Makale Özetleri

Genetiği Değiştirilmiş Organizma *(Genetically Modified Organisms)*

http://www.ilkhabergazetesi.com/wordpress/wp-content//2009/11/gdo.jpg

Hot topic: Enhancing omega-3 fatty acids in milk fat of dairy cows by using stearidonic acid-enriched soybean oil from genetically modified soybeans.

Bernal-Santos G, O'Donnell AM, Vicini JL, Hartnell GF, Bauman DE.
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Very long chain n-3 fatty acids such as eicosapentaenoic acid (EPA; 20:5n-3) are important in human cardiac health and the prevention of chronic diseases, but food sources are limited. Stearidonic acid (SDA; 18:4n-3) is an n-3 fatty acid that humans are able to convert to EPA. In utilizing SDA-enhanced soybean oil (SBO) derived from genetically modified soybeans, our objectives were to examine the potential to increase the n-3 fatty acid content of milk fat and to determine the efficiency of SDA uptake from the digestive tract and transfer to milk fat. Three multiparous, rumen-fistulated Holstein cows were assigned randomly in a 3 x 3 Latin square design to the following treatments: 1) control (no oil infusion); 2) abomasal infusion of SDA-enhanced SBO (SDA-abo); and 3) ruminal infusion of SDA-enhanced SBO (SDA-rum). The SDA-enhanced SBO contained 27.1% SDA, 10.4% alpha-linolenic acid, and 7.2% gamma-linolenic acid. Oil infusions provided 57 g/d of SDA with equal amounts of oil infused into either the rumen or abomasum at 6-h intervals over a 7-d infusion period. Cow numbers were limited and no treatment differences were detected for DMI or milk production (22.9+/-0.5 kg/d and 32.3+/-0.9 kg/d, respectively; least squares means +/- SE), milk protein percentage and yield (3.24+/-0.04% and 1.03+/-0.02 kg/d), or lactose percentage and yield (4.88+/-0.05% and 1.55+/-0.05 kg/d). Treatment also had no effect on milk fat yield (1.36+/-0.03 kg/d), but milk fat percentage was lower for the SDA-rum treatment (4.04+/-0.04% vs. 4.30+/-0.04% for control and 4.41+/-0.05% for SDA-abo). The SDA-abo treatment increased n-3 fatty acids to 3.9% of total milk fatty acids, a value more than 5-fold greater than that for the control. Expressed as a percentage of total milk fatty acids, values (least squares means +/- SE) for the SDA-abo treatment were 1.55+/-0.03% for alpha-linolenic acid (18:3n-3), 1.86+/-0.02 for SDA, 0.23 +/- <0.01 for eicosatetraenoic acid (20:4n-3), and 0.18+/-0.01 for EPA. Transfer efficiency of SDA to milk fat represented 39.3% (range=36.8 to 41.9%) of the abomasally infused SDA and 47.3% (range=45.0 to 49.6%) when the n-3 fatty acids downstream from SDA were included. In contrast, transfer of ruminally infused SDA to milk fat averaged only 1.7% (range=1.3 to 2.1%), indicating extensive rumen biohydrogenation. Overall, results demonstrate the potential to use SDA-enhanced SBO from genetically modified soybeans combined with proper ruminal protection to achieve impressive increases in the milk fat content of SDA and other n-3 fatty acids that are beneficial for human health.

Modulation of gut-associated lymphoid tissue functions with genetically modified Lactococcus lactis

Rottiers P, De Smedt T, Steidler L
Int Rev Immunol. 2009;28(6):465-86

Lactic acid bacteria are a group of taxonomically diverse, Gram-positive food-grade bacteria that have been safely consumed throughout history. The lactic acid bacterium Lactococcus lactis, well-known for its use in the manufacture of cheese, can be genetically engineered and orally formulated to deliver therapeutic proteins in the gastrointestinal tract. This review focuses on the genetic engineering of Lactococcus lactis to secrete high-quality, correctly processed bioactive molecules derived from a eukaryotic background. The therapeutic applications of these genetically modified strains are discussed, with special regards to immunomodulation.

Recent progress of flower colour modification by biotechnology

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Int J Mol Sci. 2009 Dec 15;10(12):5350-69.

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Genetically-modified, colour-altered varieties of the important cut-flower crop carnation have now been commercially available for nearly ten years. In this review we describe the manipulation of the anthocyanin biosynthesis pathway that has lead to the development of these varieties and how similar manipulations have been successfully applied to both pot plants and another cut-flower species, the rose. From this experience it is clear that down- and up-regulation of the flavonoid and anthocyanin pathway is both possible and predictable. The major commercial benefit of the application of this technology has so far been the development of novel flower colours through the development of transgenic varieties that produce, uniquely for the target species, anthocyanins derived from delphinidin. These anthocyanins are ubiquitous in nature, and occur in both ornamental plants and common food plants. Through the extensive regulatory approval processes that must occur for the commercialization of genetically modified organisms, we have accumulated considerable experimental and trial data to show the accumulation of delphinidin based anthocyanins in the transgenic plants poses no environmental or health risk.

A comparison of the effects of three GM corn varieties on mammalian health

de Vendômois JS, Roullier F, Cellier D, Séralini GE
Int J Biol Sci.;5(7):706-26.

We present for the first time a comparative analysis of blood and organ system data from trials with rats fed three main commercialized genetically modified (GM) maize (NK 603, MON 810, MON 863), which are present in food and feed in the world. NK 603 has been modified to be tolerant to the broad spectrum herbicide Roundup and thus contains residues of this formulation. MON 810 and MON 863 are engineered to synthesize two different Bt toxins used as insecticides. Approximately 60 different biochemical parameters were classified per organ and measured in serum and urine after 5 and 14 weeks of feeding. GM maize-fed rats were compared first to their respective isogenic or parental non-GM equivalent control groups. This was followed by comparison to six reference groups, which had consumed various other non-GM maize varieties. We applied nonparametric methods, including multiple pairwise comparisons with a False Discovery Rate approach. Principal Component Analysis allowed the investigation of scattering of different factors (sex, weeks of feeding, diet, dose and group). Our analysis clearly reveals for the 3 GMOs new side effects linked with GM maize consumption, which were sex- and often dose-dependent. Effects were mostly associated with the kidney and liver, the dietary detoxifying organs, although different between the 3 GMOs. Other effects were also noticed in the heart, adrenal glands, spleen and haematopoietic system. We conclude that these data highlight signs of hepatorenal toxicity, possibly due to the new pesticides specific to each GM corn. In addition, unintended direct or indirect metabolic consequences of the genetic modification cannot be excluded.

Cloned animal products in the human food chain: FDA should protect American consumers

Butler JE
Food Drug Law J. 2009;64(3):473-501.

Animal cloning is "complex process that lets one exactly copy the genetic, or inherited, traits of an animal." In 1997, Dolly the sheep was the first animal cloned and since then "scientists have used animal cloning to breed dairy cows, beef cattle, poultry, hogs and other species of livestock." Cloned animals are highly attractive to livestock breeders because "cloning essentially produces an identical copy of an animal with superior traits." The main purpose of cloning livestock is "more focused on efficiency and economic benefits of the producer rather than the overall effect of cloning on an animal's physical and mental welfare." The focus of this article is threefold. First, the science behind animal cloning is explained and some potential uses and risks of this technology are explored. Second, FDA's historical evolution, current regulatory authority, and limitations of that authority, is described. Lastly, a new regulatory vision recognizes the realities of 21st century global markets and the dynamic evolution of scientific discovery and technology.

The use of viral vectors in introducing genes into agricultural animal species

Modric T, Mergia A
Anim Biotechnol. 2009;20(4):216-30.

The use of viral vectors is a method for introducing foreign genes into various animal species. Vectors based on retro-, adeno-, flavi-, and parvoviruses have been used for research in animal species of agricultural importance, such as chickens, quail, swine, cows, goats, sheep, fish, crustaceans, and mollusks. Viral vectors allow for efficient transgenic integration into host genome or for transient expression of the transgenic construct in somatic tissues. Because of that, viral vectors are important tools for research and potentially other biotechnology applications such as improving animal production qualities and introducing disease resistance, thus improving food quality and safety. Other uses may include generating animal models of human diseases and using animals as bioreactors for production of therapeutic proteins. Each vector type provides a unique set of advantages and limitations, which are in some cases specific to an animal species or a method of introduction. This article discusses viral vector characteristics and potential applications in agriculturally important animal species. It discusses advantages and disadvantages of using viral vectors in genetic engineering of agricultural animals.

Unearthing the roles of imprinted genes in the placenta

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Placenta. 2009 Oct;30(10):823-34.

Mammalian fetal survival and growth are dependent on a well-established and functional placenta. Although transient, the placenta is the first organ to be formed during pregnancy and is responsible for important functions during development, such as the control of metabolism and fetal nutrition, gas and metabolite exchange, and endocrine control. Epigenetic marks and gene expression patterns in early development play an essential role in embryo and fetal development. Specifically, the epigenetic phenomenon known as genomic imprinting, represented by the non-equivalence of the paternal and maternal genome, may be one of the most important regulatory pathways involved in the development and function of the placenta in eutherian mammals. A lack of pattern or an imprecise pattern of genomic imprinting can lead to either embryonic losses or a disruption in fetal and placental development. Genetically modified animals present a powerful approach for revealing the interplay between gene expression and placental function in vivo and allow a single gene disruption to be analyzed, particularly focusing on its role in placenta function. In this paper, we review the recent transgenic strategies that have been successfully created in order to provide a better understanding of the epigenetic patterns of the placenta, with a special focus on imprinted genes. We summarize a number of phenotypes derived from the genetic manipulation of imprinted genes and other epigenetic modulators in an attempt to demonstrate that gene-targeting studies have contributed considerably to the knowledge of placentation and conceptus development.

Transgenic plants as vital components of integrated pest management

Kos M, van Loon JJ, Dicke M, Vet LE
Trends Biotechnol. 2009 Nov;27(11):621-7.

Although integrated pest management (IPM) strategies have been developed worldwide, further improvement of IPM effectiveness is required. The use of transgenic technology to create insect-resistant plants can offer a solution to the limited availability of highly insect-resistant cultivars. Commercially available insect-resistant transgenic crops show clear benefits for agriculture and there are many exciting new developments such as transgenic plants that enhance biological control. Effective evaluation tools are needed to ascertain that transgenic plants do not result in undesired non-target effects. If these conditions are met, there will be ample opportunities for transgenic plants to become key components of environmentally benign and durable pest management systems. Here we discuss the potential and challenges for incorporating transgenic plants in IPM.

Perceptions, knowledge and ethical concerns with GM foods and the GM process

Knight AJ
Public Underst Sci. 2009 Mar;18(2):177-88.

Compared to their European counterparts, the American public has been characterized as relatively unknowledgeable and indifferent about genetically modified foods. To evaluate these claims, six focus groups were held in three Arkansas cities to: (1) determine the extent of knowledge the public possesses about genetically modified foods; (2) detail perceived benefits and risks associated with agricultural biotechnology applications; and (3) explore lay perceptions about the genetic modification process itself. Participants demonstrated partial knowledge, and tended to overestimate the number of genetically modified foods. However, participants tended to be familiar with debates surrounding benefits, risks and moral issues associated with agricultural biotechnology applications. Findings also showed that while participants were not overly concerned about combining genes between plants, they were concerned about inserting animal genes into plants. If these results are any indication, moral and ethical issues will dominate any discussion of foods derived from a mixture of animal and plant genes.

Review of animal models designed to predict the potential allergenicity of novel proteins in genetically modified crops

Ladics GS, Knippels LM, Penninks AH, Bannon GA, Goodman RE, Herouet-Guicheney C
Regul Toxicol Pharmacol. 2009 Oct 1.

The safety assessment of genetically modified crops involves the evaluation of the potential allergenicity of novel proteins by using several in silico and in vitro endpoints. In this publication, the variables and questions associated with the development of in vivo models are examined and several unpublished results are presented. Both rodent and non-rodent (dog and pig) models have been investigated using various routes of administration with purified proteins or food extracts, with or without the use of an adjuvant. The ideal model should be simple, reproducible across laboratories over time, specific and sensitive enough for distinguishing a threshold beyond which relevant allergenicity would be predicted and, for ranking proteins correlated with the allergic responses in humans, and acceptable under animal care. Preliminary data suggest that a few appear promising; however, further evaluation of these models is required. In particular, more extensive validation testing with additional allergenic and non-allergenic material should be performed before using them in the safety assessment of genetically modified crops.

Molecular toolbox for the identification of unknown genetically modified organisms

Ruttink T, Demeyer R, Van Gulck E, Van Droogenbroeck B, Querci M, Taverniers I, De Loose M
Anal Bioanal Chem. 2009 Nov 25.

Competent laboratories monitor genetically modified organisms (GMOs) and products derived thereof in the food and feed chain in the framework of labeling and traceability legislation. In addition, screening is performed to detect the unauthorized presence of GMOs including asynchronously authorized GMOs or GMOs that are not officially registered for commercialization (unknown GMOs). Currently, unauthorized or unknown events are detected by screening blind samples for commonly used transgenic elements, such as p35S or t-nos. If (1) positive detection of such screening elements shows the presence of transgenic material and (2) all known GMOs are tested by event-specific methods but are not detected, then the presence of an unknown GMO is inferred. However, such evidence is indirect because it is based on negative observations and inconclusive because the procedure does not identify the causative event per se. In addition, detection of unknown events is hampered in products that also contain known authorized events. Here, we outline alternative approaches for analytical detection and GMO identification and develop new methods to complement the existing routine screening procedure. We developed a fluorescent anchor-polymerase chain reaction (PCR) method for the identification of the sequences flanking the p35S and t-nos screening elements. Thus, anchor-PCR fingerprinting allows the detection of unique discriminative signals per event. In addition, we established a collection of in silico calculated fingerprints of known events to support interpretation of experimentally generated anchor-PCR GM fingerprints of blind samples. Here, we first describe the molecular characterization of a novel GMO, which expresses recombinant human intrinsic factor in Arabidopsis thaliana. Next, we purposefully treated the novel GMO as a blind sample to simulate how the new methods lead to the molecular identification of a novel unknown event without prior knowledge of its transgene sequence. The results demonstrate that the new methods complement routine screening procedures by providing direct conclusive evidence and may also be useful to resolve masking of unknown events by known events.