

A multi-omics integrated study deciphers biology of the rumen and lipid metabolism

YANG Ji & LI Meng-Hua*

CAS Key Laboratory of Animal Ecology and Conservation Biology, Institute of Zoology, Chinese Academy of Sciences, Beijing 100101, China

Received July 10, 2014; accepted July 17, 2014; published online July 30, 2014

Citation: Yang J, Li MH. A multi-omics integrated study deciphers biology of the rumen and lipid metabolism. *Sci China Life Sci*, 2014, 57: 951–953, doi: 10.1007/s11427-014-4718-y

Sheep (*Ovis aries*), as one of the earliest domesticated ruminant livestock, can effectively make use of plant fibers via the rumen, and provide multiple products such as meat, milk and wool for human. However, molecular mechanism of the digestion and lipid metabolism for ruminants has been largely unexplored. The publishing of the complete genomes of cattle (*Bos taurus*) in 2009 [1] and later two other ruminant livestock, i.e., yak [2] and goat [3], have opened a new window to the biology and evolution of ruminants. Quite recently, *Science* published a high-quality sheep reference genome assembly and its comparisons with those of goat and cattle. The findings identified two sets of genes that are associated with rumen evolution and lipid metabolism, respectively [4].

This study was conducted by an international collaborative team led by Prof. Wang Wen from Kunming Institute of Zoology, Chinese Academy of Sciences, consisting of as many as 63 researchers from 27 institutions in China, USA, UK, EU, Australia and New Zealand. By performing syntenic comparisons across the 11 mammalian genomes (Figure 1), the investigators identified 321 expanded gene subfamilies in the ruminant branch, of which 73 were ruminant specific. By further integrating RNA-Seq transcriptome data and a survey of gene structure, the researchers found that multiple ruminant specific genes show copy number variations (CNVs) and/or tissue-specific gene expression, particularly for the genes involved in the evolution

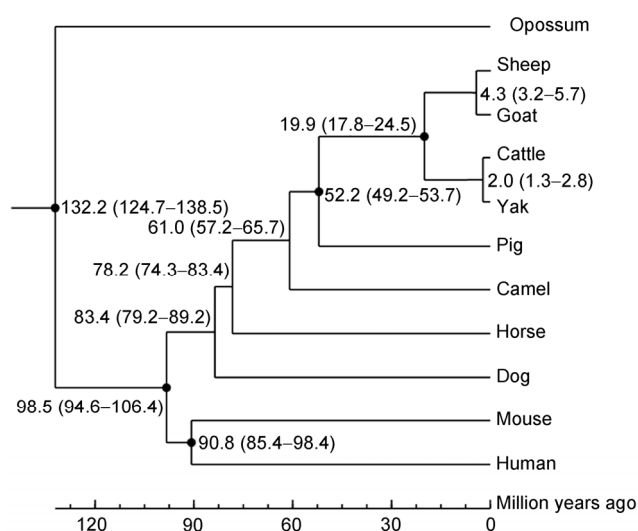


Figure 1 Phylogenetic tree constructed from the 4850 single-copy orthologous genes on 4-fold degenerate sites using the MrBayes program. The divergence time before present (Mya) and its confidence interval of the selected species were generated by the PAML McMc algorithm based on the molecular clock model.

of rumen and lipid metabolism [4].

The rumen is a highly specialized organ harboring a complex microbial flora. To my best knowledge, Dr. Jiang and his colleagues for the first time identified several previously not or poorly annotated genes such as *TCHHL2*, *PRD-SPRR11* and *LCE7A*, which are specifically expressed

*Corresponding author (email: menghua.li@ioz.ac.cn)

in the rumen [4]. These genes encode proteins related to keratinized epidermal structure development and play important roles in the formation of rumen substrate surface. Identification and characterization of these novel rumen specific structural proteins have provided critical insights into understanding the modified functions during rumen evolution.

Ruminants have a specialized metabolic pathway for the utilization of volatile fatty acids (VFAs), which are their major nutritional resource. Dr. Jiang and his colleagues revealed that in contrast to almost all other mammals (being single-copy), monoacylglycerol-O-acyltransferase (MOGAT3) have multiple duplicated copies in the genomes of cattle, sheep and goat. Different copies of the gene show highly differentiated levels of expression between skin and liver or duodenum in sheep. However, MOGAT3 is an important liver enzyme in human and no expression of functional MOGAT3 was detected in human skin. Thus, the expression of MOGAT3 in ruminant skin indicates that there may be an alternative pathway for triacylglyceride (TAG) synthesis [4].

The sheep complete genome was sequenced after other widespread livestock such as cattle, horse, pig, and goat. The sheep multi-omics integrated study by Jiang et al. [4] provided novel insights into the genetic basis of ruminant biology from the aspects of digestion, lipid metabolism, wool follicle development and reproduction. To meet the increasing global demand of mutton consumption, breeders can take better advantage of genomic information by applying molecular marker assisted breeding (MAS) for e.g. specialized mutton sheep. In 2013, ~4000000 tons of mutton was produced in China, accounting for ~32% of the world's total mutton production. Meanwhile, ~259000 tons of mutton, being ~20% of the world trade volume of sheep meat, was imported into China. The National Meat Development Plan (2013–2020), which was issued by the National Development and Reform Commission (NDRC) of China, aimed to increase the mutton production from 4000000 tons to 5180000 tons by the end of 2020. Along with the implementation of the grazing ban in order to restore the grassland since 1999, it would be particularly necessary to accelerate the application of whole genome information in marker-assisted breeding for specialized mutton sheep in China in the near future.

- 1 Bovine Genome Sequencing and Analysis Consortium, Elsik CG, Tellam RL, Worley KC, Gibbs RA, Muzny DM, Weinstock GM, Adelson DL, Eichler EE, Elnitski L, Guigó R, Hamernik DL, Kappes SM, Lewin HA, Lynn DJ, Nicholas FW, Reymond A, Rijnkels M, Skow LC, Zdobnov EM, Schook L, Womack J, Alioto T, Antonarakis SE, Astashyn A, Chapple CE, Chen HC, Chrast J, Câmara F, Ermolaeva O, Henrichsen CN, Hlavina W, Kapustin Y, Kiryutin B, Kitts P, Kokocinski F, Landrum M, Maglott D, Pruitt K, Sapojnikov V, Searle SM, Solovyev V, Souvorov A, Ucla C, Wyss C, Anzola JM,

Gerlach D, Elhaik E, Graur D, Reese JT, Edgar RC, McEwan JC, Payne GM, Raison JM, Junier T, Kriventseva EV, Eyraes E, Plass M, Donthu R, Larkin DM, Reecy J, Yang MQ, Chen L, Cheng Z, Chitko-McKown CG, Liu GE, Matukumalli LK, Song J, Zhu B, Bradley DG, Brinkman FS, Lau LP, Whiteside MD, Walker A, Wheeler TT, Casey T, German JB, Lemay DG, Maqbool NJ, Molenaar AJ, Seo S, Stothard P, Baldwin CL, Baxter R, Brinkmeyer-Langford CL, Brown WC, Childers CP, Connelley T, Ellis SA, Fritz K, Glass EJ, Herzig CT, Iivanainen A, Lahmers KK, Bennett AK, Dickens CM, Gilbert JG, Hagen DE, Salih H, Aerts J, Caetano AR, Dalrymple B, Garcia JF, Gill CA, Hiendler SG, Memili E, Spurlock D, Williams JL, Alexander L, Brownstein MJ, Guan L, Holt RA, Jones SJ, Marra MA, Moore R, Moore SS, Roberts A, Taniguchi M, Waterman RC, Chacko J, Chandrabose MM, Cree A, Dao MD, Dinh HH, Gabisi RA, Hines S, Hume J, Jhangiani SN, Joshi V, Kovar CL, Lewis LR, Liu YS, Lopez J, Morgan MB, Nguyen NB, Okwuonu GO, Ruiz SJ, Santibanez J, Wright RA, Buhay C, Ding Y, Dugan-Rocha S, Herdandez J, Holder M, Sabo A, Egan A, Goodell J, Wilczek-Boney K, Fowler GR, Hitchens ME, Lozado RJ, Moen C, Steffen D, Warren JT, Zhang J, Chiu R, Schein JE, Durbin KJ, Havlak P, Jiang H, Liu Y, Qin X, Ren Y, Shen Y, Song H, Bell SN, Davis C, Johnson AJ, Lee S, Nazareth LV, Patel BM, Pu LL, Vattathil S, Williams RL Jr, Curry S, Hamilton C, Sodergren E, Wheeler DA, Barris W, Bennett GL, Eggen A, Green RD, Harhay GP, Hobbs M, Jann O, Keele JW, Kent MP, Lien S, McKay SD, McWilliam S, Ratnakumar A, Schnabel RD, Smith T, Snelling WM, Sonstegard TS, Stone RT, Sugimoto Y, Takasuga A, Taylor JF, Van Tassell CP, Macneil MD, Abatepaulo AR, Abbey CA, Ahola V, Almeida IG, Amadio AF, Anatriello E, Bahadue SM, Biase FH, Boldt CR, Carroll JA, Carvalho WA, Cervelatti EP, Chacko E, Chapin JE, Cheng Y, Choi J, Colley AJ, de Campos TA, De Donato M, Santos IK, de Oliveira CJ, Deobald H, Devinoy E, Donohue KE, Dovc P, Eberlein A, Fitzsimmons CJ, Franzin AM, Garcia GR, Genini S, Gladney CJ, Grant JR, Greaser ML, Green JA, Hadsell DL, Hakimov HA, Halgren R, Harrow JL, Hart EA, Hastings N, Hernandez M, Hu ZL, Ingham A, Iso-Touru T, Jamis C, Jensen K, Kapetis D, Kerr T, Khalil SS, Khatib H, Kolbehari D, Kumar CG, Kumar D, Leach R, Lee JC, Li C, Logan KM, Malinverni R, Marques E, Martin WF, Martins NF, Maruyama SR, Mazza R, McLean KL, Medrano JF, Moreno BT, Moré DD, Muntean CT, Nandakumar HP, Nogueira MF, Olsaker I, Pant SD, Panzitta F, Pastor RC, Poli MA, Poslusny N, Rachagani S, Ranganathan S, Razpet A, Riggs PK, Rincon G, Rodriguez-Osorio N, Rodriguez-Zas SL, Romero NE, Rosenwald A, Sando L, Schmutz SM, Shen L, Sherman L, Southey BR, Lutzow YS, Sweedler JV, Tammen I, Telugu BP, Urbanski JM, Utsunomiya YT, Verschoor CP, Waardenberg AJ, Wang Z, Ward R, Weikard R, Welsh TH Jr, White SN, Wilming LG, Wunderlich KR, Yang J, Zhao FQ. The genome sequence of taurine cattle: a window to ruminant biology and evolution. *Science*, 2009, 324: 522–528

- 2 Qiu Q, Zhang G, Ma T, Qian W, Wang J, Ye Z, Cao C, Hu Q, Kim J, Larkin DM, Auvel L, Capitanu B, Ma J, Lewin HA, Qian X, Lang Y, Zhou R, Wang L, Wang K, Xia J, Liao S, Pan S, Lu X, Hou H, Wang Y, Zang X, Yin Y, Ma H, Zhang J, Wang Z, Zhang Y, Zhang D, Yonezawa T, Hasegawa M, Zhong Y, Liu W, Zhang Y, Huang Z, Zhang S, Long R, Yang H, Wang J, Lenstra JA, Cooper DN, Wu Y, Wang J, Shi P, Wang J, Liu J. The yak genome and adaptation to life at high altitude. *Nat Genet*, 2012, 44: 946–949
- 3 Dong Y, Xie M, Jiang Y, Xiao N, Du X, Zhang W, Tosser-Klopp G, Wang J, Yang S, Liang J, Chen W, Chen J, Zeng P, Hou Y, Bian C, Pan S, Li Y, Liu X, Wang W, Servin B, Sayre B, Zhu B, Sweeney D, Moore R, Nie W, Shen Y, Zhao R, Zhang G, Li J, Faraut T, Womack J, Zhang Y, Kijas J, Cockett N, Xu X, Zhao S, Wang J, Wang W. Sequencing and automated whole-genome optical mapping of the genome of a domestic goat (*Capra hircus*). *Nature Biotech*, 2013, 31: 135–141

- 4 Jiang Y, Xie M, Chen W, Talbot R, Maddox JF, Faraut T, Wu C, Muzny DM, Li Y, Zhang W, Stanton JA, Brauning R, Barris WC, Hourlier T, Aken BL, Searle SM, Adelson DL, Bian C, Cam GR, Chen Y, Cheng S, DeSilva U, Diken K, Dong Y, Fan G, Franklin IR, Fu S, Fuentes-Utrilla P, Guan R, Highland MA, Holder ME, Huang G, Ingham AB, Jhangiani SN, Kalra D, Kovar CL, Lee SL, Liu W, Liu X, Lu C, Lv T, Mathew T, McWilliam S, Menzies M, Pan S, Robelin D, Servin B, Townley D, Wang W, Wei B, White SN, Yang X, Ye C, Yue Y, Zeng P, Zhou Q, Hansen JB, Kristiansen K, Gibbs RA, Flicek P, Warkup CC, Jones HE, Oddy VH, Nicholas FW, McEwan JC, Kijas JW, Wang J, Worley KC, Archibald AL, Cockett N, Xu X, Wang W, Dalrymple BP. The sheep genome illuminates biology of the rumen and lipid metabolism. *Science*, 2014, 344: 1168–1173

Open Access This article is distributed under the terms of the Creative Commons Attribution License which permits any use, distribution, and reproduction in any medium, provided the original author(s) and source are credited.