.35 in the BB breed. In the BB population, the loss of genetic diversity due to unequal founder contribution and genetic drift was 4.30% within the last decade. Since 1994 (cohort 6) N_{enf} was only somewhat higher than N_{ge}, which indicates that most of the genetic drift was accumulated over the non-founder generations (Stachowicz et al., 2011). The results furthermore indicate that the loss of genetic diversity was mainly caused by genetic drift as it was shown already for other populations

(Stachowicz et al., 2011; Melka and Schenkel, 2010; Toro et al., 2000). However loss of genetic diversity is probably underestimated due to the depth of the pedigree.

Variance Components

Estimated genetic parameters and variance components for the litter traits NBA and NW are presented in Table 2. The estimated heritability of 0.12 for NBA is in accordance with most of the results from the literature, e.g. for the pig breeds Landrace (Noguera et al., 2002) and Large White (Ferraz and Johnson, 1993). For NW, the heritability of 0.12 was higher than reported by Van and Duc (1999) for the breeds Mong Cai (0.09) and Large White (0.10). However, different strategies for genetic analyses of litter size have been applied. The most common strategy is to define litter size in different parities as different traits and to apply a series of univariate calculations (e.g. Noguera et al., 2002), the application of multiple trait models (e.g. Fernández et al., 2008), or at least to distinguish between litter size in parity 1 and following parities (e.g. Gernand et al., 2010). A further alternative prior to the genetic analyses is to pre-adjust litter size for the effect of parity (e.g. Ferraz and Johnson, 1993). Additionally and in analogy to our modeling, repeatability models for NBA or NW have been applied (e.g. Fernández et al., 2008). Justification of such a repeatability model is based on a similar genetic background and high genetic correlations for litter size between consecutive parities. Preliminary analyses revealed r_g = 0.74 for NBA between parity 1 and 2, and r_g = 0.99 for NBA between parity 2 and 3. Piles et al. (2006) compared repeatability models and multiple-trait models for genetic analyses of litter size in rabbits. In their study, genetic correlations for litter size between different parities lower than 0.8 favored a multiple-trait model, but selection response and accuracies of EBVs from the multiple-trait and the repeatability model were almost identical.

Estimates of genetic parameters when analyzing female fertility traits in commercial pig populations may be biased due to cross-fostering, but cross-fostering is commonly not practiced in the BB population. The genetic correlation between NBA and NW was very high (r_g = 0.96), and indicating that an identical genetic background is involved in the phenotypic expression of both female fertility traits. A similar result (r_g = 0.91) was found by Kaplon et al. (1991) in a Polish Large White herd, where also cross-fostering was not practiced.

Table 2. Estimated Heritabilities (diagonal), genetic correlation (above diagonal), residual correlation (below diagonal), additive genetic variance ($\hat{\sigma}_a^2$), service sire variance ($\hat{\sigma}_\mathrm{s}^2$), permanent environmental variance ($\hat{\sigma}_\mathrm{p}^2$) and residual variance ($\hat{\sigma}_\mathrm{e}^2$) for the traits 'number of piglets born alive' and 'number of piglets weaned' with corresponding SE in parentheses

	Trait	
Trait	Number born alive	Number weaned
Number born alive	0.12 (0.04)	0.96 (0.03)
Number weaned	0.86 (0.01)	0.12 (0.03)
$\hat{\sigma}_a^2$	0.61 (0.22)	0.56 (0.20)
$\hat{\sigma}_\mathrm{s}^2$	0.13 (0.07)	0.16 (0.08)
$\hat{\sigma}_\mathrm{p}^2$	0.25 (0.15)	0.08 (0.13)
$\hat{\sigma}_\mathrm{e}^2$	4.08 (0.14)	4.00 (0.13)

For NBA, the estimated additive genetic variance was 0.61, which is in agreement with results by Van der Lende et al. (1999). Also the relatively high additive genetic variance for NW (0.56) indicates the possibility of improvements for female fertility in the BB population through selection. Genetic variance is only one parameter with impact on selection response. Others are selection intensity and generation intervals. Strong impact of population and herd size on selection intensity in pig breeding programs was reported in early investigations by Freeden and Martin (1967). Both obstacles, the small population size and the extremely small herd structure in combination with natural service sires are relevant for the endangered BB breed. Furthermore, different BB breeders have different breeding objectives and a variety of breeding strategies across herds exists. Breeding on a variety of traits hampers selection response in a single trait, but may maintain genetic diversity and can be interpreted as a strength rather than a weakness of a pig breeding program, especially for an endangered breed characterized by a small population size. In both traits, the variance of the service sire was relatively high, probably due to the practice of natural services and differences in fertilizing capacity and/or the direct impact of the boar on embryo viability (Van der Lende et al., 1999).

Optimum Genetic Contributions and Mating Designs

For different scenarios with a constraint at genetic relationships in the range from 0.23 to 0.27, the number of selected sires and the expected average genetic value are depicted in Figure 3.

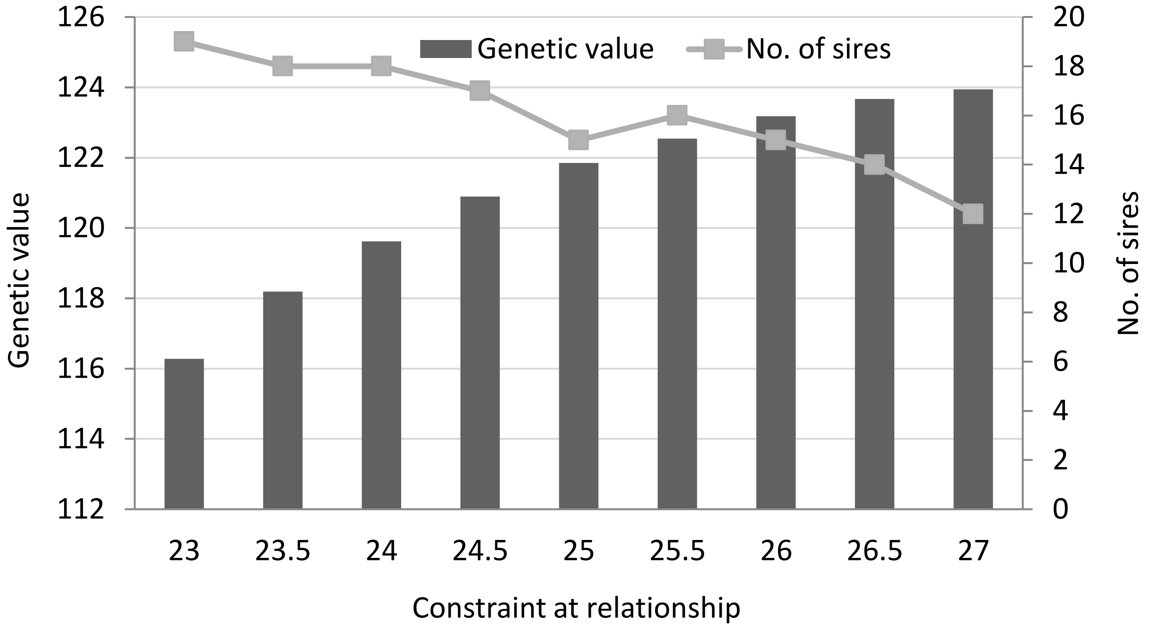

Figure 3. Genetic value of selected parents and number of selected sires at different constraints for average genetic relationships.

In the scenario with the highest constraint (= lowest level of average relationships at 0.23), the optimal number of selected sires was 19, and the average genetic value of the selected parents was 116.3. Considering the scenario with the most relaxed constraint (= highest level of allowed relationship at 0.27), the number of sires decreased to 12, and the average genetic value of the parents increased to 123.9. With increased constraints on relationships, an increase in the number of selected sires along with a decrease in the average genetic value of parents was observed. Hence, higher genetic gain was achieved when fewer sires were selected and higher genetic relationships were allowed. This was also observed in other species, i.e. dairy cattle (König and Simianer, 2006), horses (Niemann et al., 2009) and poultry (König et al., 2010). However, Figure 3 also illustrates marginal genetic progress when changing constraints in the "upper level": When increasing the constraint at relationship from 0.23 to 0.235, average EBV increased by 1.9 points. The EBV is only 0.2 points larger when relaxing relationships from 0.265 to 0.27. Consequently, the optimal decision for selection is a compromise between the constraint at relationship and genetic progress. The decision depends on the ultimate goal: Increasing genetic gain while keeping inbreeding at an acceptable level, or reduced inbreeding by keeping constant genetic progress (König et al., 2010).

Based on selected sows and boars with their optimal genetic contributions, specific mating plans were designed to produce piglets in the next generation. Using NSB-Mate and AI-Mate, average additive genetic relationships were lower compared to the average relationships obtained from all possible matings among OGC-selected sows and boars (Table 3).

Table 3. Additive genetic relationships between optimum genetic contribution selected sows and boars: All = average of all possible mating combinations without considering suggested mating frequencies, AI = mating design based on the simulated annealing algorithm as developed by Sonesson and Meuwissen (2002) and allowing artificial insemination, NSB = mating design accounting for natural service boars, i.e. verifying availability of sows and boars in same regions

	Additive genetic relationships for matings										
	No. of		Mean			Minimum			Maximum		
Scenario	boars	matings (NSB)	All	NSB	AI	All	NSB	AI	All	NSB	AI
0.23	19	23	0.208	0.151	0.159	0.000	0.000	0.000	0.636	0.227	0.215
0.24	18	10	0.215	0.179	0.167	0.000	0.058	0.000	0.665	0.229	0.227
0.25	15	23	0.220	0.175	0.178	0.000	0.000	0.000	0.665	0.228	0.233
0.26	15	25	0.227	0.180	0.188	0.000	0.000	0.000	0.665	0.228	0.233
0.27	12	25	0.232	0.191	0.197	0.000	0.000	0.000	0.665	0.293	0.247

The effect of the mating design on the average genetic gain was negligible. For example for the scenario where we constrained the relationship at 0.25, average genetic merit was: EBV = 121.85 for all possible matings, EBV = 120.36 for NSB-Mate and EBV = 121.73 when applying AI-Mate. Due to the additional restriction in NSB-Mate (mating was only possible within specific regions), higher average relationships were expected compared to AI-Mate (mating without restrictions). However, no substantial differences were found, because NSB-Mate could not fulfill the requested number of 30 matings (Table 3). In some specific regions, the required numbers of boars were not available. Average additive genetic relationships from selected matings were reduced in the range from 23.6% (scenario 0.23) to 15.1% (scenario 0.27) when applying OGC in combination with AI-Mate. Hence, a general availability of boars via artificial insemination can reduce inbreeding in the next generation as previously shown by e.g. Simianer et al. (2003) and König et al. (2010).

Breeding Strategy

Management of inbreeding whilst considering genetic gain in the traits of interest is a crucial strategy for maintaining endangered breeds. High increase of inbreeding in the recent generations associated with a small effective population size reflects the necessity for an inbreeding management in the BB breed. The current breeding strategy initiated by the breeding organization, i.e. avoiding matings of close related sows and boars, decreased inbreeding in the population. However, results for inbreeding and coancestry have shown that this effect was only valid in short term. Selection based on the OGC-concept is expected to manage inbreeding and genetic relationship in a long-term perspective, by constraining genetic relationship of selected parents. The OGC results confirmed tendencies that have been observed in large populations, i.e. an increase of genetic gain and a reduced number of selected boars along with relaxed constraints in allowed genetic relationships. Due to diminishing rates in genetic gain and following the current level of inbreeding (F = 0.121) and of coancestry (f = 0.132), an optimal value of allowed genetic relationships may be around 25%. Specific mating designs using SAA and based on suggested genetic contributions can substantially reduce inbreeding in the next generations. However, natural service is a common practice in the BB population and mating designs have to account for this circumstance. An own mating algorithm included the further restriction of matings only in specified region, but restricted availability of boars in some regions could not fulfill all of the suggested genetic contributions. Hence, artificial insemination is imperative to increase genetic gain while constraining additive-genetic relationships in the BB population, and for an effective use of the available "genetic potential". However, for OGC-applications, availability of EBV is imperative, but up to now, routine genetic evaluation is not performed. For the only traits currently systematically recorded in the BB breed (NBA and NW), reliable genetic parameters were estimated. Extension of the recording system is suggested, i.e. including further traits of relevance that reflect meat quality and pig welfare. Hence, next steps will focus on recording of new phenotypes, estimation of genetic parameters for new phenotypes, and combining EBVs for new phenotypes with EBVs for NBA or NW in an overall breeding goal.

Conservation programs generally might be more successful when combining genetic diversity with economy. For example, other endangered local pig breeds like the Iberian pigs (Toro et al., 2000) or the Nustrale pig (Casabianca et al., 2012) successfully established a high market price for specific products and combined this with aspects of the conservation program.

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KAPITEL 3

From phenotyping towards breeding strategies: using *in vivo* indicator traits and genetic markers to improve meat quality in an endangered pig breed

A.D.M. Biermann, T. Yin, U.U. König von Borstel, K. Rübesam, B. Kuhn
and S. König

Department of Animal Breeding, University of Kassel
Nordbahnhofstraße 1a, 37213 Witzenhausen, Germany

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ABSTRACT

In endangered and local pig breeds of small population sizes, production has to focus on alternative niche markets with an emphasis on specific product and meat quality traits to achieve economic competiveness. For designing breeding strategies on meat quality, an adequate performance testing scheme focussing on phenotyped selection candidates is required. For the endangered German pig breed 'Bunte Bentheimer', no breeding program has been designed until now, and no performance testing scheme has been implemented. For local breeds, mainly reared in small-scale production systems, a performance test based on *in vivo* indicator traits might be a promising alternative in order to increase genetic gain for meat quality traits. Hence, the main objective of this study was to design and evaluate breeding strategies for the improvement of meat quality within the Bunte Bentheimer breed using *in vivo* indicator traits and genetic markers. The *in vivo vivo* indicator trait was backfat thickness measured by ultrasound (BF_{iv}), and genetic markers were allele variants at the RYR1 locus. In total, 1116 records of production and meat quality traits were collected, including 613 *in vivo* ultrasound measurements and 713 carcass and meat quality records. Additionally 700 pigs were genotyped at the RYR1 locus. Data were used 1.) To estimate genetic (co)variance components for production and meat quality traits, 2.) To estimate allele substitution effects at the RYR1 locus using a selective genotyping approach, and 3.) To evaluate breeding strategies on meat quality by combining results from quantitative-genetic and molecular-genetic approaches. Heritability for the production trait BF_{iv} was 0.27, and 0.48 for backfat thickness measured on carcass. Estimated heritabilities for meat quality traits ranged from 0.14 for meat brightness to 0.78 for the intramuscular fat content (IMF). Genetic correlations between BF_{iv} and IMF were higher than estimates based on carcass backfat measurements (0.39 vs. 0.25). The presence of the unfavorable n allele was associated with increased electric conductivity, paler meat and higher drip loss. The allele substitution effect on IMF was unfavourable, indicating lower IMF when the n allele is present. A breeding strategy including the phenotype (BF_{iv}) combined with genetic marker information at the RYR1 locus from the selection candidate, resulted in a 20% increase in accuracy and selection response when compared to a breeding strategy without genetic marker information.

Keywords: Endangered pig breed, meat quality, halothane gene, ultrasound indicator traits, breeding strategies

IMPLICATIONS

Based on estimates for genetic (co)variance components, breeding program scenarios showed that the use of *in vivo* ultrasound measurements for backfat thickness successfully improved the ultimate breeding goal “meat quality” in the endangered pig breed Bunte Bentheimer. Selection response for meat quality in terms of intramuscular fat content was enhanced by including genetic marker information at the RYR1 locus from selection candidates. Alternative selection strategies aiming on alternative traits that do not rely on *ex vivo* measurements for related animals (full sibs, half sibs or progeny) might be a solution to achieve economic competiveness in niche markets for breeds characterized by small population and herd sizes.

INTRODUCTION

The Bunte Bentheimer (**BB**) belongs to the local and endangered pig breeds, having their area of origin in the northwestern region of Germany. Due to the increasing importance of higher lean meat percentage since the middle of the 20th century, and due to the restricted use of fatty pig breeds, the population size of the BB breed has decreased substantially. In the 1990s, only one BB breeding farm remained, and the effective population size decreased to a critical value of Ne = 9 (Biermann *et al.*, 2014). However, the preservation of the population succeeded, and is currently organized by the breeding organization ‘NORDSCHWEIN e.V.’ and the association ‘Verein zur Erhaltung des Bunten Bentheimer Schweines e.V.’. Detailed analyses of the BB population structure based on pedigree data were conducted by Biermann *et al.* (2014).

Conventional pig breeding programs typically have a strong emphasis on increasing lean meat percentage by reducing backfat, improving feed conversion ratios, increasing daily gain and increasing litter size. The inferiority of local breeds concerning these traits requires an alternative production method focusing on niche markets to achieve economic competiveness. In several countries, local breeds were already used for the production of high-quality products (Pugliese and Sirtori, 2012). The breeding program of the Iberian breeds, for example, target traits related to the production of high quality dry-cured products (e.g. carcass conformation traits as well as meat and fat quality traits (Fernández *et al.*, 2003)). For the BB breed, no breeding program along with an overall breeding goal has been established. Accordingly, this pig breed was not under target-orientated genetic selection over decades.

Implementing a breeding program in the BB population initially requires the availability of genetic variance components and heritabilities, as well as the phenotypic and genetic correlations between traits of interest. For the estimation of genetic parameters for meat quality traits, phenotypes have to be generated through the use of meat samples from slaughtered animals. However, phenotyping of selection candidates for meat quality traits based on the carcass or meat samples is prohibitive, as it requires that these individuals are slaughtered. Furthermore, with a focus on endangered breeds of small population sizes and kept in small-scale production systems, there is a lack of suitable infrastructure for organized performance testing of full and half-sibs or of progeny. Therefore, these breeds are in need of alternative breeding programs based on alternative phenotypes. Pimentel and König (2012) suggested the application of a novel ultrasound recording technique to beef cattle selection candidates with the ultimate aim to achieve genetic progress for meat quality traits. Selection response for an overall breeding goal based on the phenotypic indicator trait "ultrasound measurement" from the selection candidate was comparable to the selection response realized by genomic selection strategies targeting the trait “marbling score”. In pigs, ultrasound measurements are mostly used to measure backfat and loin muscle depth in living pigs, or to determine correlations between ultrasound measurements and carcass composition (e.g. Ayuso *et al.*, 2013). Using *in vivo* ultrasound measurements from highly correlated traits (e.g. backfat measurements) might be an alternative and a practical approach to achieve genetic progress for meat quality traits (especially IMF) in the BB population.

Another approach to achieve genetic progress for meat quality traits is the utilization of genetic markers or of major genes. One well known major gene in pig breeding is the halothane (ryanodine receptor, RYR1) gene, which causes malignant hyperthermia (Fujii *et* *al.*, 1991). The halothane gene is of major relevance for German pig breeding programs with the two main objectives being reduction of stress susceptibility and improvement of meat quality. For the BB breed, divergent allele frequencies at the RYR1 locus compared to conventional pig breeds are expected, because of the restricted gene flow originating from conventional breeds (Piétrain and Landrace), and due to divergent breeding strategies. Such theories were postulated by Pugliese and Sirtori (2012) for other local breeds.

The main objective of this study was to design and to evaluate breeding strategies for the improvement of meat quality within the BB breed based on parameter estimates from quantitative genetic and molecular genetic analyses. Specifically, the overall aim included the following tasks: 1.) The estimation of genetic variance components, heritabilities, and phenotypic and genetic correlations for production traits (*in vivo* ultrasound measurements and carcass measurements) and for meat quality traits, 2.) The estimation of allele substitution effects at the RYR1 locus on production and meat quality traits using a selective genotyping approach, and 3.) The evaluation of breeding strategies on meat quality by combining results from quantitative-genetic and molecular-genetic approaches.

MATERIAL AND METHODS

Animals and Traits

The genealogical background of the BB breed is described in detail by Biermann *et al.* (2014). Pigs of the BB breed are almost exclusively reared and kept in small-scale organic or low-input family farms. With regard to the participating farms, the number of slaughtered animals per farm ranged from five pigs per year to five pigs per week. Hence, data collection was focused on eight contract herds to ensure a meat quality trait flow in short (mostly weekly) intervals. Data recording included in total 1116 pigs of equal sex ratio from September 2011 to August 2013. A subset of 613 pigs was used for *in vivo* ultrasound measurements, while carcass and meat quality trait records were available from 713 pigs. Pigs from the eight different farms were slaughtered in eight different abattoirs. 700 pigs with phenotypes were genotyped at the RYR1 locus. Additionally, parents and grandparents without phenotypic records were genotyped, resulting in a total of 1014 pigs being genotyped for their RYR1 status. The pedigree included 2797 individuals and was traced back through 16 generations.

Production traits included lean meat content and backfat thickness. Trait recording for *in vivo* ultrasound measurements was accomplished on farms using Piglog 105 (Carometec Food Technology). *In vivo* lean meat content (**LMC_{iv}**) and *in vivo* backfat thickness (**BF_{iv}**) were obtained from measurements between the third and fourth last rib and 7 cm from the midline. In slaughtered pigs, lean meat content (**LMC**) and backfat thickness (**BF**) were determined using the Fat-O-Meater (Carometec Food Technology). In small abattoirs, LMC and BF were estimated using the "Two-Point-Method” (Bach and Sack, 1987). From a sample of 75 pigs, LMC and BF were available from both measurement techniques Fat-O-Meater and “Two-Point-Method”. The regression equation from this sample was used to calculate LMC and BF for all pigs on an identical “Fat-O-Meater basis”.

For determining meat quality traits, meat samples taken in the abattoir were analysed in the meat laboratory at University of Kassel. Meat samples from slaughtered pigs were taken within 1-5 hours *post mortem* from the *M. longissimus dorsi* between the third and fourth last rib. The samples of 5-10 cm in thickness were stored in a labelled plastic bag and transported to the laboratory under cooled conditions. Meat quality traits included pH-value, electric conductivity, brightness of the meat, drip loss, cooking loss, shear force, marbling and intramuscular fat content. The pH-value, electric conductivity and meat brightness were recorded using the technical equipment "pH-Star", "LF-Star" and "Opto-Star" (Matthäus, Klausa, Germany) 24 hours *post mortem* (**pH_{24}**, **EC_{24}**, **$Opto_{24}$**), and 48 hours *post mortem* (**EC_{48}**, **$Opto_{48}$**). For drip loss determination, a 1.5 cm thick slice was taken in abattoirs from each meat sample directly after cutting the sample from the carcass. Fat was trimmed from the slices, which afterwards were weighted and packed in a separately labelled plastic bag. Drip loss was defined as the difference between the weight before and after a storage time of 24 hours (**DL_{24}**), 48 hours (**DL_{48}**) and 72 hours (**DL_{72}**) at a temperature of 8 °C. Cooking loss (**CL**) was recorded 48 hours *post mortem* using a 1.5 cm slice of the meat sample which was heated to a core temperature of 75 °C. CL was defined as the difference between the weight before and after cooking. Subsequently, shear force (**SF**) of the cooking slice was measured using the Warner-Bratzler Chatillon shear force fixture. Marbling (**MAR**) was determined by a trained technician and using a subjective scale (1 = no marbling; 2 = little marbling; 3 = medium marbling; 4 = strong marbling, and 5 = very strong marbling). The remaining meat sample was used to determine the intramuscular fat content (**IMF**) with Near Infrared Spectroscopy (FOSS NIR

Systems, Hamburg, Germany). Number of observations and descriptive statistics for production and meat quality traits as analyzed in the present study are summarized in Table 1.

Table 1. Number of animals (N), mean (Mean), standard deviation (s.d.), minimum (Min) and maximum (Max) for production and meat quality traits

Trait[1]	Unit	N	Mean	s.d.	Min	Max
LMC_{iv}	[%]	613	47.56	4.66	34.20	63.90
LMC	[%]	500	42.55	4.09	27.60	64.00
BF_{iv}	[mm]	613	24.31	5.69	6.00	39.00
BF	[mm]	503	31.68	4.73	17.00	48.98
pH_{24}		667	5.55	0.14	5.05	6.04
EC_{24}	[mS/s]	633	4.62	2.90	1.10	9.87
EC_{48}	[mS/s]	674	6.52	2.36	1.20	9.93
$Opto_{24}$	[0=bright; 90=dark]	661	74.39	7.23	48.83	88.70
$Opto_{48}$	[0=bright; 90=dark]	679	74.18	6.96	49.43	89.50
DL_{24}	[%]	658	3.06	2.60	0.02	14.37
DL_{48}	[%]	657	4.80	2.86	0.80	18.76
DL_{72}	[%]	635	6.47	3.03	0.64	20.11
CL	[%]	680	33.03	3.17	12.08	42.01
SF	[kg/cm²]	681	10.10	2.45	4.30	18.83
MAR	[score 1-5]	674	2.24	0.81	1.00	5.00
IMF	[%]	686	1.57	0.49	0.77	3.99

[1] LMC_{iv} = lean meat content measured by ultrasound on the live animal; BF_{iv} = backfat thickness measured by ultrasound on the live animal; LMC = lean meat content measured on the carcass; BF = backfat thickness measured on the carcass; pH_{24} = pH-value measured 24 h p.m.; EC_{24} = electric conductivity measured 24 h p.m.; $Opto_{24}$ = meat brightness measured 24 h p.m.; DL_{24} = drip loss measured 24 h p.m.; EC_{48} = electric conductivity measured 48 h p.m.; $Opto_{48}$ = meat brightness measured 48 h p.m.; DL_{48} = drip loss measured 48 h p.m.; DL_{72} = drip loss measured 72 h p.m.; MAR = marbling; CL = cooking loss; SF = shear force; IMF = intramuscular fat content.

The explanatory variable “weight of pigs at the slaughtering date” ranged from 52 kg to 164 kg with a mean value of 102 kg. Weights of pigs for the *in vivo* ultrasound measurements ranged from 56 kg to 163 kg with a mean value of 105 kg.

Estimation of Genetic Parameters

Variance components and heritabilities for production and meat quality traits were generated from univariate animal models. For the estimation of covariance components and genetic correlations, bivariate animal models for all trait combinations were applied. Mixed model equations were solved using the AI-REML procedure, as implemented in the DMU software package (Madsen and Jensen, 2000). The following genetic statistical model was applied to all traits:

$$y_{ijklmn} = \mu + S_i + H_j + RYR1_k + a_l + L_{lm} + b_1 SW_{ijklmn} + e_{ijklmn}$$

where

y_{ijklmn} = observation for production/meat quality traits of the *l-th* pig

μ = overall mean

S_i = fixed effect of the *i-th* sex of the *l-th* pig

H_j = fixed effect of the *j-th* herd where the *l-th* pig was bred/fattened

$RYR1_k$ = fixed effect of the *k-th* RYR1 genotype of the *l-th* pig

a_l = random additive genetic effect of the *l-th* pig

L_{lm} = random *m-th* common environment effect of litter of *l-th* pig

SW_{ijklmn} = weight at the test/slaughtering date of the *l-th* pig

b_1 = linear regression of the production/meat quality trait on the weight at the test/slaughtering date

e_{ijklmn} = random residual effect

The (co)variance structure of random effects for the bivariate model was:

$$\operatorname{var}\begin{bmatrix} a_1 \\ a_2 \\ cl_1 \\ cl_2 \\ e_1 \\ e_2 \end{bmatrix} = \begin{bmatrix} g_{11}A & g_{12}A & 0 & 0 & 0 & 0 \\ g_{21}A & g_{22}A & 0 & 0 & 0 & 0 \\ 0 & 0 & l_{11} & l_{12} & 0 & 0 \\ 0 & 0 & l_{21} & l_{22} & 0 & 0 \\ 0 & 0 & 0 & 0 & r_{11} & r_{12} \\ 0 & 0 & 0 & 0 & r_{21} & r_{22} \end{bmatrix}$$

where index $_1$ indicates the first and index $_2$ indicates the second production or meat quality trait; a_1 and a_2 = vectors of random genetic animal effects for the two traits; cl_1 and cl_2 = vectors of random common environmental effects of the litter for the two traits; e_1 and e_2 = vectors of random residual effects for the two traits; g_{11} = additive genetic variance for the first trait, $g_{12} = g_{21}$ = additive genetic covariance between both traits, g_{22} = additive genetic variance for the second trait; l_{11} = common environmental variance of the litter for the first trait, $l_{12} = l_{21}$ = common environmental covariance of the litter between both traits, l_{22} = common environmental variance of the litter for the second trait; r_{11} = residual variance for the first trait, $r_{12} = r_{21}$ = residual covariance between both traits, r_{22} = residual variance for the second trait; and **A** = an additive genetic relationship matrix.

Estimation of Allele Substitution Effects at the RYR1 Locus

For estimation of marker effects for production and meat quality traits at the RYR1 locus, a selective genotyping approach was used. The selection of extreme phenotypes with regard to meat quality was based on residuals for IMF using the following statistical model:

$$Y_{ijk} = \mu + S_i + H_j + \beta X_k + e_{ijk}$$

where

Y_{ijk} = observation for IMF of the kth pig

S_i = fixed effect of the ith sex of the pig

H_j = fixed effect of the jth herd of the pig

X_k = weight at the slaughtering date of pig k

β = linear regression of IMF on the weight at the slaughtering date

e_{ijk} = random residual effect for IMF

Group A consisted of 100 pigs with the highest values for IMF residuals and group B included 100 pigs with the lowest values for IMF residuals (Figure 1).

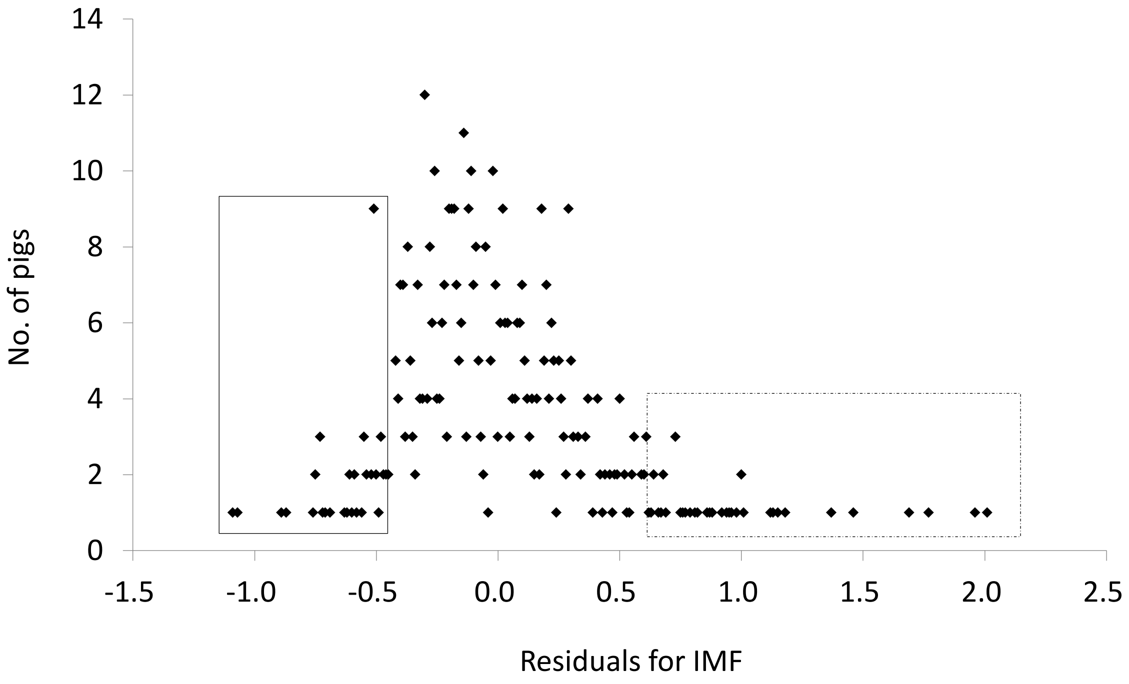

Figure 1. Distribution of residuals for the meat quality trait IMF. Pigs from extreme groups extracted for selective genotyping are highlighted within dashed lines (= highest values for IMF residuals = group A) and solid lines (= lowest values for IMF residuals = group B). (Style of figure according to Sharma *et al.*, 2006 and Bagheri *et al.*, 2013).

For the estimation of allele substitution effects at the RYR1 locus, methodology for selective genotyping data, as suggested by Henshall and Goddard (1999), was applied. Methodology is based on a logistic model and by defining the RYR1 genotype as a dependent and binary trait. Heterozygous pigs with genotype Nn received the score = 1, and homozygous pigs with genotype NN received the score = 0. For the analysis of binary data, a generalized linear mixed model (GLMM) with a logit link function was applied. The statistical model for estimating the probability of genotype Nn versus a genotype NN was defined as follows:

$$\text{logit}(\pi_r) = \log\left\lfloor \frac{\pi_r}{1-\pi_r} \right\rfloor = a + b_1 Yr + S_s + H_t + b_2 SW_r$$

π_r	= probability of the genotype Nn of a pig r
a	= intercept
Y_r	= observation for the production/meat quality trait of pig r
b_1	= linear regression of genotype Nn on the phenotypic value of the production/meat quality trait
S_s	= fixed effect of the sth sex of the pig
H_t	= fixed effect of the tth herd of the pig
SW_r	= weight at slaughtering date of pig r
b_2	= linear regression of IMF on the weight at the slaughtering date

The estimated slope of the regression coefficient b_1 was used for the calculation of allele substitution effects at the RYR1 locus, i.e., the contrast α of the heterozygous genotype Nn to the homozygous genotype NN with regard to the production and meat quality trait of interest. Henshall and Goddard (1999) introduced the following equation which was used in the present study:

$$\alpha = \frac{-1+\sqrt{1+b_1^2\sigma_X^2}}{b_1}$$

with σ_X^2 denoting the phenotypic variance of the production and meat quality trait in the unselected base population.

Breeding Strategies on Meat Quality

Genetic gain in meat quality for an ultimate breeding goal including only meat quality (100% of the economic weight on the meat quality trait), and considering different combinations of phenotypic and genomic information (index) sources, was assessed by applying the selection index theory. The theoretical framework for combining phenotypic and genomic data as described by Dekkers (2007) was translated into the computer algorithm SIG-R (Pimentel and König, 2012). SIG-R was used to evaluate the following three relevant and basic breeding program scenarios that can be applied to the BB population: 1. Scenario PHENO_REL = phenotypic information for the meat quality trait IMF from slaughtered full-sibs of the selection candidate, 2. Scenario PHENO_OWN = phenotypic information for ultrasound measurements (BF_{iv}) from the selection candidate used as indicator trait for IMF, and 3. Scenario PHENO_OWN_MARKER = phenotypic information (BF_{iv}) of the selection candidate combined with the genomic information RYR1 status of the selection candidate referred to as genetic marker for IMF. Relevant quantitative genetic parameters for the three scenarios were: h^2 for IMF = 0.78, h^2 for BF_{iv} = 0.27, genetic correlation between IMF and BF_{iv} = 0.39, phenotypic correlation between IMF and BF_{iv} = 0.25, phenotypic standard deviation for IMF = 0.49%, and phenotypic standard deviation for BF_{iv} = 5.69 mm.

The approach for the evaluation of the scenario PHENO_OWN_MARKER combined quantitative genetic parameter estimates with allele substitution effects for IMF at the RYR1 locus. The allele substitution effect α_{IMF} of the N allele was 0.207. Hence, the additive genetic variance for IMF explained by the genetic marker was:

$$\sigma^2_{m\_IMF} = 2p(1-p)\alpha_{IMF}{}^2 = 0.351\%^2$$

with p = 0.87 denoting the allele frequency of the desired N allele. Matrices and vectors for selection index calculations combining phenotypic information and marker were: Matrix

$$\mathbf{P} = \begin{bmatrix} \sigma^2_{BFiv} & \mathrm{cov}_{BFiv:m\_IMF} \\ \mathrm{cov}_{BFiv:m\_IMF} & \sigma^2_{m\_IMF} \end{bmatrix}$$

including the (co)variance components for both information "traits" IMF marker and phenotypic observation for BF_{iv} from the selection candidate where σ^2_{BFiv} = phenotypic variance for BF_{iv} and $\mathrm{cov}_{BFiv:m\_IMF}$ = covariance between BF_{iv} and the marker for IMF; the (co)variance matrix

$$\mathbf{G} = \begin{bmatrix} \sigma^2_{a\_BFiv} & \mathrm{cov}_{BFiv:m\_IMF} \\ \mathrm{cov}_{BFiv:m\_IMF} & \sigma^2_{m\_IMF} \end{bmatrix}$$

between information "traits" and the breeding value for IMF where $\sigma^2_{a\_BFiv}$ = additive genetic variance for BF_{iv}; and vector

$$\mathbf{w} = \begin{bmatrix} 1 \\ 0 \end{bmatrix}$$

representing the economic weight for the IMF phenotype.

The equation $\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{w}$ was solved, where b-values = weighting factors in IMF genetic evaluations for BF_{iv} and the IMF marker genotype of the selection candidate (boar or sow). The evaluation criteria for the different breeding scenarios were the correlation between index and aggregate genotype (= accuracy of the estimated breeding value (**EBV**) for the selection candidate (r_{TI})), and selection response per generation by assuming a selection intensity of i = 1.

RESULTS AND DISCUSSION

Genetic Parameters for Production and Meat Quality Traits

At the phenotypic scale, and when compared to conventional pig breeds, traits recorded in the BB population are characterized by a large variation and a wide range (Table 1). Such a high variation at the phenotypic scale reflects the substantial differences in housing and feeding systems across herds. In addition, different pre-slaughter conditions, especially when comparing technical processes in large-scale commercial slaughterhouses with small abattoirs, may have influence on meat traits variability.

Heritabilities for production traits (LMC_{iv}, LMC, BF_{iv}, BF) were in a moderate range from 0.27 to 0.48 (Table 2) and correspond with estimates from previous studies (van Wijk *et al.*, 2005; Schwab *et al.*, 2010). Estimates for *in vivo* traits were lower in comparison to the same traits measured on the carcass. This is probably due to the higher common environmental litter variance for the *in vivo* traits caused by a greater number of *in vivo* measured full-sibs compared to the number of slaughtered full-sibs. Estimated heritabilities for meat quality traits ranged from 0.14 for $Opto_{24}$ to 0.78 for IMF (Table 2). Our results are in agreement with the estimates of several other studies in conventional populations (de Vries *et al.*, 1994; Suzuki *et al.*, 2005; van Wijk *et al.*, 2005; Borchers *et al.*, 2007; Gjerlaug-Enger *et al.*, 2010; Schwab *et al.*, 2010; Dodenhoff *et al.*, 2011). Hence, explanations for trait specific heritabilities are summarized in those studies, and will not be discussed in detail in the current context of endangered breeds.

Phenotypic and genetic correlations between all production and meat quality traits are presented in Table 3. Phenotypic correlations between *in vivo* traits with the same traits from the carcass were moderate to high, and significantly different from zero. Genetic correlations among production traits were very high, i.e., r_g = 0.94 between LMC_{iv} and LMC, and r_g = 0.96 between BF_{iv} and BF. These results agree with the high genetic correlations between ultrasound and carcass measurements found by Lo *et al.* (1992) with r_g = 0.87 for lean meat area, and r_g = 0.85 for backfat. They conclude that a high genetic correlation in combination with moderate heritability favors selection based on ultrasound measurements to improve carcass characteristics. The phenotypic correlation coefficients between production and meat quality traits in this study were not significantly different from zero in most cases. As an exception, moderate phenotypic correlation coefficients were found between IMF and the production traits. Genetic correlations between IMF and the production traits were moderate and confirm the results by Lo *et al.* (1992) and by Schwab *et al.* (2010). Quantitative genetic parameter estimates for production and meat quality traits in the BB population reflect estimates in conventional and local pig breeds, and are a solid basis for designing breeding strategies on meat quality in the BB population.

Table 2. Variance components (σ_a^2 = additive genetic variance, σ_{cl}^2 = common litter environmental variance, σ_e^2 = residual variance) and heritabilities (h^2) for production and meat quality traits from the univariate model (corresponding standard errors of estimates in brackets)

	Genetic parameters			
Trait[1]	σ_a^2	σ_{cl}^2	σ_e^2	h^2
LMC_{iv}	3.87 (2.20)	2.41 (0.79)	7.06 (1.15)	0.29 (0.06)
LMC	5.87 (2.36)	1.31 (0.86)	8.30 (1.68)	0.38 (0.05)
BF_{iv}	4.85 (2.91)	3.73 (1.10)	9.26 (1.51)	0.27 (0.06)
BF	9.12 (3.14)	0.11 (0.83)	9.70 (2.18)	0.48 (0.04)
pH_{24}	0.00 (0.00)	0.01 (0.00)	0.01 (0.00)	0.18 (0.06)
EC_{24}	4.47 (1.24)	0.43 (0.31)	2.28 (0.77)	0.62 (0.04)
EC_{48}	1.59 (0.81)	0.84 (0.30)	2.75 (0.54)	0.31 (0.05)
$Opto_{24}$	6.44 (5.93)	6.57 (2.64)	32.13 (4.29)	0.14 (0.06)
$Opto_{48}$	6.32 (5.11)	8.68 (2.71)	28.19 (3.57)	0.15 (0.06)
DL_{24}	2.20 (0.83)	0.00 (0.19)	3.37 (0.56)	0.40 (0.04)
DL_{48}	3.44 (1.13)	0.00 (0.24)	3.77 (0.74)	0.48 (0.03)
DL_{72}	2.05 (1.13)	0.00 (0.32)	5.80 (0.83)	0.26 (0.04)
CL	5.34 (1.38)	0.54 (0.35)	3.06 (0.84)	0.60 (0.04)
SF	1.81 (0.78)	0.52 (0.28)	3.44 (0.53)	0.31 (0.05)
MAR	0.33 (0.11)	0.07 (0.04)	0.28 (0.07)	0.48 (0.05)
IMF	0.19 (0.04)	0.04 (0.01)	0.02 (0.02)	0.78 (0.05)

[1] Abbreviations are defined in Table 1.

Table 3. Genetic (above diagonal) and phenotypic correlations[1] (below diagonal) among production and meat quality traits from a series of bivariate models (Corresponding standard errors of genetic correlations in brackets)

Traits[2]	LMC$_{iv}$	LMC	BF$_{iv}$	BF	pH$_{24}$	EC$_{24}$	EC$_{48}$	Opto$_{24}$	Opto$_{48}$	DL$_{24}$	DL$_{48}$	DL$_{72}$	CL	SF	MAR	IMF
LMC$_{iv}$		0.94 (0.12)	-0.99 (0.01)	-0.97 (0.10)	0.82 (0.52)	-0.24 (0.23)	0.10 (0.32)	-0.28 (0.55)	0.07 (0.42)	0.18 (0.32)	0.05 (0.27)	0.07 (0.35)	0.33 (0.25)	0.36 (0.33)	-0.31 (0.25)	-0.43 (0.19)
LMC	0.48 ***		-0.93 (0.12)	-0.99 (0.03)	0.71 (0.26)	-0.16 (0.26)	-0.18 (0.33)	-0.65 (0.55)	-0.04 (0.44)	-0.03 (0.32)	-0.03 (0.29)	-0.09 (0.36)	0.38 (0.25)	0.89 (0.25)	-0.20 (0.28)	-0.22 (0.21)
BF$_{iv}$	-0.98 ***	-0.47 ***		0.96 (0.11)	-0.54 (0.48)	0.29 (0.23)	-0.06 (0.33)	0.27 (0.58)	0.04 (0.44)	-0.17 (0.33)	-0.09 (0.28)	-0.16 (0.38)	-0.43 (0.26)	-0.31 (0.33)	0.24 (0.26)	0.39 (0.19)
BF	-0.45 ***	-0.91 ***	0.44 ***		-0.68 (0.26)	0.20 (0.24)	0.17 (0.31)	0.52 (0.57)	0.07 (0.42)	0.14 (0.29)	0.10 (0.27)	0.18 (0.34)	-0.11 (0.24)	-0.62 (0.28)	0.24 (0.26)	0.25 (0.19)
pH$_{24}$	-0.04 ns	0.02 ns	0.07 ns	-0.02 ns		-0.39 (0.34)	0.79 (0.47)	0.01 (0.58)	0.34 (0.53)	-0.20 (0.37)	-0.31 (0.34)	-0.27 (0.43)	0.53 (0.35)	0.60 (0.38)	0.64 (0.35)	-0.17 (0.29)
EC$_{24}$	-0.19 **	-0.08 ns	0.17 *	0.10 *	-0.15 ***		0.85 (0.10)	-0.58 (0.25)	-0.16 (0.30)	0.86 (0.08)	0.79 (0.10)	0.92 (0.12)	-0.21 (0.20)	-0.61 (0.24)	0.33 (0.22)	-0.17 (0.17)
EC$_{48}$	-0.10 ns	-0.02 ns	0.09 ns	0.03 ns	0.01 ns	0.71 ***		-0.35 (0.44)	0.33 (0.51)	0.62 (0.21)	0.52 (0.22)	0.47 (0.30)	0.21 (0.24)	-0.22 (0.33)	-0.05 (0.29)	-0.63 (0.25)
Opto$_{24}$	0.05 ns	0.01 ns	-0.03 ns	0.01 ns	0.16 ***	-0.49 ***	-0.31 ***		0.52 (0.42)	-	-	-0.53 (0.36)	-0.01 (0.34)	0.33 (0.40)	-0.84 (0.29)	-0.71 (0.29)
Opto$_{48}$	0.03 ns	-0.05 ns	0.02 ns	0.07 ns	0.19 ***	-0.43 ***	-0.27 ***	0.77 ***		-0.19 (0.33)	-0.18 (0.32)	-0.04 (0.44)	0.33 (0.35)	0.70 (0.37)	-0.35 (0.35)	-0.77 (0.30)
DL$_{24}$	-0.11 ns	-0.01 ns	0.10 ns	0.04 ns	-0.18 ***	0.78 ***	0.54 ***	-0.56 ***	-0.53 ***		0.84 (0.06)	0.91 (0.10)	-0.24 (0.24)	-0.39 (0.30)	0.36 (0.29)	-0.04 (0.23)
DL$_{48}$	-0.11 ns	0.00 ns	0.10 ns	0.02 ns	-0.17 ***	0.76 ***	0.57 ***	-0.52 ***	-0.52 ***	0.93 ***		-	-0.00 (0.21)	-0.21 (0.27)	-	-0.18 (0.19)
DL$_{72}$	-0.12 ns	-0.08 ns	0.10 ns	0.09 *	-0.22 ***	0.66 ***	0.50 ***	-0.48 ***	-0.46 ***	0.84 ***	0.92 ***		0.17 (0.26)	-0.17 (0.35)	-0.39 (0.29)	-0.28 (0.25)
CL	0.13 ns	0.02 ns	-0.13 ns	0.00 ns	0.06 ns	-0.03 ns	0.04 ns	-0.12 **	0.05 ns	-0.07 ns	-0.03 ns	0.06 ns		0.08 (0.23)	-0.18 (0.20)	-0.18 (0.16)
SF	0.11 ns	0.03 ns	-0.07 ns	-0.02 ns	0.19 ***	-0.24 ***	-0.24 ***	0.05 ns	0.12 **	-0.14 ***	-0.17 ***	-0.13 **	0.26 ***		0.16 (0.28)	-0.16 (0.22)
MAR	-0.22 **	-0.10 *	0.20 **	0.09 ns	0.10 **	0.00 ns	0.06 ns	-0.10 *	-0.11 **	-0.08 *	-0.10 *	-0.16 ***	-0.09 *	-0.08 *		0.86 (0.08)
IMF	-0.29 ***	-0.25 ***	0.25 ***	0.24 ***	-0.08 *	-0.01 ns	-0.08 *	-0.17 ***	-0.17 ***	-0.03 ns	-0.07 ns	-0.07 ns	0.04 ns	-0.01 ns	0.53 ***	

[1] Significance level: *** = *P ≤ 0.001*, ** = *P ≤ 0.01*, * = *P ≤ 0.05*, ns = *P > 0.05*.

[2] Abbreviations are defined in Table 1.

Allele Frequencies and Allele Substitution Effects for Meat Quality Traits at the RYR1 Locus

For the entire BB population, including 1014 genotyped pigs, the frequency of the unfavorable n allele at the RYR1 locus was q = 0.13, and p = 0.87 for the favorable allele N. Genotype frequency was 0.757 for NN, 0.226 for Nn, and 0.017 for nn. Pugliese and Sirtori (2012) reviewed allele frequencies at the RYR1 locus for several native pig breeds located in the southern part of Europe. Allele frequency q of the unfavorable n allele was zero for the Italian breeds Casertana, Nero Siciliano and Apulo Calabrese, for the Iberian pig sub-strain Manchado de Jabugo, as well as for the French breed Basque. In the local French breeds Bayeux and Blanc de l'Ouest, allele frequency of the n allele was comparably high (q = 0.44 and q = 0.34, respectively). The authors assumed introgression from commercial breeds such as Landrace or Piétrain.

Using the selective genotyping approach, the frequency of the favorable NN genotype was significantly higher in group A, representing the 100 pigs with the highest residuals for IMF. Accordingly, within this group, a higher percentage of the favorable N allele was observed (Table 4).

Table 4. Genotypic and allele frequencies (p = frequency for the N allele and q frequency for the n allele) at the RYR1 locus for 100 pigs with the highest residuals for IMF (group A) and for 100 pigs with the lowest residuals for IMF (group B)

	Genotype		Allele	
Group	NN	Nn	p	q
A	0.84	0.16	0.92	0.08
B	0.67	0.33	0.84	0.16
Test- statistic[1]	χ^2 = 7.81			
P- value	*P* = 0.0052			

[1] Application of a chi-square test for genotype frequencies for a 2 x 2 contingency table (two groups A and B, and two genotypes NN and Nn; d.f. = 1).

Frequency of the N allele was p = 0.92 in group A, and p = 0.84 in group B. The detrimental impact of the unfavorable n allele on meat quality traits was reflected by estimated allele substitution effects (Table 5).

Table 5. Allele substitution effect α (= effect of the unfavorable n allele) at the RYR1 locus for production and meat quality traits, and regression coefficients (b-value) from the logistic model

	Difference Nn vs. NN		
Trait[1]	α (in general units)	α (in s.d. units)	b-value[2]
LMC	0.83	0.20	0.05 ns
BF	-0.89	0.19	-0.04 ns
pH_{24}	-0.01	0.07	-0.48 ns
EC_{24}	2.28	0.79	0.32 ***
EC_{48}	1.70	0.72	0.35 **
$Opto_{24}$	-3.45	0.48	-0.07 **
$Opto_{48}$	-4.00	0.58	-0.09 **
DL_{24}	2.10	0.81	0.37 ***
DL_{48}	2.22	0.78	0.32 ***
DL_{72}	2.10	0.69	0.26 ***
CL	0.50	0.19	0.05 ns
SF	0.71	0.29	0.12 ns
MAR	-0.47	0.59	-0.79 **
IMF	-0.21	0.42	-0.90 *

[1] Abbreviations are defined in Table 1.

[2] Significance level: *** = $P \leq 0.001$, ** = $P \leq 0.01$, * = $P \leq 0.05$, ns = $P > 0.05$.

The highest values for α (in s.d. units) were estimated for EC, Opto, DL, MAR and IMF and ranged from 0.42 to 0.81. The presence of the n allele was associated with an increased EC, lower values for Opto (paler color), and a higher amount of DL, i.e., the typical characteristics reflecting pale, soft and exudative (PSE) meat (e.g., Rosenvold and Andersen, 2003; Borchers *et al.*, 2007). Allele substitution effects were unfavorable for traits depicting the fat content of meat (MAR and IMF), and further indicating lower fat content when the n allele is present. The negative effect of the n allele on fat content is also documented by Zhang *et al.* (2007) and coincides with the well-documented positive effect of the n allele on LMC (Rosenvold and Andersen, 2003). In this study, however, the effect on LMC was small (α in s.d. units = 0.20), and the regression coefficient from the logistic model (b-value = 0.05) was not significant. This likely reflects the absence of target-orientated artificial selection on LMC in the BB population. Our results demonstrate the future opportunity to use genetic marker information at the RYR1 locus for improvements of meat quality traits in the BB population.

Evaluation of Breeding Strategies for the Improvement of Meat Quality

Different breeding strategies (Table 6) aimed at improving IMF, which was defined as the ultimate breeding goal. Breeding on improved IMF implies correlated increase in backfat, which is undesired in commercial pig breeds. For the BB meat production aiming on a market niche, and with a strong focus on gourmet restaurants, increase of backfat is without detrimental economic impact. For scenarios including phenotypic information from slaughtered full-sibs (PHENO_REL), accuracies of EBV were 0.44 including one full-sib, and 0.52 including two full-sibs. Selection response for IMF per generation was 0.19%, and 0.23%, respectively. Performance tests for selection candidates including ultrasound measurements (BF_{iv}) from the selection candidate as an information source (PHENO_OWN) resulted in lower accuracy of EBV and selection response compared to PHENO_REL. BF_{iv} is less heritable than IMF ($h^2 = 0.27$ vs. $h^2 = 0.78$), causing lower accuracy and genetic gain when used as an index trait. Similar results were found by Newcom *et al.* (2005). In their study, selection on IMF based on carcass traits revealed higher genetic gain ($h^2 = 0.42$ for the carcass trait; genetic gain for IMF = 0.75%) compared to selection based on IMF ultrasound measurements ($h^2 = 0.25$ for the ultrasound measurement; genetic gain for IMF = 0.32%). Schwab *et al.* (2010) also predicted higher selection response per generation for carcass IMF compared to ultrasonic IMF (0.49% vs. 0.29%). However, the following essential practical aspects support selection strategies based on *in vivo* ultrasound information directly from potential selection candidates: 1. Independence from the number of available full-sibs, 2. Redundancy of elaborate trait recording and analysis schemes for meat samples, and 3. Availability of *in vivo* measurements as an on-farm breeding and management tool.

Genetic gain and accuracy of EBVs substantially increased when including both index sources the ultrasound measurement and genetic marker information at the RYR1 locus from selection candidates. When adding the RYR1 status as a genetic marker to a selection candidates phenotype (scenario PHENO_OWN_MARKER), the accuracy of EBV and selection response increased by 20%. A similar strategy was suggested by Pimentel and König (2012) for the improvement of the meat quality trait "marbling score" in beef cattle. With regard to the high average generation interval and to the small effective population size within the BB population (Biermann *et al.*, 2014), a rigorous breeding program aiming at eliminating the undesired allele at the RYR1 locus is difficult to implement. Hence, a combination of ultrasound information with marker information used as selection index information sources might be a suitable compromise. Recommendations predominantly consider practical conditions and applications that can be implemented in small-scale production systems and for endangered populations. Recently, more candidate genes for meat quality, and specifically for IMF, have been reported (Schwab *et al.*, 2009; Han *et al.*, 2012). These candidate genes can be included in breeding program scenarios by extending the scenario "PHENO_OWN_MARKER" to a broader variety of relevant genes affecting meat quality traits in pigs.

Table 6. Correlation between index and aggregate genotype (r_{TI}) and selection response from one round of selection for different breeding scenarios (section intensity = 1)

Scenario[1]	Breeding goal	Index traits	Information sources	r_{TI}	Selection response
PHENO_REL	IMF	IMF	1 Full-sib[2]	0.44	0.19
PHENO_REL	IMF	IMF	2 Full-sibs[2]	0.52	0.23
PHENO_OWN	IMF	BF_{iv}	Selection candidate	0.20	0.09
PHENO_OWN_MARKER	IMF	BF_{iv} + RYR1	Selection candidate	0.24	0.11

[1] Scenarios as explained in the materials and methods.

[2] Full-sibs of the selection candidate.

A breeding focus on meat quality traits is imperative, because the economic competiveness of the BB population might only be realized when implementing and expanding breeding activities to achieve improved product quality. Such an approach is justified because meat from the BB is offered, e.g., in gourmet restaurants and in delicatessen stores, in high price segments.

CONCLUSIONS

Estimated genetic parameters for production and meat quality traits in the BB population reflect estimates in conventional populations, and represent basic principles for implementing breeding strategies on meat quality. The unfavorable n allele at the RYR1 locus is still present in the BB population with a frequency of $q = 0.13$. Allele substitutions effects on meat quality traits were significant and exhibit the future need for using genetic marker information at the RYR1 locus to improve meat quality traits in this population. Selection response and accuracy of selection increased by 20% when considering the genetic marker information at the RYR1 locus from selection candidates as an additional information source. A breeding strategy based on *in vivo* indicator traits can be directly applied on pig farms to potential selection candidates. Such a breeding strategy will improve meat quality within a moderate range. The combination of quantitative-genetic and molecular-genetic approaches is a practical and most efficient approach to achieve genetic progress in endangered and small populations.

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KAPITEL 4

Economic values and evaluation of breeding schemes for non-market traits with applications to an endangered pig breed

A.D.M. Biermann, E. Rommelfanger, J. Anthe, H. Frevert and S. König

Department of Animal Breeding, University of Kassel
Nordbahnhofstraße 1a, 37213 Witzenhausen, Germany

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ABSTRACT

For the sustainable conservation of local breeds, alternative breeding programs are needed to compete against conventional breeds. Alternative breeding strategies in pig production place more emphasis on meat and sensorial quality for economical competiveness. Hence, two main objective of this study were 1.) to derive economic values for meat and sensorial quality traits based on a consumer's survey, and 2.) to design and to evaluate alternative breeding schemes for the endangered German pig breed "Bunte Bentheimer" (BB). The consumer survey included a total of 101 respondents, which were asked for their willingness to pay (WTP) for tasted meat samples, and for further quality trait characteristics concerning the appearance of meat, presented as photographs. Based on the average WTP for different quality classes, economic values were derived. Economic values per trait unit using tasted meat samples were -0.78 € for shear force (SF), 57.52 € for intramuscular fat content (IMF), -0.43 € for meat color (COL) and 14.65 € for drip loss (DL). In contrast, economic values for same appearance traits, but based on the WTP using photographs (O_COL and O_DL), were -2.72 € and -5.18 €. Those divergent results indicate utilization of photographs for the derivation of economic weights for traits which are not ascertainable by tasting (e.g., color and drip loss). Economic values from the first part were used to design and to evaluate alternative breeding schemes for the BB breed. Breeding goals were defined in order to improve meat and sensorial quality. Economic evaluation criteria were discounted profit and annual genetic gain. Breeding schemes using an on-station test for full-sibs of selection candidates were not profitable due to high breeding costs. As an alternative, a breeding scheme based on phenotypes for *in vivo* ultrasound measurements for backfat thickness (BF_{iv}), were designed. BF_{iv} can directly be recorded on selection candidates and was considered as index trait to improve meat quality. Discounted profit for this breeding scheme was positive denoted with 35.92 € per animal due to a substantial reduction of breeding costs. As expected, annual genetic gain for IMF was lower compared to direct selection on IMF, but desirable higher genetic gain for SF was achieved. In consequence, profitability and furthermore sustainability of alternative breeding programs primarily depends on its applicability and corresponding breeding costs. A breeding scheme based on the index trait BF_{iv} measured on selection candidates implies low breeding costs, and simultaneously moderate genetic gain for meat quality traits.

Keywords: economic values; non-market traits; meat quality; breeding strategies; endangered pig breed

INTRODUCTION

Sustainable conservation of local breeds demands well-organized long-term breeding programs adjusted to prevalent production systems and markets (FAO, 2007). In the population of the German endangered pig breed Bunte Bentheimer (**BB**), the whole meat value chain from production up to marketing strategies is organized by producers from small-scaled and low-input production systems. To compete against conventional breeds and conventional meat production, alternative breeding strategies are required with strong emphasis on meat and sensorial quality in breeding goals.

The development of breeding goals via selection index methodology requires economic weights for all traits used in the breeding goal. The economic weight or economic value of a trait reflects its marginal utility and can be derived for traits with direct revenues using profit functions. Such a classical approach was presented by de Vries (1989) for fertility and production traits for pigs in The Netherlands, and also applied by Serenius and Muhonen (2007) for pig production in Finland. The derivation of economic values presupposes an accurate calculation of profit functions, being challenging for traits with low or without any market-related relevance. For the assessment of economic values for non-market traits without direct revenues, a method is suggested based on survey technology and on individual preferences, i.e. the so called contingent valuation methodology (**CVM**) (Mitchell and Carson, 1993). Basically, when applying CVM, a target group is asked for their willingness to pay (**WTP**) for a change of a specific good. CVM was used for the valuation of people's WTP for animal welfare (Bennett and Blaney, 2003) or the determination of breeding goal traits for the South German Heavy Horse (Edel and Dempfle, 2004). Furthermore, von Rohr et al. (1999) derived economic values for meat quality traits for pig production in Switzerland by surveying meat technology experts. Experts were asked for their WTP for different carcass quality classes. Results of this study were adapted to the German pig breeding program in Bavaria in order to derive economic values for the quality traits intramuscular fat content and pH-value in sire lines (Habier et al., 2004). However, economic values for commercial meat markets might differ from economic values in same traits for specific value chains in niche markets. Hence, it is imperative to derive economic values for meat quality traits based on the structure and payment system for niche markets. Market specific economic weights are the basis for the development and evaluation of alternative breeding strategies. As one example addressing specific niche market requirements, Schierenbeck et al. (2009) derived economic weights for functional conformation traits using auction prices from heifers sold on elite markets. For market-oriented smallholder pig production in Vietnam, Roessler et al. (2008) used choice experiments to assess farmers' preferences for breeding traits. In an ongoing study, Roessler et al. (2009) evaluated the current recording scheme with regard to genetic gain and discounted profit by applying the software package ZPLAN (Willam et al., 2008). Täubert et al. (2011) enhanced the ZPLAN program in order to include possibilities for the evaluation of genomic information, and to make the software more "user-friendly". The modified software package ZPLAN+ was used e.g. for the evaluation of breeding strategies against boar taint in pigs (Haberland et al., 2014), or for the evaluation of breeding programs in chicken (Sitzenstock et al., 2013). So far, economic evaluations on a population wide scale did not address alternative breeding programs for endangered pig breeds combined with a focus on novel traits without direct revenues. Hence, the main objectives of this study were twofold: 1.) to derive economic values for non-market and niche-oriented traits based on a consumer's survey using CVM, and 2.) to design alternative pig breeding schemes along with an economic evaluation applying deterministic calculations using the software package ZPLAN+.

MATERIAL AND METHODS

Traits

Our approach for the evaluation of breeding program scenarios included marketable and non-marketable traits. The fertility trait "number of piglets born alive" (**NBA**) was considered as a marketable trait, and meat and sensorial quality traits as non-marketable traits.

Estimations of breed specific phenotypic and genetic (co)variance components, as one prerequisite for the evaluation of breeding strategies, were subject of previous studies for fertility and meat quality traits. In the present study, sensorial quality traits measured by a trained panel were additionally recorded. In Table 1, an overview about data sources and phenotypic population parameters for all traits are given. For the evaluation of sensorial quality traits meat samples, in total 47 BB pigs from 5 different farms were analyzed. Information about participating farms and animals are given in Biermann et al. (2015). Meat samples were also analyzed with regard to instrumental measured meat quality. This was necessary for further steps concerning the derivation of the economic values. Meat quality traits were recorded according to Biermann et al. (2015) and included electric conductivity (**EC**), brightness of the meat (**COL**), and drip loss (**DL**), measured 48 hours post mortem, respectively. Furthermore, shear force (**SF**), marbling (**MAR**), and intramuscular fat content (**IMF**) were recorded. Meat samples were recorded in small abattoirs and traits were analyzed in the meat laboratory at Kassel University. For the sensorial trait evaluation, meat slices of 1.5 cm thickness were frozen and thawed 24 hours before testing during a temperature of 7°C. Just before sensorial evaluation, slices were released from fat, covered in aluminum foil, and heated to a core temperature of 75°C using a contact grill. One slice of each meat sample was used for the sensorial analysis by a trained panel, including six panelists. After a training phase of six weeks and eight training sessions according to DIN 10961: 1996-08 (Deutsches Institut für Normung e.V., 1996), samples were tested within six sessions. A consensus profile (DIN 10967-2: 2002-05; Deutsches Institut für Normung e.V., 2002a) was applied to evaluate the following sensory attributes: tenderness (**TS**), juiciness (**JS**), and chewiness (**CS**). For TS and JS, a 6-point category scale was anchored on the left end with a low intensity of the sensory attribute, and on the right end with a high intensity of the sensory attribute, i.e. for TS: not tender to very tender, and for JS: not juicy to very juicy. TS was defined as the force required to compress the sample of meat between molar teeth on the first bite, and JS as the degree of moisture inside the sample released upon chewing (Moelich et al., 2003). For CS, the 6-point category scale was defined in the other way around, i.e.: very chewy to not chewy, and the trait was defined as the number of chews required before swallowing. For the sensory evaluation, each panelist used water and unseasoned bread for neutralization. Meat slices were prepared and divided in cubes with width of 1.5 cm and length of 1.5 cm. Cubes with a temperature of about 40°C were handed to the panelists according to an appropriate testing plan (DIN 10967-4: 2002-05; Deutsches Institut für Normung e.V., 2002b).

Table 1. Phenotypic population parameters (Mean = population mean and σ_p = phenotypic standard deviation) for fertility, meat and sensorial quality traits in the BB population

Trait[1]	Unit	Mean	σ_p	Reference
Fertility				
NBA	piglets	9.15	2.56	Biermann et al. (2014)
Meat Quality				
BF_{iv}	mm	24.31	5.69	Biermann et al. (2015)
EC	mS/s	6.52	2.36	
COL	0 = bright; 90 = dark	74.18	6.96	
DL	%	4.80	2.86	
SF	kg/cm³	10.10	2.45	
MAR	score	2.24	0.81	
IMF	%	1.57	0.49	
Sensorial Quality				
TS	score	4.00	0.84	Present study
JS	score	3.05	0.61	
CS	score	3.97	0.65	

[1] NBA = number of piglets born alive; BF_{iv} = backfat thickness measured by ultrasound on the live animal; EC = electric conductivity; COL = meat brightness; DL = drip loss; SF = shear force; MAR = marbling; IMF = intramuscular fat content; TS = tenderness score evaluated by a trained panel (0 = not tender and 5 = very tender); JS = juiciness score evaluated by a trained panel (0 = not juicy and 5 = very juicy); CS = chewiness score evaluated by a trained panel (0 = very chewy and 5 = not chewy).

Derivation of Economic Values

The economic value for NBA was calculated as the first derivative of the profit function P, based on the biological parameters, variable costs, and returns of the BB breed being presented and defined in Table 2. Economic value or marginal utility for NBA per sow and year was calculated according to Simianer (2002) using a classical profit function:

$$\frac{\partial P}{\partial n_{NBA}} = \left\{ [n_L \times (1-s) \times SW \times Pr] - \begin{bmatrix} n_L \times \left(1-\frac{s}{2}\right) \times \ vC_p + \\ n_L \times (1-s) \times (d_e - \ d_b) \times vC_f + \\ n_L \times (1-s) \times (w_e - \ w_b) \times FC_f \times CF_f \end{bmatrix} \right\}.$$

As a further extension, the economic value was expressed per fattening pig, while the number of fattening pigs was defined as: $n_L \times n_{NBA} \times (1-s)$.

Derivation of economic values for non-market traits based on the approach by von Rohr et al. (1999) requires trait classifications. All analyzed meat samples (n = 47) were classified for each trait under study according to the corresponding phenotypic standard deviation, and considering that each class includes almost the same number of samples. For traits addressing the appearance of meat (COL, DL, MAR) an additionally classification was done to provide these traits secondary as photographs, being furthermore termed as the optical meat quality traits (**O_COL**, **O_DL**, **O_MAR**). For each class of the traits O_COL and O_MAR, such a photograph of an original meat sample was chosen which optimally represents the respective meat characteristics. For O_DL, samples were artificially modified to represent different amounts of drip loss (Anthe, 2015). Trait classifications with respective thresholds for quality classes are presented in Table 3.

Ongoing, different price levels were assigned to each quality class. Prices for meat and sensorial quality traits were derived based on a consumer survey, i.e. by assessing a consumers' WTP for tasted meat samples. The consumer test comprised 101 respondents being recruited based on regular consumption of pork, and being familiar with the product under study. Also for the consumer test, meat slices of the 47 BB meat samples were prepared as previously described. Each respondent received five different test samples for tasting. After the tasting of each sample, consumers were asked for their WTP in relation to the price they usually pay for the same kind of meat (in this case loin). Each sample was at least tasted by two, and at most by 20 consumers, resulting in a total of 409 consumer appreciations. With regard to optical quality traits, consumers appraised different characteristics of the traits, and were also asked for their WTP for each characteristic in relation to the price they usually pay for this kind of meat. Numbers of consumers' appreciation per quality class are presented in Table 3.

Table 2. Biological technical coefficients of the Bunte Bentheimer (BB) population and corresponding costs and prices for ecological pig production in Germany

Description	Abbreviation	Value	Unit
Biological parameters of the BB population			
Reproduction cycle		0.48[1]	years
Productive lifetime females		2.4[1]	years
Productive lifetime males		3.1[1]	years
Age at first reproduction females (farrowing)		1.33[1]	years
Age at first reproduction males (farrowing)		1.0[1]	year
Number of litter per sow and year	n_L	2.1[1]	litter
Number of piglets born alive	n_{NBA}	9.15[1]	piglets
Piglet losses until the begin of the fattening period	s	0.15[2]	percentage
Age at the beginning of fattening period	d_b	75[2]	days
Life weight at the beginning of fattening period	w_b	30[2]	kg
Age at the end of fattening period	d_e	296[3]	days
Life weight at the end of fattening period	w_e	129[3]	kg
Slaughter weight	SW	102[3]	kg
Feed conversion during fattening period	FC_f	3.25[2]	
Costs and prices for ecological pig production			
Variable costs per piglet until fattening period	vC_p	20.00[2]	€
Variable costs per fattening pig and day	vC_f	0.15[2]	€
Costs per kg fattener feed	CF_f	0.40	€
Prices per kg slaughter weight	Pr	3.00	€

[1] Data sources: Biermann et al. (2014).

[2] Estimated according to the BB population.

[3] Data sources: Biermann et al. (2015).

Table 3. Quality classes for meat, sensorial, and optical traits; averaged consumers WTP[1], and number of consumers' appreciations (n) per class

Trait[2]	Class 1	Class 2	Class 3
Meat Quality			
EC	< 5.5	5.5 – 7.5	> 7.5
WTP	93.70	89.78	86.23
n	188	135	86
COL	< 76.6	76.6 – 83.3	> 83.3
WTP	86.54	91.59	94.19
n	129	154	126
DL	< 2.8	2.8 – 5.6	> 5.6
WTP	85.22^{a}	97.56^{b}	89.80
n	156	144	109
SF	< 7.8	7.8 – 10.5	> 10.5
WTP	90.08	96.09^{c}	85.03^{d}
n	120	156	133
MAR	1	> 1	
WTP	92.58	88.96	
n	206	203	
IMF	< 1.4	1.4 – 1.9	> 1.9
WTP	93.05	86.95	92.82
n	146	146	117
Sensorial Quality			
TS	< 3.8	3.8 – 4.6	> 4.6
WTP	86.70^{a}	88.29	97.57^{b}
n	157	114	138
JS	< 2.7	2.7 – 3.3	> 3.3
WTP	98.05^{c}	80.66^{a,d}	91.56^{b}
n	135	109	165
CS	< 3.75	3.75 – 4.4	> 4.4
WTP	86.45^{a}	89.07	97.58^{b}
n	154	121	134
Optical Quality			
O_COL	< 60.0	60.0 – 70.0	> 70.0
WTP	66.20^{c,e}	102.26^{a,f}	87.27^{b,d}
n	101	101	101
O_DL	< 3.0	3.0 – 6.0	> 6.0
WTP	115.20^{e}	89.41^{e,f}	51.80^{f}
n	101	101	101
O_MAR	1	2 – 3	4 – 5
WTP	88.25^{e}	105.35^{f}	95.93
n	101	101	101

[1] WTP = willingness to pay for tasted meat samples in percent of the usually paid price for loin, determined by 101 respondents.

[2] Appreciation of Table 1; O_COL = optical brightness presented as photography; O_DL = optical drip loss presented as photography; O_MAR = optical marbling presented as photography.

^{a,b} = $p < 0.05$; ^{c,d} = $p < 0.01$; ^{e,f} = $p < 0.001$; different letters indicate differences according to the specified significance level.

Prices per class were calculated by averaging all available appreciations within one quality class (averaged consumers WTP). Statistical comparison of calculated means (averaged consumers WTP) per quality class was performed using the Wilcoxon rank sum test. Averaged consumers WTP were expressed in percent to the usually paid price (Table 3), because respondents mentioned different price levels (market values (€ per kg meat) range between 7.23 € and 28.43 € (Anthe, 2015)). Finally, hypothetical prices per carcass and quality class were calculated as: $Pr \times SW \times averaged\ consumers\ WTP\ (\%)/100$.

Economic values for meat, sensorial, and optical quality traits were derived using the following equation (von Rohr et al., 1999):

$$EV(\mu) = \frac{1}{\sigma\sqrt{2\pi}} \sum_{i=1}^{n} Pr_i \times \left(e^{-\frac{1}{2}\left(\frac{B_{i-1} - \mu}{\sigma}\right)^2} - e^{-\frac{1}{2}\left(\frac{B_i - \mu}{\sigma}\right)^2} \right),$$

where μ is the population mean of the trait, σ is the phenotypic standard deviation of the trait, n is the number of quality classes, Pr_i is the price within the i^{th} quality class, and B_i is the upper boundary of the i^{th} quality class.

The following example illustrates the methodology (Figure 1): previously to the test, respondents have to define their minimum, maximum, and mean WTP for the product under study. Afterwards consumers' WTP was recoded using a scale with a total length of 18.8 cm. The left end was anchored with the consumers minimum WTP (WTP_{min}), and on the right end with the consumers maximum WTP (WTP_{max}). The middle of the scale (9.4 cm) represents the consumers usually paid price (WTP_{mean}) for the product under study.

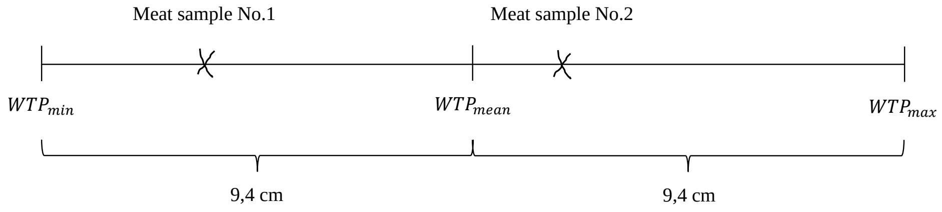

Figure 1. Scale to determine the consumers WTP for tasted meat samples and optical meat quality traits.

Given the following example: a respondent specified a WTP_{min} of 6.00 €, a WTP_{max} of 10.00 €, and a WTP_{mean} of 7.23 € per kg/loin. After tasting meat sample No. 1, $\mathrm{WTP}_{\mathrm{No.1}}$ was marked at 4.4 cm on the scale. In this case, WTP for sample No.1 was lower than the usually paid price. Hence, for $WTP_{No.x}$ < 9.4, $WTP_{No.x}$ in € was calculated as:

$$WTP_{No.x} = WTP_{min} + \frac{WTP_{No.x}}{9.4} \times (WTP_{mean} - WTP_{min}).$$

For sample No. 1, the respondent is willing to pay 6.58 €, being 90.05% of the usually paid price. After tasting meat sample No. 2, $\mathrm{WTP}_{\mathrm{No.2}}$ was marked at 12.2 cm on the scale. In this case, WTP for sample No.2 was higher than the usually paid price. If $WTP_{No.x}$ > 9.4, the $WTP_{No.x}$ in € was calculated as:

$$WTP_{No.x} = WTP_{mean} + \frac{(WTP_{No.x} - 9.4)}{9.4} \times (WTP_{max} - WTP_{mean}).$$

For sample No. 2, the respondent is willing to pay 8.06 €, being 111.41% of the usually paid price. Finally, after averaging all available appreciations within one quality class, an averaged WTP of for example 80% within a quality class results in 244.8 € per carcass, and is defined as the hypothetical price for pigs within this quality class.

Breeding Schemes

Economic evaluation of possible breeding schemes for the BB population was accomplished with deterministic calculations and using the software package ZPLAN+ (Täubert et al., 2010). As a major element of deterministic calculations, ZPLAN+ combines discounted gene flow theory (Hill, 1974) and selection index methodology (Hazel, 1943). A population size of 400 BB herdbook sows and 100 BB herdbook boars, reflecting the current active breeding stock was the basis for the deterministic modeling. All animals were considered as selection candidates, and included in performance testing schemes. Modeling of different breeding scenarios based on the reproduction parameters and biological-technical coefficients, as presented in Table 2. Population characteristics and genetic parameters were adopted from previous BB studies (Biermann et al., 2015; Biermann et al.,

2014) and economic values for traits in the breeding goal were values from the present study (Table 1 and Table 4). For the two selection groups sows and boars, selection intensity on the sow selection pathway was i = 1.89, and i = 1.40 for boars. Breeding programs were designed and evaluated for an investment period of 10 years. Discounted costs and discounted returns both were scheduled with interest rates of 2.5%. Different breeding scenarios were compared in terms of discounted profit and natural genetic gain. Discounted profit per animal accounts for discounted returns after deducting discounted breeding costs. Annual natural genetic gain per trait describes the average genetic superiority of the progeny of the selected animals in one round of selection compared to the initial population.

Table 4. Heritability (diagonal), phenotypic (below the diagonal) and genetic correlations (above diagonal), and economic values (w) for traits of the selection indices

Trait[1]	NBA	IMF	BF_{iv}	COL	DL	SF
NBA	**0.12**[3]	0.00[2]	0.00[2]	0.00[2]	0.00[2]	0.00[2]
IMF	0.00[2]	**0.78**[3]	0.39[3]	-0.77[3]	-0.18[3]	-0.16[3]
BF_{iv}	0.00[2]	0.25[3]	**0.27**[3]	0.04[3]	-0.09[3]	-0.31[3]
COL	0.00[2]	-0.17[3]	0.02[3]	**0.15**[3]	-0.18[3]	0.70[3]
DL	0.00[2]	-0.07[3]	0.10[3]	-0.52[3]	**0.48**[3]	-0.21[3]
SF	0.00[2]	-0.01[3]	-0.07[3]	0.12[3]	-0.17[3]	**0.31**[3]
w	13.37	57.52	0.00	-2.72[4]	-5.18[4]	-0.78

[1] NBA = number of piglets born alive; IMF = intramuscular fat content; BF_{iv} = backfat thickness measured by ultrasound on the live animal; COL = meat brightness; DL = drip loss; SF = shear force.

[2] Assumptions based on results of Hermesch et al. (2000).

[3] Results of Biermann et al. (2015).

[4] Results based on the optical quality traits (O_COL and O_DL).

The basic breeding scenario (**scenario I**) was modeled in order to represent the current situation in the BB population. Selection is only based on routinely measured reproduction performance (NBA = 100% of the breeding goal). For scenario I, no variable and fixed cost components were assigned, because NBA is directly recorded by farmers without the need for additional recording technique or cost components for logistic infrastructure.

Alternative breeding schemes were modeled targeting on specific product quality by including meat quality traits in breeding goals and indices. The first alternative scenario additionally considered on-stations tests for IMF (**scenario II**). For improving meat palatability, a selection index was constructed only including meat quality traits COL, DL, SF, and IMF (**scenario III**). Variable costs for both scenarios were assessed with 200 € per selection candidate for the on-station test. A further alternative scenario (**scenario IV)** also focused on product quality, but based on *in vivo* indicator trait measurements for backfat thickness measured by ultrasound (**BF_{iv}**). The BF_{iv} measurement technique and BB population parameters are described by Biermann et al. (2015). Assessed variable costs for the on-field test comprised 25 € per selection candidate. Description of breeding scenarios along with their variations of information sources are presented in Table 5.

Table 5. Breeding goals, index traits, selection groups and information sources, and variable costs for the different breeding scenarios

Scenario[1]	Breeding goal	Index traits[2]	Selection groups and Information sources		Variable costs (€)
			Sows	Boars	
I	NBA	NBA	Selection candidate		0.00
			Dam[3]; 2 Full-sibs[4]	Dam[3]; 2 Full-sibs[4]	
II	NBA	NBA	Selection candidate		200.00
			Dam[3]; 2 Full-sibs[4]	Dam[3]; 2 Full-sibs[4]	
	IMF	IMF	2 Full-sibs[5]	2 Full-sibs[5]	
III	IMF COL DL SF	IMF COL DL SF	2 Full-sibs[5]	2 Full-sibs[5]	200.00
IV	NBA	NBA	Selection candidate		25.00
			Dam[3]; 2 Full-sibs[4]	Dam[3]; 2 Full-sibs[4]	
	IMF	BF_{iv}	Selection candidate	Selection candidate	
			Dam[3]; 2 Full-sibs[4]	Dam[3]; 2 Full-sibs[4]	
			2 Full-sibs[5]; Sire[3]	2 Full-sibs[5]; Sire[3]	

[1] Scenarios as explained in the materials and methods.

[2] Appreciation of Table 4.

[3] Dams and sires of the selection candidate.

[4] Full-sibs (breeding) of the selection candidate.

[5] Full-sibs (fattening) of the selection candidate.

RESULTS AND DISCUSSION

Derivation of Hypothetical Prices

The WTP for each quality class expressed as the averaged consumers WTP in relation to a commonly paid price (100%) is presented in Table 3. The relative expression of WTP was chosen in order to handle consumers' different buying behavior, i.e. by concerning prices they usually pay for the product under study. For meat and sensorial quality traits, relative WTP were lower than the price consumers usually pay for this kind of meat (i.e. < 100%). In general, the palatability of meat is determined by three main characters: the texture, the juiciness, and the flavor of meat (Warriss, 2010; Bredahl et al., 1998). In the present study, traits that can be directly related to meat texture are SF measured instrumental, as well as TS and CS determined by a trained panel. Among these traits, highly significant (*$P < 0.0001$*) phenotypic correlation were found (r_p = -0.66 between SF and TS; r_p = -0.71 between SF and CS; and r_p = 0.76 between TS and CS). Such a pronounced relationship between instrumental measured shear force and sensory analysis was also found by Bejerholm and Barton-Gade (1986) for pork meat, as well as for beef (Destefanis et al., 2008). For meat samples with the highest SF values (class 3), the lowest consumers WTP were found (85.03% of the usually paid price). Accordingly, consumers WTP were increased for meat samples revealing high TS and CS values (class 3 with 97.57% and 97.58%, respectively). Generally, juiciness of meat is related to the following traits considered in the present study: DL, traits reflecting the fat content (MAR and IMF), and JS. However, the phenotypic correlation between JS and DL was low (r_p = -0.28), and also small and not significant ($P > 0.05$) between JS with MAR and between JS with IMF. Results are in accordance with non-significant correlations between JS and DL as reported by Huff-Lonergan et al. (2002). Correlations between juiciness and lipid content were also not significant in the present study, and supporting results by Fortin et al. (2005). Hence, improved juiciness due to higher fat content, caused by promoted flow of saliva in the mouth (Warriss, 2010), could not be verified in our study. The highest average consumers WTP was calculated for samples showing medium amount of DL (class 2 with 97.56%) and low JS (class 1 with 98.05%). Consumers WTP was highest for less fat content (class 1 of IMF and MAR), but not different ($P > 0.05$) from other classes. Results indicate a consumers' tendency towards dryer meat and less fat content. In general, consumers preferred meat characterized by high tenderness, but simultaneously low juiciness and small amounts of fat and therefore less flavored pork. The relative WTP for the optical quality traits revealed a consumer's preference for meat showing medium brightness (O_COL class 2), medium marbling (O_MAR class 2), and low degree of drip loss (O_DL class 1). This preference probably reflects the average quality which consumers expect when buying fresh pork. Dransfield et al. (2005) identified the color of pork as the most important characteristic with regard to consumer perception, although preferences differed between countries. Among surveyed consumers, those differences were also apparent. When considering a subgroup characterized by a high WTP for products from local breeds, the determined WTP was significantly higher for darker and strong marbled meat (O_COL, O_MAR, class 3, Anthe, 2015). Such particularities concerning preferences of a potential target group might be taken into account when setting up a breeding program for the local BB breed. Preferences for pork with a low degree of drip loss were expected, and are in agreement with results by Dransfield et al. (2005). For ongoing research aiming at the derivation of economic values for non-market traits, we suggest consideration of following aspects: i) calculation of breed/population specific means and phenotypic standard deviations for traits of interest as a prerequisite for the definition of adequate quality classes, ii) the recruitment of capable test candidates reflecting identical consumer behavior, iii) training of candidates to internalize product standards (which have to be determined), and to get used to a specific kind of presentation.

Derivation of Economic Values

The economic value for the fertility trait NBA reflecting its marginal utility per fattening pig was 13.37 €. Derived economic values for meat, sensorial and optical quality traits based on averaged consumers WTP are presented in Figure 2 and Figure 3. Here, economic values are expressed as a function for alterations of the population mean in a range of the population mean ± one phenotypic standard deviation. Economic values for traits addressing the texture of meat (SF, TS, and CS) were negative at the current population mean. For SF, the economic value was slightly negative (-0.78 €/trait unit), because a large proportion of the BB population is already assigned to the optimum class with SF ranging between 7.8 and 10.5. However, for increasing palatability and to commit consumers' preferences for tender meat, stronger emphasis on SF is suggested.

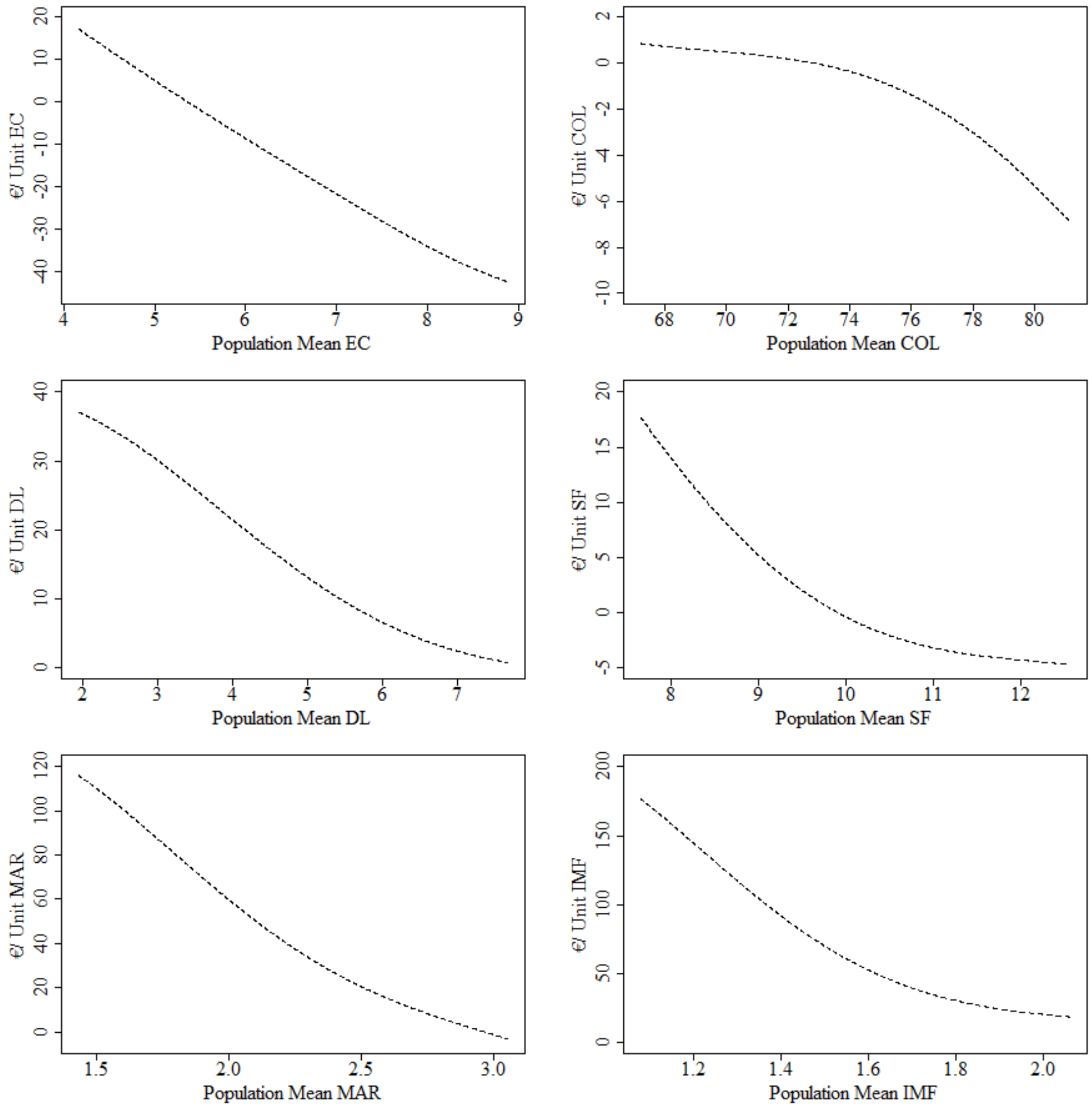

Figure 2. Economic values as a function of the population mean for EC = electric conductivity; COL = meat brightness; DL = drip loss; SF = shear force; MAR = marbling; IMF = intramuscular fat content.

Otherwise, only minor genetic improvement of SF is expected. Economic values for the sensorial quality traits TS and CS were substantially negative (-53.61 €/trait unit and -18.55 €/trait unit), because for both traits estimated population means were on an already high level. Nevertheless, improvement of the texture is advisable, since the population mean of objective measured SF is quite high with 10.10 kg/cm³. Population means for TS and CS are only based on small number of records, which requires further studies to describe the population adequately on the phenotypic scale.

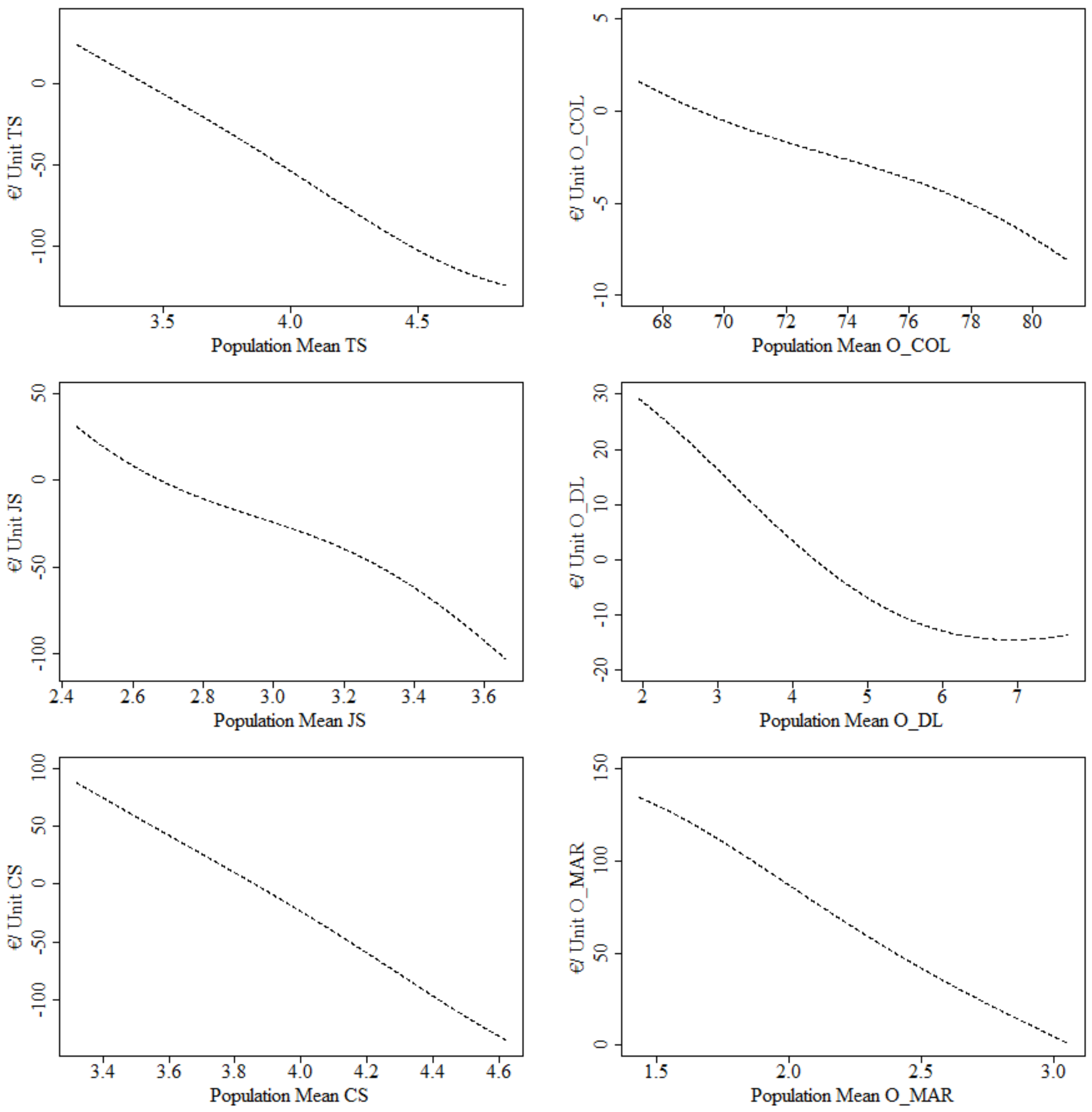

Figure 3. Economic values as a function of the population mean for TS = tenderness score evaluated by a trained panel (0 = not tender and 5 = very tender); JS = juiciness score evaluated by a trained panel (0 = not juicy and 5 = very juicy); CS = chewiness score evaluated by a trained panel (0 = very chewy and 5 = not chewy); O_COL = optical brightness presented as photographs; O_DL = optical drip loss presented as photographs; O_MAR = optical marbling presented as photographs.

Economic values for traits concerning juiciness (DL, MAR, IMF and JS) were positive for DL, MAR, and IMF, and negative for JS at the current population mean. Positive economic values for DL are in contradiction with the ultimate goal, i.e. the reduction of DL. Such a surprising result reveals that DL might not affect consumers' perception when consuming pork, and discloses weakness of a method based only on consumers WTP for tasted meat samples. However, DL as well as COL and MAR impact consumers' purchase decision (Bredahl et al., 1998), and therefore suggesting elementary economic importance. As expected, the economic value based on consumers WTP for different characteristics of DL presented as photographs (O_DL) was negative with -5.18 € per trait unit. As illustrated in Figure 3, the economic value for O_DL is positive for a population mean lower than 4% drip loss. Afterwards, for higher DL population means, economic values were negative. Those findings from the present study confirm the general assumption, i.e. considering drip losses up to 4% as acceptable. Furthermore, we illustrated the general possibility to derive economic values for DL based on photographs. An attribute being most important for palatable meat is the fat content, affecting simultaneously flavor, juiciness, and tenderness (Warriss, 2010; Bejerholm and Barton-Gade, 1986). For all traits associated with fat content (MAR, IMF, and O_MAR), positive and high economic values were derived (38.10 €, 57.52 €, and 64.16 € per trait unit, respectively). The optimum for marbling is a marbling score close to 3 for both descriptors MAR and O_MAR, and an associated IMF in the range of 2 to 3%. For higher population means, economic values were negative. Similar target values for IMF were suggested for conventional pig breeding programs in Switzerland (von Rohr et al., 1999), as well as in Gemany for the Bavarian sire cross line (Habier et al., 2004) when aiming on improvements for meat palatability. For breeding strategies with a strong focus on palatability, it is imperative to include palatability traits into breeding goals, along with a high economic weight. Both components high economic weights in combination with high heritabilities will ensure long term selection response for the trait of interest. This is also valid when considering genetic markers or genomic breeding values (König et al., 2009).

In addition to palatability, appearance of meat influences consumers purchase decisions. Beside drip loss and marbling, meat color is an important consumer selection criterion (Dransfield et al., 2005; Bredahl et al., 1998), especially for fresh meat. Economic values for traits reflecting meat color (COL, O_COL) were negative for population means larger than 70.0 units (Figure 2 and Figure 3), indicating that the optimum color is close to 70.0 units. Similar to DL, the color of the meat does not affect consumers' perception when consuming pork, but instead has an obvious purchase impact. Hence, for the derivation of economic values for traits without an effect on consumers' perception when consuming meat, but impacting the purchase decision, WTP generally should be based on photographs rather than tasting of meat.

Economic values in the present study were derived based on the approach suggested by von Rohr et al. (1999). But in contrast to von Rohr et al. (1999), we derived hypothetical prices based on a consumer survey instead of interviews with meat technology experts. Economic values for the quality traits COL, DL, and IMF from both studies are compared in Figure 4. For neutral comparisons, economic values are depicted in € per phenotypic standard deviation. Economic values for DL from both studies were quite similar. This is also the case for COL, but estimates based on different record techniques and therefore have to be interpreted contrarily. In the study of von Rohr et al. (1999), decreasing COL will lead to darker color, while in the present study, decreasing COL results in brighter meat color. When defining breeding goals for meat quality, consumers' perception and preferences are elementary and should therefore be the central element of the strategy (Verbeke et al., 1999). The color (in this case the brightness) of the meat is highly correlated with IMF (r_g = -0.77), which implies that brighter meat is related to increased IMF. Economic values for IMF differed substantially, and were substantially higher in the present study.

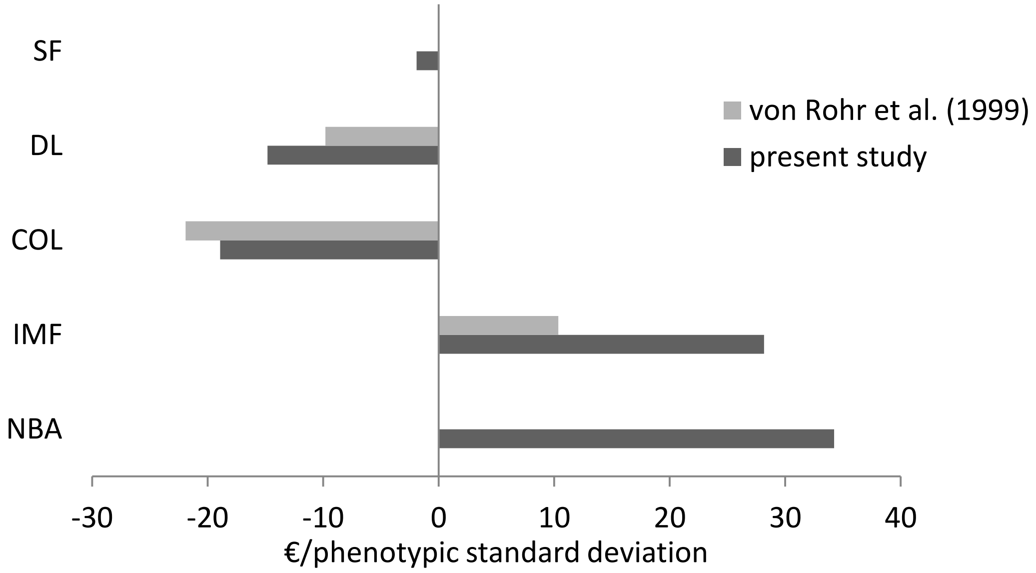

Figure 4. Economic values in € per phenotypic standard deviation for the present study and economic values based on von Rohr et al. (1999).

Economic Evaluation of Breeding Schemes

For the basic breeding scheme of the BB population, and by neglecting additional cost components, discounted profit per animal and investment period was large (32.22 €). Despite positive denoted profit of the current breeding scheme, annual genetic gain for single meat quality traits fail (Figure 5). This is due to low and inconsistent genetic correlations between NBA and meat quality traits (Hermesch et al., 2000). Solanes et al. (2009) also estimated low genetic correlation of $r_g = 0.12$ between NBA and IMF for a Duroc pig line, and expected only little effects on IMF when basing selection on NBA. Hence, for prospective breeding strategies targeting on specific product and meat quality, incorporation of appropriate meat quality traits directly into breeding goals is imperative. Alternatively to the basic breeding scheme, two scenarios (scenario II and scenario III) were modeled by including meat quality as information sources (= index traits). Scenario II included NBA and IMF. Consequently, genetic gain for other meat quality traits based on genetic correlations with IMF. Selection in scenario III only based on meat quality traits (IMF, COL, DL, and SF). Genetic gain for IMF, BF_{iv}, and COL was similar in both scenarios II and III. Annual genetic gain for DL and SF was larger when incorporating these traits directly into the index. For both scenarios, recording of meat quality information sources was associated with high breeding costs, especially when implementing an on-station test for full-sibs of selection candidates. Despite high discounted returns, both scenarios were not profitable (discounted profit scenario II = -80.15 €/animal, and scenario III = -33.91 €/animal). Breeding costs can be decreased by reducing, e.g., the number of tested animals from 400 to 60 sows, and from 100 to 30 boars. Indeed, a positive discounted profit per animal of 11.13 € (scenario II) and 29.97 € (scenario III) was realized, but simultaneously, genetic gain decreased. Additionally, application of such breeding schemes requires a two-step selection procedure, e.g. based on breeding values for fertility in the first step, while the second selection step is based on full-sibs performance for meat quality traits. Such a breeding scheme implies demanding organizational efforts, and its implementation in a small-scale breeding organization might be the huge challenge. When optimizing breeding schemes for smallholder production systems, higher breeding costs, e.g. for performance testing or for logistic efforts, have major impact on long-term sustainability and profitability (Rössler et al., 2009). In order to reduce cost components, another alternative breeding scheme was modeled based on performance testing directly accomplished in participating herds. This scheme (scenario IV) was adapted to small-scale and low-input production systems, and also aimed at the improvement of meat quality. Index traits were NBA and BF_{iv}, whereas BF_{iv} was recorded (own performance of selection candidates via ultrasound) to improve highly correlated IMF. Discounted profit for scenario IV was large and positive with 35.92 € per animal. Annual genetic gain for IMF was lower as obtained for scenario II and III. As expected, when basing selection on BF_{iv}, backfat thickness significantly increased. Nevertheless, results also exhibit desirable and highest genetic gain for SF when using the index trait BF_{iv}. This is due to moderate genetic correlation between BF_{iv} with SF. Genetic gain was even higher when compared to direct selection on SF (scenario IV vs. III; Figure 5). Decrease in instrumental measured SF simultaneously will improve meat tenderness, i.e. tenderness as evaluated by a trained panel (r_p between SF and TS = -0.66). Similar ideas were presented by Schwab et al. (2010), based on r_g = -0.79 between Instron tenderness and a tenderness score evaluated by a trained panel. This close genetic relationship is important for improving palatability and consumers' acceptance. However, if marketing strategies strongly depend on conventional market requirements, increasing backfat thickness will cause economic loss due to the correlated decrease in lean meat percentage. Hence, implementation of suggested breeding strategies (especially scenarios II, III, and IV) require a specific niche market structure (Pugliese and Sirtori, 2012) in order to ensure profitability of pig production. One successful breeding program is established for the Iberian pig breed, focusing on specific meat and product quality (Fernández et al., 2003). Another example is the breeding program for the German Schwaebisch-Haellisches pig (Bühler and Postler, 2004). Especially for niche market production, it might be reasonable to fulfill product specific standards for novel traits, while maintaining genetic and phenotypic variation. The presented concept of a breeding program design can be combined with specific mating plans as elaborated by Biermann et al. (2014) to ensure long-term genetic diversity of the BB breed.

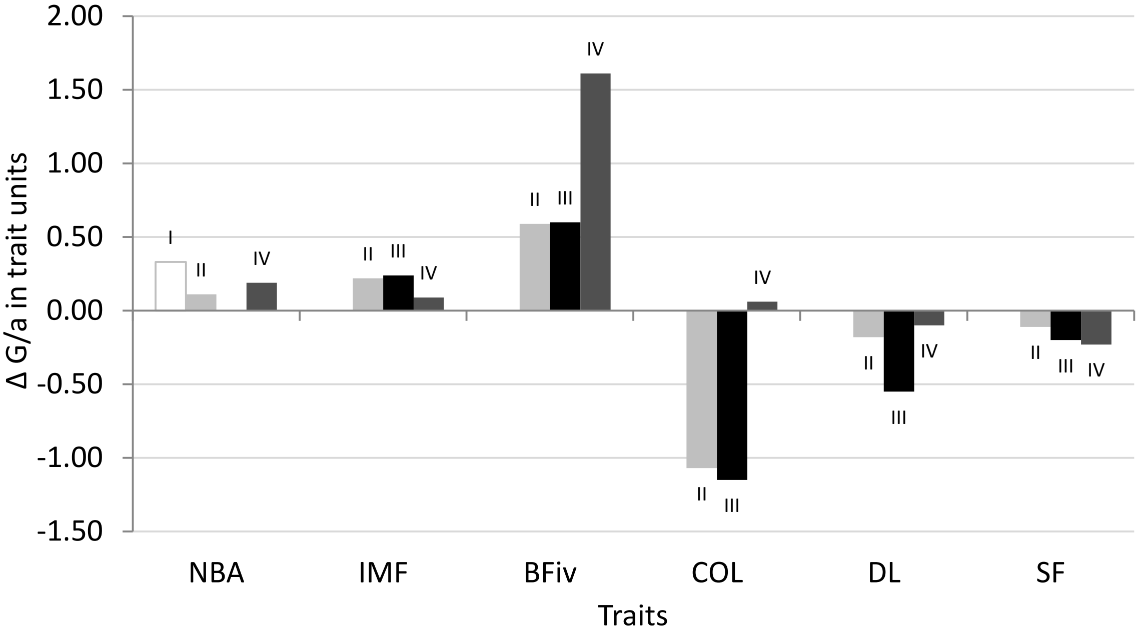

Figure 5. Annual genetic gain in trait units for all traits and scenarios; scenario I = white; scenario II = light grey; scenario III = black; and scenario IV = dark grey. NBA = number of piglets born alive; IMF = intramuscular fat content; BFiv = backfat thickness measured with ultrasound; COL = meat brightness; DL = drip loss; SF = shear force.

CONCLUSIONS

Results indicate the possibility and feasibility to derive economic values based on a consumer's survey and their WTP for tasted meat samples. For traits which are not ascertainable by tasting, results suggest determination of consumers WTP based on photographs. Deterministic evaluations of pig breeding schemes favored "low cost" breeding program designs in order to ensure profitability and sustainability of a niche breeding program. Hence, to avoid expensive performance tests of selection candidates or of related animals (e.g. full-sibs) for meat quality traits, we suggest recording of highly correlated and cost efficient indicator traits as index sources. In the case of the BB breed, selection response for meat quality traits was moderate when implementing BF_{iv} recording for sows and boars.

ACKNOWLEDGMENTS

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KAPITEL 5

Allgemeine Diskussion

In den Kapiteln 2, 3 und 4 wurden die jeweiligen Ergebnisse bereits im Vergleich zu anderen Studien diskutiert. In diesem Kapitel sollen die gewonnenen Erkenntnisse aus den einzelnen Kapiteln in Hinblick auf die Entwicklung eines Zuchtprogramms für die Rasse Bunte Bentheimer diskutiert werden. Bei der Gestaltung und Umsetzung von Zuchtprogrammen, insbesondere für bedrohte und lokale Rassen, kann auf internationale (FAO, 2007 und 2010) und nationale (Fachbeirat Tiergenetische Ressourcen, 2013) Richtlinien und Empfehlungen zurückgegriffen werden. Für die Entwicklung eines Zuchtprogrammes für die Bunte Bentheimer Population sind der aktuellen Situation angepasst die folgenden beiden Punkte von wesentlicher Relevanz: 1.) Die Festlegung der Zuchtziele unter besonderer Berücksichtigung der rassespezifischen Eigenschaften und genetischen Populationsparametern und 2.) Die Definition der für die Umsetzung erforderlichen Zuchtmaßnahmen, von der Leistungsprüfung bis hin zur Anpaarungsplanung. Als dritter, auf den ersten beiden Punkten aufbauend, müssen geeignete Kriterien zur regelmäßigen Überprüfung des Zuchtprogrammes ausgewählt und ggf. entsprechende Anpassung der Zuchtziele und/oder Zuchtmaßnahmen vorgenommen werden (Fachbeirat Tiergenetische Ressourcen, 2013). Letztgenannter soll aber nicht mehr Bestandteil dieser Arbeit sein.

Erkenntnisse zur Festlegung eines (einheitlichen) Zuchtziels

Das aktuelle Zuchtziel des Bunten Bentheimer Schweines wird offiziell durch den Verein zur Erhaltung des Bunten Bentheimer Schweines e.V. durch folgende Eigenschaften definiert:

- „hohe Fruchtbarkeit
- lange Nutzungsdauer
- stressstabil und robust
- genügsam in der Haltung
- exzellente Fleischqualität“

Für die Gestaltung eines Zuchtprogrammes fehlt allerdings die Festlegung konkreter Merkmale, die im Gesamtzuchtwert entsprechend ihrer ökonomischen Bedeutung zusammengefasst werden. Als geeignete Zuchtzielmerkmale sind jene Merkmale zu betrachten, die zur Realisierung des allgemein formulierten Zuchtziels beitragen und die rassetypischen Eigenschaften widerspiegeln unter Berücksichtigung der populationsgenetischen Parameter. Nicht alle aufgeführten Ziele eignen sich dabei für eine direkte züchterische Bearbeitung im Sinne einer Zuchtwertschätzung. Die gewünschte Stressstabilität wird bereits durch konsequente Sanierungsmaßnahmen bezüglich des RYR1 Gens bearbeitet. Die genetische Disposition zur Stressanfälligkeit durch das RYR1 Gen und eine populationsspezifische Analyse ist Bestandteil von Kapitel 3 und soll an dieser Stelle nicht weiter behandelt werden. Die Genügsamkeit der Tiere in der Haltung ist insofern von Bedeutung, als sie die Umgänglichkeit und somit oft auch den Arbeitsaufwand erheblich beeinflussen kann und daher auch einen ökonomischen Aspekt beinhaltet. Dennoch ist die Erfassung von Verhaltensmerkmalen oft sehr zeitintensiv und mit hohem Arbeitsaufwand verbunden. Die genetische Disposition für Verhaltensmerkmale ist generell eher gering. Für Merkmale der Mütterlichkeit schätzten Grandinson et al. (2003) Heritabilitäten von 0,06 (SE = 0,03) für den Ferkel-Schrei-Test, bei dem die Reaktion der Sau auf abgespieltes Ferkelgeschrei erfasst wird, und $h^2 = 0{,}08$ (SE = 0,04) für ein Merkmal, das die Reaktion der Sau auf das Handling von Ferkeln widerspiegelt. Für ein Verhaltensmerkmal, das sich auf die Umgänglichkeit während einer Wiegeprozedur bezieht, schätzen Holl et al. (2010) Heritabilitäten von 0,23. Für das gleiche Merkmal wurden in der vorliegenden Arbeit Schätzwerte von 0,17 (SE = 0,06) erreicht, basierend auf 505 Beobachtungen während der Ultraschallmessungen an Zucht-und Masttieren. Es konnten allerdings keine signifikanten phänotypischen Korrelationen zu Fleischleistungs- oder Fleischqualitätsmerkmalen festgestellt werden. Lediglich zu den unten beschriebenen Exterieurmerkmalen „Rahmen“ und „Bemuskelung“ konnten Korrelationen von -0,10 und -0,12 bei einem Signifikanzniveau von $p < 0{,}05$ ermittelt werden. Tiere mit einer guten Ausprägung dieser Merkmale zeigten somit weniger Aktivität während der Ultraschallmessungen. Dennoch ist der Nutzen züchterischer Bearbeitung von Verhaltensmerkmalen fraglich. Ein gutes Betriebsmanagement und eine positive Tier-Mensch-Beziehung werden bei diesen stark umweltbedingten Merkmalen vermutlich größeren Nutzen erzielen als eine aufwändige Zuchtstrategie.

Fruchtbarkeitsmerkmale

Der Populationsdurchschnitt für die Fruchtbarkeitsmerkmale „Anzahl lebend geborener Ferkel je Sau und Wurf“ (NBA) und „Anzahl abgesetzter Ferkel je Sau und Wurf“ (NW) lag bei 9,15 und 8,56, wobei 3008 Beobachtungen berücksichtigt wurden (Kapitel 2). Für eine züchterisch wenig bearbeitete Rasse liegen diese Leistungen zunächst in einem guten Bereich. An dieser Stelle sei allerdings anzumerken, dass insbesondere die ersten Würfe mit geringen Leistungen in der Vergangenheit oft nicht gemeldet wurden, so dass von einer leichten Überschätzung des Populationsdurchschnittes auszugehen ist. Beide Fruchtbarkeitsmerkmale sind die einzigen Leistungsaufzeichnungen, die weitestgehend routinemäßig ab dem Jahr 1985 für diese Rasse vorliegen. In Abbildung 1 ist der genetische Trend anhand eines Relativzuchtwertes (standardisiert auf einen Mittelwert von 100 und einer Standardabweichung von 20) für NBA und NW nach den Geburtsjahrgängen der Zuchtsauen aufgezeigt. Da die Anzahl der Tiere je Jahrgang stark schwankte, wurden angepasst an Kapitel 2 entsprechende Kohorten gebildet und die durchschnittlichen Relativzuchtwerte berechnet.

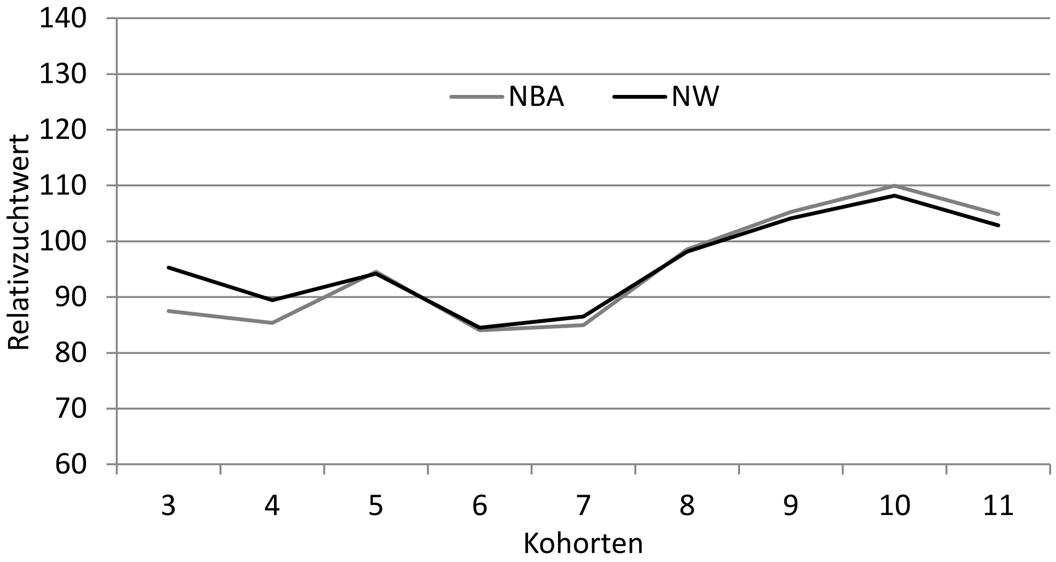

Abbildung 1: Genetischer Trend der Fruchtbarkeitsmerkmale „lebend geborene Ferkel je Sau und Wurf“ (NBA) und „abgesetzter Ferkel je Sau und Wurf“ (NW) anhand eines standardisierter Relativzuchtwert (Mittelwert = 100 und Standardabweichung = 20) nach Kohorten (Kapitel 2).

Ab Kohorte 7 (Jahrgänge 1997, 1998 und 1999) ist ein deutlicher positiver Trend für beide Merkmale zu verzeichnen, erst in den jüngsten Jahrgänge (Kohorte 11) scheint dieser Trend wieder abzunehmen. Durch Einbeziehung dieser Fruchtbarkeitsmerkmale im Zuchtziel und der entsprechenden ökonomischen Gewichtung könnte der bisherige positive genetische Trend weiter verfolgt werden.

Fleischqualitätsmerkmale

Die Umsetzung einer exzellenten Fleischqualität in einem Zuchtprogramm erweist sich als etwas komplizierter, da hier eine genaue Definition dieses Zuchtzieles fehlt und verschiedene Auslegungen möglich sind. Hinzu kommt, dass sich unterschiedliche Vermarktungsformen in Abhängigkeit von den lokalen Gegebenheiten am Markt etabliert haben. Während einige Betriebe auf eine direkte Vermarktung setzen, durch den Verkauf auf Wochenmärkten, in Hofläden oder an Gaststätten, gehen andere den Weg über Marktpartner, die den Vertrieb zu z.B. Fleischerfachgeschäften regulieren. Im letzteren Fall erfolgt der Verkauf der Tiere an die Marktpartner, wobei sich die Preise neben einem Aufschlag für Ökoschweine oder artgerechte Tierhaltung an dem konventionellen Zahlungssystem orientieren, also in erster Linie am Magerfleischanteil der Schlachtkörper. Diese Unterschiede in der Vermarktung führen letztendlich zu innerbetrieblichen und divergenten Zuchtzielen und erschweren die Umsetzung eines einheitlichen Zuchtziels. Während ein marktorientierter Betrieb intern zur Erlössteigerung auf erhöhte Magerfleischanteile abzielt, favorisiert ein nischenorientierter Betrieb Zuchttiere, die besonders schmackhaftes Fleisch erzeugen, d.h. dieser Betrieb bevorzugt sehr fettreiche Schlachttiere mit guter Marmorierung und hohem intramuskulären Fettgehalt (IMF). In Kapitel 3 konnte gezeigt werden, dass der Magerfleischanteil, gemessen am lebenden Tier mittels Ultraschall (LMC_{iv}) bei den Bunten Bentheimern durchschnittlich bei 47,56% lag und der durchschnittlichen Magerfleischanteil der Schlachtköper (LMC) bei 42,55%. Der mittlere IMF Gehalt lag mit 1,57% unter dem für diese Rasse erwarten Wert. Der oben genannte Betriebseffekt könnte mitunter Grund dafür sein. Zur Verdeutlichung dieses Effektes sind in Tabelle 1 die Mittelwerte ausgewählter Fleischleistungs- und Fleischqualitätsmerkmale der vier größten Betriebe dargestellt. Betrieb A und B stehen dabei für eine Nischenvermarktung und Betrieb C und D sind auf die Vermarktung durch Marktpartner angewiesen.

Tabelle 1: Mittelwerte ausgewählter Merkmale der Fleischleistung und Fleischqualität nach Betrieb

	Nischenvermarktung		Vermarktung durch Marktpartner	
	Betrieb A	Betrieb B	Betrieb C	Betrieb D
LMC[1]	40,74 ^{a}	41,92 ^{b}	45,40 ^{c}	43,18 ^{d}
LMC_{iv}	46,91 ^{a}	46,53 ^{a}	49,48 ^{b}	47,55 ^{a}
IMF	1,52 ^{a}	2,00 ^{b}	1,29 ^{c}	1,44 ^{a}
SF	11,57 ^{a}	10,21 ^{b}	8,80 ^{c}	9,41 ^{d}

[1] LMC = Magerfleischanteil gemessen am Schlachtkörper; LMC_{iv} = Magerfleischanteil gemessen am lebenden Tier mittels Ultraschall; IMF = intramuskulärer Fettgehalt; SF = Scherkraft.

^{a,b,c,d} unterschiedliche Buchstaben stehen für einen signifikanten Unterschied von $p < 0{,}05$.

Die Betriebe A und B weisen im Durchschnitt geringere Magerfleischanteile auf als Tiere der Betriebe B und D. Aufgrund der negativen Korrelation zwischen LMC und IMF (siehe Kapitel 3) spiegelt sich das auch in den mittleren IMF Gehalten wider, wobei insbesondere Betrieb B und C stark divergieren. Tabelle 2 zeigt, dass insbesondere in Betrieb B im Schnitt eine außerordentlich lange Mastdauer erzielt wird. Daher ist anzunehmen, dass die durchschnittlich höheren IMF Gehalte mitunter auch darauf zurückzuführen sind.

Tabelle 2: Mittleres Schlachtalter und Schlachtgewicht nach Betrieb mit den entsprechenden Standardabweichungen in Klammern

	Nischenvermarktung		Vermarktung durch Marktpartner	
	Betrieb A	Betrieb B	Betrieb C	Betrieb D
Schlachtalter	285,15	374,03	274,50	271,72
[Tagen]	(38,32)	(69,29)	(30,53)	(31,75)
Schlachtgewicht	107,09	99,34	94,75	102,44
[kg]	(8,79)	(16,66)	(6,60)	(7,65)

Ein weiterer Aspekt der Fleischqualität, der insbesondere in Hinblick auf die Vermarktung relevant ist, ist die sensorischen Qualität. Wie in Kapitel 4 beschrieben, wurden Fleischproben unterschiedlicher Betriebe unter standardisierten Bedingungen zubereitet und anschließend durch ein geschultes Panel hinsichtlich Geruch, Textur und Geschmack beurteilt (0 = nicht erkennbar bis 5 = sehr stark erkennbar) mit einer anschließenden Gesamtbeurteilung (0 = gefällt mir gar nicht bis 5 = gefällt mir sehr). Die Ergebnisse für Fleischproben von Betrieb B und C sind in Abbildung 2 gegenübergestellt.

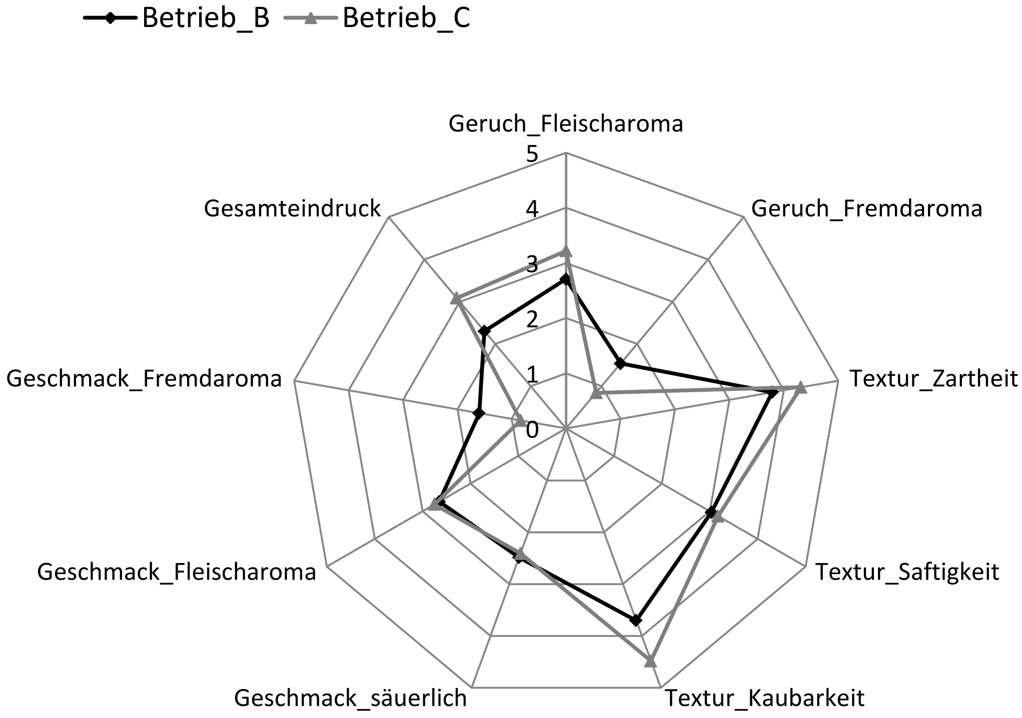

Abbildung 2: Ergebnisse der sensorischen Bewertung durch ein geschultes Panel (Kapitel 4) bezüglich Geruch, Textur, Geschmack (0 = nicht erkennbar bis 5 = sehr stark erkennbar) und Gesamteindruck (0 = gefällt mir gar nicht bis 5 = gefällt mir sehr) für Fleischproben der Betriebe B und C.

Die Ergebnisse zeigen, dass Proben von Betrieb C in der Gesamtbewertung signifikant besser abschnitten. In Bezug auf die Textur war dieser Betrieb ebenfalls in allen Merkmalen überlegen. Weitere Unterschiede zeigten sich hinsichtlich der Fremdaromen, die sowohl durch Riechen als auch Schmecken erfasst wurden. Der Unterschied war allerdings nur signifikant für die geschmacklichen Fremdaromen, die in Betrieb B stärker erkennbar waren. Die Ursachen für die Unterlegenheit von Betrieb B in Bezug auf die sensorische

Qualität sind vermutlich sehr mannigfaltigen Ursprungs und lassen sich im Rahmen dieser Untersuchung zunächst nur vermuten. Die Schmackhaftigkeit von Fleisch und damit einhergehende Akzeptanz durch den Konsumenten werden maßgeblich durch die Attribute Zartheit, Saftigkeit und Geschmack/Geruch des Fleisches bestimmt (Warriss, 2010; Bredahl et al., 1998). Für Betrieb B wurden durchschnittlich höhere instrumental erhobene Scherkraftwerte (SF) erfasst als für Betrieb C (Tabelle 1). Die phänotypische Korrelation zwischen SF und durch das Panel beurteilte Zartheit war erwartungsgemäß negativ (r_p = -0,66; p < 0,001), da mit steigender Scherkraft die Zartheit des Fleisches abnimmt. Sowohl Tabelle 1, als auch Abbildung 2 zeigen, dass die Proben von Betrieb B im Schnitt zäher als Proben von Betrieb C waren. Aufgrund des extrem hohen durchschnittlichen Schlachtalters in Betrieb B ist dies als naheliegende Ursache zu betrachten, da mit steigendem Alter die Quervernetzungen im Kollagen zunehmen. Des Weiteren wurden in Betrieb B im Vergleich zu Betrieb C durchschnittlich höhere Skalenwerte bezüglich der Fremdaromen angegeben. Es ist anzunehmen, dass diese im Zusammenhang mit den höheren IMF Gehalt der Proben standen. Dennoch waren generell keine signifikanten Korrelationen zwischen IMF und der sensorischen Beurteilung festzustellen. Die genauen Ursachen für diese Abweichungen vom „normalen“ Fleischgeschmack können im Rahmen dieser Studie somit nicht festgestellt werden. Für eine weitere Erforschung dieser Ursache sind eine umfangreiche Futtermittelanalyse auf dem Betrieb sowie eine genaue Überprüfung des Fettsäuremusters der Fleischproben allerdings zu empfehlen.

Diese betriebliche Gegenüberstellung ermöglicht es den Betrieben durch Optimierung von Produktionsprozessen die Fleischqualität im Sinne des betriebsspezifischen Zuchtzieles zu verbessern. Aus züchterischer Sicht und mit Hinblick auf die Gestaltung eines Zuchtprogrammes für die Rasse Bunte Bentheimer verdeutlicht diese Gegenüberstellung der Betriebe die eigentliche Herausforderung, den unterschiedlichen Strategien bei der Gestaltung eines Zuchtprogrammes gerecht zu werden. Aufgrund der deutlichen Unterlegenheit bezüglich des Magerfleischanteils im Vergleich zu handelsüblichen Schlachtschweinen ist von einer Zucht auf dieses Merkmal eindeutig abzuraten. Vielmehr sollten Schwächen (geringer MFA) als Stärken (erhöhter Fettgehalt) betrachtet werden und im Rahmen eines Zuchtprogrammes auf Merkmale wie IMF eingegangen werden. Eine hohe genetische Varianz und Heritabilität für IMF (Kapitel 3) sprechen aus züchterischer Sicht für eine Bearbeitung dieses Merkmals.

Weitere mögliche Zuchtzielmerkmale

Neben den Fruchtbarkeits- und Fleischqualitätsparametern (Kapitel 2, 3 und 4) wurden im Rahmen der Eigenleistungsprüfung im Feld Merkmale des Exterieur und die Lebendtagszunahme (die durchschnittliche Tageszunahme je Lebenstag von der Geburt bis zum Prüfzeitpunkt; LTZ) an insgesamt 613 Zucht- und Masttieren erfasst. In der BB Population erfolgt eine Exterieurbeurteilung bei der Körung von Jungebern als Grundvoraussetzung für die Herdbuchaufnahme. Die Beurteilung der Merkmale Rahmen (RA), Fundament (FUN) und Bemuskelung (BEM) erfolgt auf einer dreistufigen, subjektiven Bewertungsskala. Das Merkmal Rahmen beinhaltet die äußere Erscheinung, die Höhe und die Länge des Zuchttieres. Beim Fundament wird die Vorder- und Hinterhand berücksichtigt. Die Bemuskelung bezieht sich auf die Ausprägung von Schulter, Kotelett und Schinken. Die Benotung ist wie folgt definiert:

1 = unterdurchschnittlich, zuchtuntauglich, bedingt tauglich
2 = durchschnittlich, zuchttauglich
3 = überdurchschnittlich, besonderes zuchttauglich.

Die Nachteile dieses Bewertungssystems liegen darin, dass durch das Zusammenfassen von Merkmalen keine Rückschlüsse auf Einzelmerkmale gezogen werden können und Informationen zur phänotypischen Ausprägung der Einzelmerkmale fehlen. Zur Abschätzung des genetischen Hintergrundes dieser Merkmale, sowie mögliche genetische Zusammenhänge zu Leistungsmerkmalen, wäre aber genau dies notwendig. Die geschätzten Heritabilitäten mit entsprechenden Standardfehlern für RA, FUN und BEM lagen mit 0,00 (SE = 0,06), 0,06 (SE = 0,05) und 0,02 (SE = 0,05) in einem sehr geringen Bereich und sind aus züchterischer Sicht eher unbrauchbar, da sie keine Rückschlüsse auf ein konkretes Merkmal zulassen. Alternativ zu einem benotenden System hat sich daher im Bereich der Tierzucht das lineare Bewertungssystem bewährt, in der Rinderzucht, Pferdezucht (Stock et al. 2013), aber auch in der Schweinezucht. Die auf diesem System basierenden Heritabilitäten vom BHZP im Jahr 2002 veröffentlicht (Henne, 2002), lagen für die Rahmenhöhe und Rahmenlänge, zwischen 0,07 und 0,11. Für Merkmale des Fundamentes wurden Werte zwischen 0,03 und 0,20 geschätzt. Für die Bemuskelung von Rücken und Schinken wurden Werte zwischen 0,12 und 0,25 angegeben. Für eine erfolgreiche Zuchtwertschätzung für Exterieurmerkmale beim Bunten Bentheimer wäre die Einführung eines linearen Bewertungssystems notwendig. Dennoch, das aktuelle Bewertungssystem wird angewandt, um möglichst zuchttaugliche und gut konditionierte Zuchttiere zu selektieren. In Abbildung 3 und 4 ist dargestellt in welchem Zusammenhang die Bonitierung mit der Rückenspeckdicke (erfasst mittels Ultraschall (BF_{iv})) und LTZ steht.

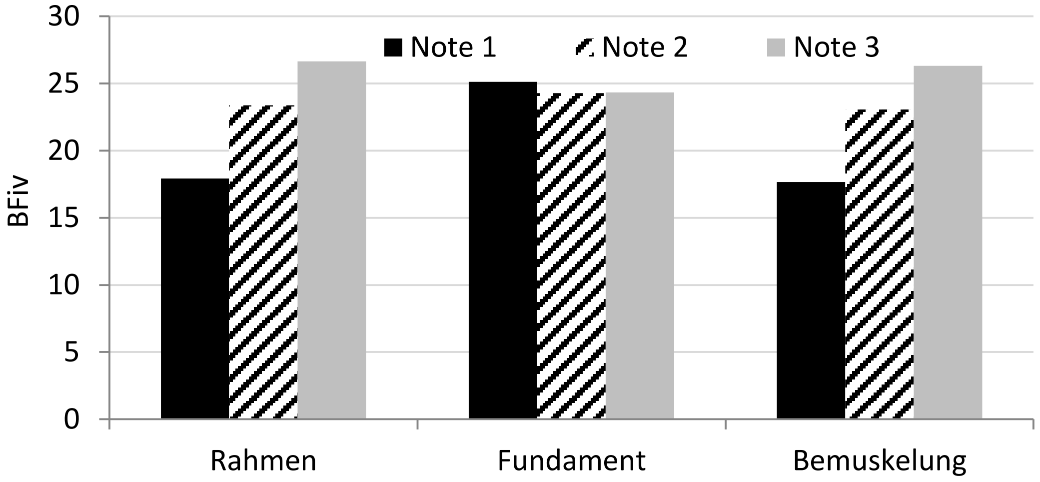

Abbildung 3: Rückenspeckdicke (BF_{iv}) in Abhängigkeit von der subjektiven Benotung bezüglich der Merkmale Rhamen, Fundament und Bemuskelung.

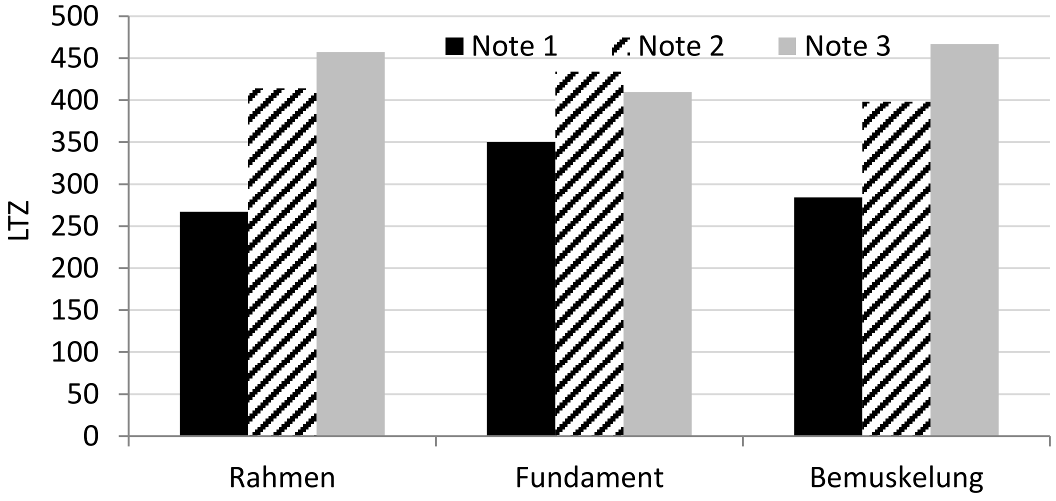

Abbildung 4: Lebendtagszunahme (LTZ) in Abhängigkeit von der subjektiven Benotung bezüglich der Merkmale Rahmen, Fundament und Bemuskelung.

Die Abbildungen 3 und 4 verdeutlichen zunächst, dass offenbar ein positiver Zusammenhang zwischen BF_{iv} und LTZ besteht, da sich in den Merkmalen RA und BEM ein ähnliches Bild abzeichnet. Mit steigender Benotung steigt auch BF_{iv} bzw. LTZ an. Dies ist begründet in einer relativ engen genetischen Beziehung (r_g = 0,45; SE = 0,16) zwischen BF_{iv} und LTZ. Zu einem vergleichbaren Ergebnis kamen bereits Hovenier et al. (1992) mit einer genetischen Korrelation von r_g = 0,57 (SE = 0,11). Vielmehr verdeutlichen die Abbildungen aber, dass die Selektion auf eine besondere Zuchttauglichkeit (Benotung = 3) bezüglich des Rahmens und der Bemuskelung zur Auswahl fettreicherer Zuchttiere führt. Dieser Zusammenhang sollte bei der Selektion von Jungebern, aber auch bei der Remontierung von Jungsauen berücksichtigt werden. In einem Zuchtziel, das auf höhere IMF Gehalte abzielt, kann dieser Zusammenhang als Vorteil genutzt werden. Zur Bewertung eines potentiellen Fleischansatzvermögens eignet es sich allerdings weniger. Zu dem Exterieurmerkmal FUN konnte kein nennenswerter Zusammenhang festgestellt werden. Dem Merkmalskomplexes Fundament sollte allerdings besondere Beachtung geschenkt werden, da Probleme mit dem Fundament neben Fruchtbarkeitsstörungen zu den häufigsten Abgangsursachen zählen und somit auch in einer geringeren Nutzungsdauer resultieren. Tarrés et al. (2006) zeigten in einer Studie in der Schweiz, dass für Large White Sauen mit dem besten Index für Exterieurmerkmale ein geringeres Risiko bestand, ausgemerzt zu werden und sich daher ein indirekter Selektionserfolg für die Nutzungsdauer ergibt. In einer aktuellen Studie zeigen Le et al. (2015), dass ein gewünschter genetischer Zusammenhang zwischen Fruchtbarkeitsmerkmalen und Merkmalen des Exterieur, erfasst an 5 Monate alten Tieren, besteht. Sauen mit einer besseren Gesamtbenotung der Beine, zeigten auch eine bessere Leistung in Bezug auf das Fruchtbarkeitsmerkmal NBA. Die züchterische Berücksichtigung von Exterieurmerkmalen, insbesondere des Merkmalskomplexes Fundament, könnte somit sowohl Nutzungsdauer und Fruchtbarkeit, aber auch die Widerstandsfähigkeit (Robustheit) positiv beeinflussen. Eine erfolgreiche Zuchtwertschätzung hinsichtlich dieses Merkmalskomplexes würde allerding eine Datenerfassung basierend auf einem linearen Bewertungssystem voraussetzen.

Zusammensetzung eines möglichen Selektionsindex

Nach genauer Definition des Zuchtziels und Festlegung konkreter Zuchtzielmerkmale werden diese, entsprechend ihrer wirtschaftlichen Gewichtung, in einem Gesamtzuchtwert zusammengefasst. In Kapitel 4 wurden für das Fruchtbarkeitsmerkmal NBA und ausgewählte Fleischqualitätsmerkmale ökonomische Gewichte abgeleitet. Für Merkmale ohne direkte Marktrelevanz ist die Ableitung ökonomischer Gewichte durch spezielle Befragungsmethoden möglich (Kapitel 4) oder auch anhand von Auktionspreisen (Lind, 2006). Aufgrund der oben beschriebenen positiven Auswirkung eines guten Exterieurs beim Schwein, hat dieser Merkmalskomplex durchaus Berechtigung im Zuchtziel berücksichtigt zu werden. Im dänische Zuchtprogramm (Dan Avl, 2015) wir das Fundament beispielsweise mit einem relativen Gewicht von 5% für die Vaterrasse und 2% für die Mutterrasse im Zuchtziel berücksichtigt. Für das Fundament wird ein wirtschaftliches Gewicht von 16,75 € angegeben. In einem Zuchtprogramm für eine Rasse wie dem Bunten Bentheimer Schwein, mit einem weniger marktorientierten Zuchtziel, würde zur Erzeugung von möglichst langlebigen und robusten Tieren eine prozentual höhere Gewichtung im Zuchtziel Sinn machen. In Tabelle 3 ist in Anlehnung an die Ergebnisse aus Kapitel 4 ein theoretisches Zuchtziel abgebildet mit dem Schwerpunkt auf Fruchtbarkeit (NBA), Fleischqualität (IMF) und Exterieur, beispielsweise als ein Index aus RA, FUN, BEM. Basierend auf den in Kapitel 4 abgeleiteten ökonomischen Gewichten für NBA und IMF und einer relativen Gewichtung von 2/3 ergibt sich für das Exterieur ein theoretisches ökonomisches Gewicht von 18 € je Merkmalseinheit, bei einer angenommenen genetischen Standardabweichung von 1,00.

Tabelle 3: Möglicher Selektionsindex und ökonomische Gewichtung (w) für die Rasse Bunte Bentheimer

Merkmal [1]	Relative Gewichtung im Zuchtziel	w* σ_g	σ_g	w/Einheit
NBA	22%	12,00	0,89	13,37 €
IMF	45%	25,00	0,43	57,52 €
Exterieur	33%	18,00	1,00	18,00 €

[1] NBA = lebend geborene Ferkel je Sau und Wurf; IMF = intramuskulärer Fettgehalt; Exterieur = Index aus Rahmen, Fundament und Bemuskelung.

Für eine ausführliche Zuchtplanungsrechnung fehlen allerding die notwendigen populationsgenetischen Parameter für lineare Exterieurmerkmale. Für diesen Zweck würde sich aufbauend auf den bisherigen Ergebnissen ein Folgeprojekt anbieten.

Erkenntnisse zur Festlegung geeigneter Zuchtmaßnahmen

Zur Realisierung der definierten Zuchtziele im Rahmen eines Zuchtprogramms sind anschließend entsprechende Zuchtmaßnahmen festzulegen, die der aktuelle Situation der Population angepasst sind. Die erforderliche Leistungsprüfung sollte mit der Struktur der Betriebe wirtschaftlich und praktisch vereinbar sein. Bereits etablierten Vermarktungsstrategien sollten im Rahmen des Zuchtprogramms berücksichtigt werden. Des Weiteren ist insbesondere in kleinen und bedrohten Populationen dem aktuellen Gefährdungsgrad und der Inzuchtsituation bei der Festlegung der Zuchtmaßnahmen besondere Beachtung zu schenken.

Geeignete Leistungsprüfung für kleine Betriebsstrukturen

Für die Umsetzung der gewünschten Zuchtziele ist es nicht nur erforderlich, dass die Zuchtzielmerkmale eine gewisse genetische Varianz und Erblichkeit aufweisen, sondern sie müssen im Rahmen einer Leistungsprüfung erfassbar sein. In kleinen Populationen und unter kleinstrukturierten Produktionsbedingungen sollte eine möglichst praxisorientierte Art der Leistungsprüfung gewählt werde, die durch geringen Arbeits- und Kostenaufwand in den Produktionsablauf integriert werden kann. Eine Feldprüfung ist daher einer Stationsprüfung allein aus ökonomischen Beweggründen vorzuziehen. Die oben gennannten Fruchtbarkeitsmerkmale können problemlos durch die Landwirte selbst erfasst und der Zuchtorganisation gemeldet werden. Für die Schlachtleistungsmerkmale LMC und BF konnte in Kapitel 3 gezeigt werden, dass die gleichen Merkmale erfasst, mittels Ultraschall am lebenden Tier, geeignete Hilfsmerkmale sind. Genetische Korrelationen von $r_g = 0{,}94$ zwischen LMC_{iv} und LMC und $r_g = 0{,}96$ zwischen BF_{iv} und BF versprechen einen sehr guten korrelierten Selektionserfolg. Die Erfassung von Fleischqualitätsmerkmalen ist generell mit einem besonders hohen und kostspieligen Aufwand verbunden. Basierend auf den geschätzten genetischen Korrelationen zwischen den Ultraschallmessungen und der Fleischqualität konnte gezeigt werden, dass die Selektion auf BF_{iv} mit einer Verbesserung der Fleischqualität in Form eines erhöhten IMF Gehaltes einhergeht. Dies wird auch in den in Kapitel 3 und 4 vorgestellten Zuchtplanungsrechnungen deutlich. Der geringere Zuchtfortschritt im Vergleich zur direkten Erfassung von IMF steht den deutlich geringeren variablen Kosten einer Feldprüfung gegenüber und spricht vom derzeitigen Standpunkt aus für eine Leistungsprüfung in Form einer Feldprüfung. Neben den Ultraschallmessungen als Bestandteil der Feldprüfung könnte diese um eine lineare Exterieurbeurteilung erweitert werden zur indirekten Verbesserung der Fruchtbarkeit, Nutzungsdauer und Widerstandsfähigkeit (Robustheit).

Berücksichtigung unterschiedlicher Vermarktungsstrategien

Unterschiedliche Vermarktungsstrategien innerhalb einer Population können aufgrund antagonistischer innerbetrieblicher Zuchtziele langfristig zur Bildung von Subpopulationen und deren Auseinanderdriften führen. Angesichts der ohnehin geringen Populationsgröße würde das den Austausch genetischen Materials, das Inzuchtmanagement und den züchterischen Fortschritt weiter erschweren. Der Gestaltung eines nachhaltigen Zuchtprogrammes und der Bewahrung der genetischen Diversität würde damit entgegengewirkt werden. Um einer marktorientierten und nischenorientierten Vermarktungsstrategie in einem Zuchtprogramm gleichermaßen gerecht zu werden, sei eine mögliche Option die Anwendung von Gebrauchskreuzungen. Durch die Anpaarung einer fleischreichen Rasse auf väterlicher Seite können marktfähige Schlachttiere erzeugt werden, nischenorientierte Betriebe könnten weiterhin die Vermarktung von Reinzuchttieren zur Produktion von traditionellen und regionalen Fleischprodukten praktizieren. So wäre es im Rahmen eines Reinzuchtprogrammes möglich, gezielt auf rassetypischen Eigenschaften einzugehen. Gebrauchskreuzungen mit alten Rassen findet man in diversen Ländern, sie unterstützen die Erhaltung alter, lokaler Rassen und ermöglichen gleichzeitig eine wirtschaftliche Produktion. In Polen wird die lokalen Rassen Złotnicka, die mit durchschnittlichen Magerfleischanteilen von 46% und IMF von die 2% (Grześkowiak et al., 2009) zur Produktion traditioneller Produkte eingesetzt. Die Anwendung von Gebrauchskreuzungen z.B. durch den Einsatz von Polnischer Large White, Hampshire oder Duroc auf väterlicher Seite haben sich bewährt, um Magerfleischanteile und Tageszunahmen zu verbessern (Szulc et al., 2006; Szulc et al., 2012). Im Nord-Westen Vietnams werden Yorkshire Eber mit Sauen der lokalen Rassen Ban und Mong Cai gekreuzt, zur Verbesserung des Magerfleischanteils und zur Erzeugung marktkonformer Schlachttiere (Rössler et al., 2009; Herold et al., 2010). Solch eine Strategie würde es auch bei den Bunten Bentheimern ermöglichen, unterschiedliche Vermarktungsformen im Rahmen eines Zuchtprogramms gleichzeitig bestehen zu lassen und ein einheitliches Zuchtziel innerhalb der Population zu verfolgen.

Inzuchtmanagement

In Zuchtprogrammen für bedrohte Rassen ist für den langfristigen und nachhaltigen Erfolg einerseits die wirtschaftliche Konkurrenzfähigkeit von Bedeutung, aber andererseits die Bewahrung der genetischen Diversität. Geringe Populationsgrößen gehen oft einher mit bereits hohen Inzucht- und Verwandtschaftskoeffizienten. Beim Bunten Bentheimer lag der durchschnittliche Inzuchtkoeffizient der letzten Jahrgänge bereits über 12% mit steigender Tendenz (Kapitel 2). Für die Gestaltung eines Zuchtprogramms und die Auswahl geeigneter Zuchtmaßnahmen ist es daher unerlässlich, Instrumentarien zur Inzuchtkontrolle zu integrieren. Die geeignete Methode dazu wurde in Kapitel 2 vorgestellt. Durch gezielte Selektion und Anpaarung ist es möglich, Zuchtfortschritt bei gleichzeitiger Inzuchtkontrolle zu generieren. Die vorgestellt Simulation ließe sich ebenso auf einen Gesamtzuchtwert im Sinne des definierten Zuchtziels anwenden, beispielsweise eine Kombination aus den Merkmalskomplexen Fruchtbarkeit, Fleischqualität und Exterieur. Ein Hindernis in der Bunten Bentheimer Population ist bisher allerdings die eingeschränkte Verfügbarkeit der Eber unter den Betrieben, da bisher so gut wie keine künstliche Besamung praktiziert wird. So findet ein genetischer Austausch nur unter bestimmten Betrieben statt, was die Umsetzbarkeit von konkreten Anpaarungsplänen erschwert. Die unter der Annahme des Natursprunges modellierten Szenarien müssten zukünftig so modifiziert werden, dass die vorgeschlagenen Anpaarungen auch in der Praxis umgesetzt werden können.

Entwurf eines Zuchtprogramm für die Rasse Bunte Bentheimer

Der Entwurf für das Zuchtprogramm (Abbildung 5) ist in Hinblick auf das in Tabelle 4 vorgeschlagene Zuchtziel konzipiert. Teile dieses Entwurfes wurden aus dem von Brandt (2010) vorgestellt Konzept zur ökologischen Jungsauenerzeugung übernommen.

In allen Zuchtbetrieben sollen **potentielle Selektionskandidaten** einer Eigenleistung im Feld unterzogen werden. Als potentielle Selektionskandidaten sind Tiere zu betrachten, die z.B. besonders das rassetypischen Aussehens widerspiegeln, aber auch einige Grundvoraussetzungen erfüllen, wie eine ausreichende Anzahl an Zitzen. Die Feldprüfung kann vom Zuchtleiter/Zuchtgebietsleiter bei einem durchschnittliche Prüfgewicht von 90 bis 100 kg durchgeführt werden und umfasst die Messung der Rückenspeckdicke (BF_{iv}) mittels Ultraschall und eine lineare Exterieurbeurteilung (**Feldprüfung 1**). Anhand festgelegter Grenzwerte durch den Zuchtverband werden die besten Selektionskandidaten ausgewählt, die übrigen gehen in die Mast. Die ausgewählten Selektionskandidaten werden für die Erzeugung der ersten beiden Würfe eingesetzt, sowohl Sauen als auch Eber. So können die ersten Eigenleistungen zur Fruchtbarkeit erfasst werden (**Feldprüfung 2**). Die Nachkommen aus den ersten beiden Würfen werden ausschließlich für die Mast erzeugt. Betriebe mit einer **marktorientierten Vermarktungsstrategie** können dabei zur Erzeugung marktkonformer Schlachttiere auf fleischreiche Vaterrassen zurückgreifen, wie z.B. Piétrain. Die Haltung eigener Eber wäre nicht zwingend erforderlich, wenn künstliche Besamung praktiziert werden würde. Betriebe mit **nischenorientierter Vermarktung** können zur Erzeugung von Masttieren auf den eigenen Bentheimer Bestandseber zurückgreifen. Nach den ersten beiden Würfen liegen damit Leistungsdaten aus der Feldprüfung 1 und 2 vor, so dass darauf basierend eine vollständige **Zuchtwertschätzung für alle Selektionskandidaten** durchführt werden kann. Anhand der Zuchtwerte und der maximalen zulässigen Verwandtschaft (die aufgrund der bereits hohen durchschnittlichen Inzuchtkoeffizienten mindestens unter 25% liegen sollte) werden die besten Sauen und Eber mit ihren optimalen Einsatzfrequenzen unter Anwendung der OGC-Methode selektiert (**OGC Tiere**). Durch die Umsetzung konkreter Anpaarungspläne mittels NSB-Mate lässt sich die zukünftige Inzucht der Folgegeneration noch weiter reduzieren. Dabei können zuvor die Regionen, innerhalb derer eine Anpaarung möglich ist, festgelegt werden. Die besten Nachkommen aus diesen Anpaarungen stehen dann wieder als potentiellen Selektionskandidaten zur Erstellung der nächsten Generation an Zuchttieren zur Verfügung.

Vor- und Nachteile des Zuchtprogrammes

Der Vorteil dieses Zuchtprogramm liegt insbesondere darin, dass die unterschiedlichen Vermarktungsstrategien gleichzeitig bestehen bleiben können. Es bietet Züchtern und

Haltern viel Flexibilität, da sie an kein Qualitätsprogramm gebunden sind. Es ist daher besonders auch für sehr kleine Betriebsstrukturen geeignet. Der positive Einfluss unterschiedlicher und individueller Vermarktungsstrategien lässt sich auch aufgrund der steigenden Bestandszahlen vermuten (siehe Kapitel 1, Abbildung 1). Trotz der steigenden Tierzahlen ist eine systematische und koordinierte Inzuchtkontrolle unentbehrlich, um die Bewahrung der genetischen Diversität zu gewährleisten. Darüber hinaus ist Zuchtfortschritt erstrebenswert, um rassetypische Merkmale besonderes für Vermarktungszwecke besser herauszustellen. Als rassetypisches und vermarktungsrelevantes Merkmal bietet sich der intramuskuläre Fettgehalt an. Hohe Varianzen und eine gute Erblichkeit stellen zudem gute züchterische Erfolge in Aussicht, um tatsächlich als Alleinstellungsmerkmal für diese Rasse zu fungieren. Ein weiterer Vorteil des Programmes ist, dass die Leistungsprüfungen in einem relativ kostengünstigen Umfang im Rahmen einer Feldprüfung erfolgen können.

Die Anwendung modernen Zuchttechniken, wie genomische Selektion als Alternative zu den klassischen Zuchtmaßnahmen, ist unter Berücksichtigung der aktuellen Bedingungen nicht zu rechtfertigen. Aufgrund der verhältnismäßig geringen Tierzahlen wäre allein die Aufstellung einer repräsentativen Referenzpopulation kaum möglich und die anfallenden Kosten unter Berücksichtigung der Betriebsstrukturen nicht angemessen. Hinzu kommt, dass aufgrund der bisher fast fehlenden Praktizierung der künstlichen Besamung die Verfügbarkeit der Eber stark eingeschränkt ist, sodass der Nutzen eines genomisch unterstützten Zuchtwertes eher fraglich ist.

Doch auch für dieses Zuchtprogramm besteht der Nachteil in der Herausforderung der Koordination und Umsetzung innerhalb dieser Betriebsstrukturen. Die Meldung der Selektionskandidaten, also alle Tiere, die theoretisch angepaart werden sollen, müssen an eine zentrale Stelle übermittelt werden, um darauf basierend Zuchtwerte zu schätzen und Selektions- und Anpaarungspläne zu konzipieren. Die Umsetzung der Anpaarungspläne ist wegen der Natursprungproblematik relativ aufwendig. Für die Umsetzung eines solchen Zuchtprogrammes wäre es daher notwendig, in Zusammenarbeit mit dem Verein und einer wissenschaftlichen Koordinationsstelle eine praktikable Lösung zu erarbeiten.

Eine alternative Vermarktungsstrategie

Für marktorientierte Betriebe, die nur beim dritten Wurf Reinzuchttiere erzeugen, z.B. zur Eigenremontierung, müssen Möglichkeiten erarbeitet werden, um die ausselektierten Tiere auch ohne wirtschaftliche Einbußen zu vermarkten. Eine generelle alternative Vermarktung wäre die Nutzung des überschüssigen Fettes (z.B. Rückenspeck) im Bereich der Naturkosmetik. In einigen verarbeitenden Betrieben lag der Bedarf an Speck, z.B. zur Herstellung von Würsten und Dauerwaren, weit unter dem Angebot, das durch die teils sehr fetthaltigen Schlachtköper gegeben war. Bereits in der Vergangenheit bewährte sich diese wertvolle Ressource zur Herstellung von Cremes, Salben, Lotionen und Seifen. Die gegenwärtige Akzeptanz durch den Konsumenten und die Etablierung eines Nischenmarktes müsste aber zuvor im Rahmen eines eigenen Forschungsprojektes z.B. zu alternativen Vermarktungsstrategien geprüft werden.

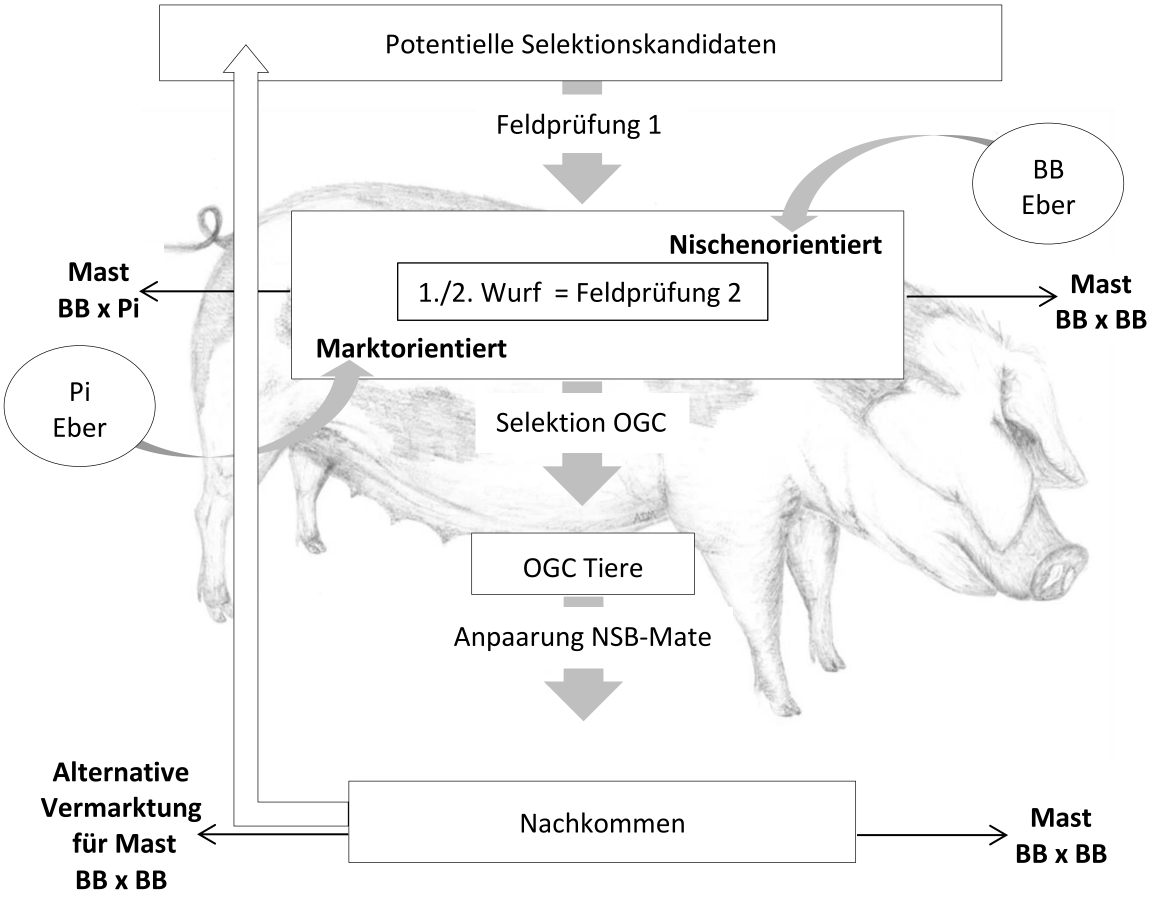

Abbildung 5: Entwurf für ein Zuchtprogramm für die Rasse Bunte Bentheimer.

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