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#### Chapter

## Breastfeeding and Gut Microbiota

Bita Najafian and Mohammad Hossein Khosravi

#### Abstract

Human breast milk (HBM) not only is a source of nutrition for infants but also contains a variety of biologically active components and bacterial species. These molecules and bacteria guide both intestinal microbiota and infantile immune system. Recently published studies have found several vital roles for gut microbiota including effects on the individual's personality, decreased predisposition to the diseases, and a variety of other health-related consequences such as possible therapeutic effects or preventing role. In this chapter the components of human breast milk and its effect on shaping the human gut microbiota have been reviewed.

Keywords: breastfeeding, gut microbiota, breast milk, microbiome

#### 1. Introduction

Today, there is no doubt that human breast milk is the most beneficial source of nutrition for infants which is the result of several years of research and evaluation. Beside known nutrients such as proteins and carbohydrates, human breast milk contains a wide range of biologically active components and microbiota [1]. Previous researches have shown that mother's intestinal microbiome is transferred to her infant through breast milk. This relationship between mother and infant plays the key role in forming a healthy intestinal microbiome which is responsible for protecting against diarrheal and respiratory illnesses as well as asthma, obesity, diabetes, atopy, and other inflammatory diseases such as inflammatory bowel diseases (IBD) [2, 3]. The presence of bacteria in human breast milk not only improves the infantile health but also promotes mother's health by a variety of mechanisms such as preventing mastitis [4]. Human milk oligosaccharides (HMOs) have the main role in developing the intestinal microbiota [1]. Their synthesis is determined by maternal genotype.

Transferring immunity from mother to infant is started from the intrauterine life and is continued by breastfeeding. Breast milk includes antibodies and immunities targeting the mother's gut and airway microbes with which her infant is likely to encounter during the very first months of birth [5]. Recently conducted researches have revealed that breast milk directly modulates the development of immune system in breastfed infants as well as provides passive protection [6].

Colostrum is the most enriched part of the breast milk of immune factors which provides an appropriate immune response when the infant is at risk of exposure to new microbes [7]. Hormones, cytokines, growth factors, chemokines, and immunoglobulins are among the bioactive factors that are transferred to infant via breastfeeding [7, 8]. In this chapter a comprehensive review has been done on the role of breastfeeding and breast milk ingredients in forming infant's intestinal microbiota.

#### 2. Microbial components of breast milk

Before year 2000, human breast milk (HBM) was considered to be sterile. Martin et al. mentioned the presence of commensal and probiotic bacteria in HBM [9]. Lactobacillus fermentum and Lactobacillus gasseri were more commonly found in breast milk samples using culture-dependent techniques [10]. Today, lactic acid bacterial strains with proven probiotic activities are referred to as probiotics [11]. Every milliliter of breast milk contains about 1000 colony-forming units of various bacterial species [12, 13]. An estimation reveals that infants receive about 800,000 bacteria from breast milk each day [14]. At birth and during delivery, infants receive a notable dose of microbes through different mechanisms such as vaginal flora which is followed by the first breastfeeding [15]. So, breast milk is the second important source of microbiota seeding in the infant's intestines [16, 17]. This has been proven by several previous epidemiologic studies in which the researchers have reported fundamental differences in gut microbiota between breastfed and formula-fed infants [18, 19]. Previous conducted researches have revealed that infantile stool and breast milk have some microbial strains, such as *Enterococcus*, Staphylococcus, Bifidobacterium, and Lactobacillus, in common [20, 21]. It also has been reported that more daily breastfeeding is attributed to more similarity between mother's milk and infant stool microbiome [17].

Newly developed methods, such as next generation sequencing, have augmented our knowledge regarding microbial composition of human breast milk. *Staphylococcus* and *Streptococcus* have been reported to be the most common microbiota families in the human's breast milk. Other families including *Bifidobacterium*, *Lactobacillus*, and *Enterobacteriaceae* family members are placed in the following ranks [22, 23]. Colostrum contains a more various number of bacterial species than do transitional and mature milk.

So far, we have no idea where the mother's milk microbiota exactly comes from; however a number of theories have come up. The first one considers that retrograde flow of breast milk from the infant's mouth to the areola and commensal skin area contaminates the milk with maternal skin flora; however, the presence of anaerobic species does not justify the commensal contamination [24–26]. On the other hand, Streptococcus which is abundant in salivary flora is also common in human breast milk microbiome, supporting the retrograde flow theory [27]. The theory of retrograde flow was first mentioned by Ramsay and colleagues where they used ultrasound technology to study the huge transmission of breast milk from the infant's mouth to the mammary gland ducts [25]. Another theory holds this belief that breast milk microbiota are originated from mother's intestinal flora, where they migrate via blood and lymphatic circulation to the mammary glands [27, 28]. Studying pregnant and lactating mice revealed that both aerobic and anaerobic organisms are translocated from gut to the mesenteric lymph nodes and mammary glands, subsequently [28]. In addition, another research team found that there are similar bacterial signatures in breast milk, lymph nodes, and dendritic cells (DC) of lactating mice [29]. Hormonal changes in late pregnancy and increased permeability of the intestinal endothelium are considered to have a supporting role for translocation of intestinal bacteria to mammary glands [27]. Hence, the origin of breast milk microbiota should be more investigated.

A variety of maternal factors have effects on the diversity of mother's milk microbiota. Previously published studies have reported that mothers with vaginal delivery have more various microbial species in their breast milk than that of those who deliver by cesarean section [30, 31]. Also, it has been reported that there is no remarkable difference for milk bacterial concentration between different genders

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or race groups as well as geographical regions [32, 33]. Various types of breast milk have different bacterial concentrations as the colostrum has lower concentrations than do transitional and mature milk. Results from comparative clinical studies have revealed that breast milk bacterial composition is affected by maternal health condition such as obesity, human immunodeficiency virus (HIV), and celiac disease [34, 35]. Also, it is expectable that maternal chemotherapy and antibiotic use decrease the microbial diversity in mother's milk [36, 37].

#### 3. Mammary gland microbiome

Recently, many efforts have been made to determine the mammary gland bacteriome in different ways [38, 39]. Biopsies from different sites of the breast have approved the viability of bacteria by culture. Human breast tissue bacteriome was shown to be similar to those of the human breast milk where the *Proteobacteria* is the main phylum [40]. Also, nipple aspirate fluid (NAF) has been recently used to determine the breast ductal bacteriome. NAF, which is secreted regularly by breast duct endothelial cells, can be easily collected using a syringe connected to the suction cup applied with a negative pressure [41, 42].

#### 4. Infant gut and what breast milk microbiota has to do

#### 4.1 HBM microbiome as anti-infective

It is believed that breast milk microbiota reduces the incidence of bacterial infections through a variety of mechanisms in breastfed infants. Commensal bacteria modulate growth and replication of pathogen bacteria through their antimicrobial power or as a result of competitive exclusion; as the *Escherichia coli*, *Shigella*, or *Salmonella* strains are inhibited by lactobacilli isolated from human breast milk [43, 44]. In a randomized clinical trial, researchers prescribed breast milk lactobacilli to infants between 6 and 12 months of age which reduced the total incidence of infections [45]. There are a variety of studies which have assessed the antimicrobial activity of the intestine; however; more studies should be conducted for assessing antimicrobial specificities of human breast milk.

#### 4.2 Immunomodulatory role

Animal studies have shown an important role for gut microbiota in increasing and modulating immune functions [46–48]. Lymphoid tissue development was shown to be altered in organs such as the spleen, lymph nodes, and thymus when there is a reduced number of microbiota in the animal intestines. The intestines without any germs have shown reduced numbers of IgA-producing cells, lamina propria CD4+ cells, and hypoplastic Peyer's patches [49]. Production of Th1 cytokines including Il-2, Il-12, and TNF-alpha by macrophages has been shown to be augmented by breast milk lactobacillus strains. Recently conducted studies have shown an improved immunologic and better Th1 response in breastfed infants that that of those fed by formula [50]. *Lactobacillus fermentum* and *Lactobacillus salivarius* have been reported as potent activators of natural killer cells and both innate and acquired immunity as a result of in vitro studies [51]. In addition, human milk metagenome has been shown to contain immunomodulatory DNA motifs which may help modulate exaggerated inflammatory responses to bacterial infection [52]. Most of these regulatory effects were not found in non-milk-derived probiotic bacteria [51].

#### 4.3 Anti-allergic role

A protective association has been discovered between human breast milk lactic acid bacteria and allergies. The main etiology of allergy has been described as the disturbance in regulation of immune system [53]. Previously published animal studies have revealed that probiotic bacteria originated from human breast milk, such as *Lactobacillus gasseri* and *Lactobacillus coryniformis*, have a modulatory role for immune response in cow milk protein sensitivity [54]. However, a conducted randomized clinical trial has shown that prescribing probiotics in the first 6 months of life does not reduce the risk of atopic eczema [55]. Other similar studies have reported that prescribing specific *Lactobacillus* and *Bifidobacterium* species to mothers has led to a reduced incidence of infant eczema in the first 2 years of life [56, 57]. This anti-allergy property of probiotics has been attributed to the downregulation in the production of Th2 cytokines by the hygiene hypothesis [54]. Another clinical study has reported that infants who have more *Klebsiella* species, as the dominant bacteria in their gut, have a higher chance for involving with Atopia, whereas the presence of *Viridans streptococci* in the gut microbiome has the contrary role [58].

#### 4.4 Antitumor properties

However not many studies have been conducted for assessing antitumor properties of the gut microbiome; there are some points in the literature [59]. *Enterococcus faecalis* and *Staphylococcus hominis*, which are isolated from human breast milk, have shown some antitumor properties against a breast cancer cell line [60]. Another similar study has reported that a subspecies of *Lactococcus lactis* has shown therapeutic effect against colon cancer [61].

#### 5. Conclusion

In this chapter we went through the definition and application of human breast milk microbiome and its role on building infant gut microbiome as well as infant's health and disease. Also mentioned is that this gut microbiome may play important roles as anti-infective, immunomodulatory, and anticancer properties. As the importance of breast milk microbiome is getting more notices, further studies should be conducted to assess it more and provide some ways for enriching mother's milk microbiome with beneficial bacteria.

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#### References

[1] Le Doare K, Holder B, Bassett A, Pannaraj PS. Mother's milk: A purposeful contribution to the development of the infant microbiota and immunity. Frontiers in Immunology. 2018;**9**:361

[2] Xu L, Lochhead P, Ko Y, Claggett B, Leong RW, Ananthakrishnan AN. Systematic review with meta-analysis: Breastfeeding and the risk of Crohn's disease and ulcerative colitis. Alimentary Pharmacology & Therapeutics. 2017;**46**(9):780-789

[3] Azad MB, Vehling L, Lu Z, Dai D, Subbarao P, Becker AB, et al. Breastfeeding, maternal asthma and wheezing in the first year of life: A longitudinal birth cohort study. European Respiratory Journal. 2017;**49**(5):1602019

[4] Jiménez E, de Andrés J, Manrique M, Pareja-Tobes P, Tobes R, Martínez-Blanch JF, et al. Metagenomic analysis of milk of healthy and mastitis-suffering women. Journal of Human Lactation. 2015;**31**(3):406-415

[5] Brandtzaeg P. The mucosal immune system and its integration with the mammary glands. The Journal of Pediatrics. 2010;**156**(2):S8-S15

[6] Mueller NT, Bakacs E, Combellick J, Grigoryan Z, Dominguez-Bello MG. The infant microbiome development: Mom matters. Trends in Molecular Medicine. 2015;**21**(2):109-117

[7] Ballard O, Morrow AL. Human milk composition: Nutrients and bioactive factors. Pediatric Clinics. 2013;**60**(1):49-74

[8] Andreas NJ, Kampmann B, Le-Doare KM. Human breast milk: A review on its composition and bioactivity. Early Human Development. 2015;**91**(11):629-635

[9] Civardi E, Garofoli F, Tzialla C, Paolillo P, Bollani L, Stronati M.
Microorganisms in human milk: Lights and shadows. The Journal of Maternal-Fetal & Neonatal Medicine.
2013;26(sup2):30-34

[10] Martín R, Langa S, Reviriego C, Jimínez E, Marín ML, Xaus J, et al. Human milk is a source of lactic acid bacteria for the infant gut. The Journal of Pediatrics. 2003;**143**(6):754-758

[11] Mohania D, Nagpal R, Kumar M, Bhardwaj A, Yadav M, Jain S, et al. Molecular approaches for identification and characterization of lactic acid bacteria. Journal of Digestive Diseases. 2008;**9**(4):190-198

[12] Cabrera-Rubio R, Collado MC, Laitinen K, Salminen S, Isolauri E, Mira A. The human milk microbiome changes over lactation and is shaped by maternal weight and mode of delivery. The American Journal of Clinical Nutrition. 2012;**96**(3):544-551

[13] Jeurink P, Van Bergenhenegouwen J, Jiménez E, Knippels L, Fernández L, Garssen J, et al. Human milk: A source of more life than we imagine. Beneficial Microbes. 2013;4(1):17-30

[14] Heikkilä MP, Saris P. Inhibition of *Staphylococcus aureus* by the commensal bacteria of human milk.
Journal of Applied Microbiology.
2003;95(3):471-478

[15] Dominguez-Bello MG, Costello EK, Contreras M, Magris M, Hidalgo G, Fierer N, et al. Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns. Proceedings of the National Academy of Sciences. 2010;**107**(26):11971-11975

#### Breastfeeding and Gut Microbiota DOI: http://dx.doi.org/10.5772/intechopen.92404

[16] Gritz EC, Bhandari V. The human neonatal gut microbiome: A brief review. Frontiers in Pediatrics. 2015;**3**:17

[17] Pannaraj PS, Li F, Cerini C, Bender JM, Yang S, Rollie A, et al. Association between breast milk bacterial communities and establishment and development of the infant gut microbiome. JAMA Pediatrics. 2017;**171**(7):647-654

[18] Azad MB, Konya T, Maughan H, Guttman DS, Field CJ, Chari RS, et al. Gut microbiota of healthy Canadian infants: Profiles by mode of delivery and infant diet at 4 months. CMAJ. 2013;**185**(5):385-394

[19] Gomez-Llorente C, Plaza-Diaz J, Aguilera M, Muñoz-Quezada S, Bermudez-Brito M, Peso-Echarri P, et al. Three main factors define changes in fecal microbiota associated with feeding modality in infants. Journal of Pediatric Gastroenterology and Nutrition. 2013;57(4):461-466

[20] Martín V, Maldonado-Barragán A, Moles L, Rodriguez-Baños M, Campo RD, Fernández L, et al. Sharing of bacterial strains between breast milk and infant feces. Journal of Human Lactation. 2012;**28**(1):36-44

[21] Benito D, Lozano C, Jiménez E, Albújar M, Gómez A, Rodríguez JM, et al. Characterization of *Staphylococcus aureus* strains isolated from faeces of healthy neonates and potential mother-to-infant microbial transmission through breastfeeding. FEMS Microbiology Ecology. 2015;**91**(3):fiv007

[22] Hunt KM, Foster JA, Forney LJ, Schütte UM, Beck DL, Abdo Z, et al. Characterization of the diversity and temporal stability of bacterial communities in human milk. PLoS One. 2011;**6**(6)

[23] Fitzstevens JL, Smith KC, Hagadorn JI, Caimano MJ, Matson AP, Brownell EA. Systematic review of the human milk microbiota. Nutrition in Clinical Practice. 2017;**32**(3):354-364

[24] Urbaniak C, Gloor GB, Brackstone M, Scott L, Tangney M, Reid G. The microbiota of breast tissue and its association with breast cancer. Applied and Environmental Microbiology. 2016;**82**(16):5039-5048

[25] Ramsay DT, Kent JC, Owens RA, Hartmann PE. Ultrasound imaging of milk ejection in the breast of lactating women. Pediatrics. 2004;**113**(2):361-367

[26] Biagi E, Quercia S, Aceti A, Beghetti I, Rampelli S, Turroni S, et al. The bacterial ecosystem of mother's milk and infant's mouth and gut. Frontiers in Microbiology. 2017;**8**:1214

[27] Rodríguez JM. The origin of human milk bacteria: Is there a bacterial entero-mammary pathway during late pregnancy and lactation? Advances in Nutrition. 2014;5(6):779-784

[28] Perez PF, Doré J, Leclerc M, Levenez F, Benyacoub J, Serrant P, et al. Bacterial imprinting of the neonatal immune system: Lessons from maternal cells? Pediatrics. 2007;**119**(3):e724-ee32

[29] Zhou X, Voigt A, Paveglio S, Weinstock G, Matson A, Davidovics Z. Similar bacterial signatures in intestinal tissues, milk, and dendritic cells of lactating mice suggest a possible enteromammary pathway. Gastroenterology. 2017;**152**(5):S172

[30] Cabrera-Rubio R, Mira-Pascual L, Mira A, Collado M. Impact of mode of delivery on the milk microbiota composition of healthy women. Journal of Developmental Origins of Health and Disease. 2016;7(1):54-60

[31] Khodayar-Pardo P, Mira-Pascual L, Collado M, Martínez-Costa C. Impact of lactation stage, gestational age and mode of delivery on breast milk microbiota. Journal of Perinatology. 2014;**34**(8):599-605

[32] Urbaniak C, Angelini M, Gloor GB, Reid G. Human milk microbiota profiles in relation to birthing method, gestation and infant gender. Microbiome. 2016;**4**(1):1

[33] Kumar H, du Toit E, Kulkarni A, Aakko J, Linderborg KM, Zhang Y, et al. Distinct patterns in human milk microbiota and fatty acid profiles across specific geographic locations. Frontiers in Microbiology. 2016;7:1619

[34] Olivares M, Albrecht S, De Palma G, Ferrer MD, Castillejo G, Schols HA, et al. Human milk composition differs in healthy mothers and mothers with celiac disease. European Journal of Nutrition. 2015;**54**(1):119-128

[35] González R, Mandomando I, Fumadó V, Sacoor C, Macete E, Alonso PL, et al. Breast milk and gut microbiota in African mothers and infants from an area of high HIV prevalence. PLoS One. 2013;8(11)

[36] Soto A, Martín V, Jiménez E, Mader I, Rodríguez JM, Fernández L. Lactobacilli and bifidobacteria in human breast milk: Influence of antibiotherapy and other host and clinical factors. Journal of Pediatric Gastroenterology and Nutrition. 2014;**59**(1):78

[37] Urbaniak C, McMillan A, Angelini M, Gloor GB, Sumarah M, Burton JP, et al. Effect of chemotherapy on the microbiota and metabolome of human milk, a case report. Microbiome. 2014;**2**(1):24

[38] Urbaniak C, Cummins J, Brackstone M, Macklaim JM, Gloor GB, Baban CK, et al. Microbiota of human breast tissue. Applied and Environmental Microbiology. 2014;**80**(10):3007-3014

[39] Hieken TJ, Chen J, Hoskin TL, Walther-Antonio M, Johnson S, Ramaker S, et al. The microbiome of aseptically collected human breast tissue in benign and malignant disease. Scientific Reports. 2016;**6**:30751

[40] Murphy K, Curley D, O'Callaghan TF, O'Shea C-A, Dempsey EM, O'Toole PW, et al. The composition of human milk and infant faecal microbiota over the first three months of life: A pilot study. Scientific Reports. 2017;7(1):1-10

[41] Chan AA, Bashir M, Rivas MN, Duvall K, Sieling PA, Pieber TR, et al. Characterization of the microbiome of nipple aspirate fluid of breast cancer survivors. Scientific Reports. 2016;**6**(1):1-11

[42] Petrakis NL. Nipple aspirate fluid in epidemiologic studies of breast disease. Epidemiologic Reviews. 1993;**15**(1):188-195

[43] Jara S, Sánchez M, Vera R, Cofré J, Castro E. The inhibitory activity of Lactobacillus spp. isolated from breast milk on gastrointestinal pathogenic bacteria of nosocomial origin. Anaerobe. 2011;**17**(6):474-477

[44] Lyons A, O'mahony D, O'brien F, MacSharry J, Sheil B, Ceddia M, et al. Bacterial strain-specific induction of Foxp3+ T regulatory cells is protective in murine allergy models. Clinical and Experimental Allergy. 2010;**40**(5):811-819

[45] Maldonado J, Cañabate F, Sempere L, Vela F, Sánchez AR, Narbona E, et al. Human milk probiotic *Lactobacillus fermentum* CECT5716 reduces the incidence of gastrointestinal and upper respiratory tract infections in infants. Journal of Pediatric Gastroenterology and Nutrition. 2012;**54**(1):55-61

[46] Arrieta M-C, Stiemsma LT, Amenyogbe N, Brown EM, Finlay B. The intestinal microbiome in early life: Breastfeeding and Gut Microbiota DOI: http://dx.doi.org/10.5772/intechopen.92404

Health and disease. Frontiers in Immunology. 2014;**5**:427

[47] Gensollen T, Iyer SS, Kasper DL, Blumberg RS. How colonization by microbiota in early life shapes the immune system. Science. 2016;**352**(6285):539-544

[48] Walker WA, Iyengar RS. Breast milk, microbiota, and intestinal immune homeostasis. Pediatric Research. 2015;77(1-2):220-228

[49] Macpherson AJ, Harris NL. Interactions between commensal intestinal bacteria and the immune system. Nature Reviews. Immunology. 2004;**4**(6):478-485

[50] Pabst H, Spady D, Pilarski L, Carson M, Beeler J, Krezolek M. Differential modulation of the immune response by breast-or formulafeeding of infants. Acta Paediatrica. 1997;**86**(12):1291-1297

[51] Perez-Cano FJ, Dong H, Yaqoob P. In vitro immunomodulatory activity of *Lactobacillus fermentum* CECT5716 and *Lactobacillus salivarius* CECT5713: Two probiotic strains isolated from human breast milk. Immunobiology.
2010;215(12):996-1004

[52] Ward TL, Hosid S, Ioshikhes I, Altosaar I. Human milk metagenome: A functional capacity analysis. BMC Microbiology. 2013;**13**(1):116

[53] Prokopakis E, Vardouniotis A, Kawauchi H, Scadding G, Georgalas C, Hellings P, et al. The pathophysiology of the hygiene hypothesis. International Journal of Pediatric Otorhinolaryngology. 2013;77(7): 1065-1071

[54] Lara-Villoslada F, Olivares M, Sierra S, Rodríguez JM, Boza J, Xaus J. Beneficial effects of probiotic bacteria isolated from breast milk. British Journal of Nutrition. 2007;**98**(S1):S96-S100

[55] Taylor AL, Dunstan JA, Prescott SL. Probiotic supplementation for the first 6 months of life fails to reduce the risk of atopic dermatitis and increases the risk of allergen sensitization in high-risk children: A randomized controlled trial. Journal of Allergy and Clinical Immunology. 2007;**119**(1):184-191

[56] Abrahamsson TR, Jakobsson T, Böttcher MF, Fredrikson M, Jenmalm MC, Björkstén B, et al. Probiotics in prevention of IgEassociated eczema: A double-blind, randomized, placebo-controlled trial. Journal of Allergy and Clinical Immunology. 2007;**119**(5):1174-1180

[57] Kim JY, Kwon JH, Ahn SH,
Lee SI, Han YS, Choi YO, et al. Effect of probiotic mix (*Bifidobacterium bifidum*, *Bifidobacterium lactis*, *Lactobacillus acidophilus*) in the primary prevention of eczema: A double-blind, randomized, placebo-controlled trial.
Pediatric Allergy and Immunology.
2010;21(2p2):e386-ee93

[58] Kirjavainen PV, Apostolou E, Arvola T, Salminen SJ, Gibson GR, Isolauri E. Characterizing the composition of intestinal microflora as a prospective treatment target in infant allergic disease. FEMS Immunology and Medical Microbiology. 2001;**32**(1):1-7

[59] Ojo-Okunola A, Nicol M, Du Toit E. Human breast milk bacteriome in health and disease. Nutrients. 2018;**10**(11):1643

[60] Hassan Z, Mustafa S, Rahim RA, Isa NM. Anti-breast cancer effects of live, heat-killed and cytoplasmic fractions of *Enterococcus faecalis* and *Staphylococcus hominis* isolated from human breast milk. In Vitro Cellular & Developmental Biology. Animal. 2016;**52**(3):337-348 Infant Feeding - Breast versus Formula

[61] Kim JY, Woo HJ, Kim Y-S, Kim KH, Lee HJ. Cell cycle dysregulation induced by cytoplasm of *Lactococcus lactis* ssp. lactis in SNUC2A, a colon cancer cell line. Nutrition and Cancer. 2003;**46**(2):197-201

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