

Finite Density QCD with Infinite Coupling Constant Limit

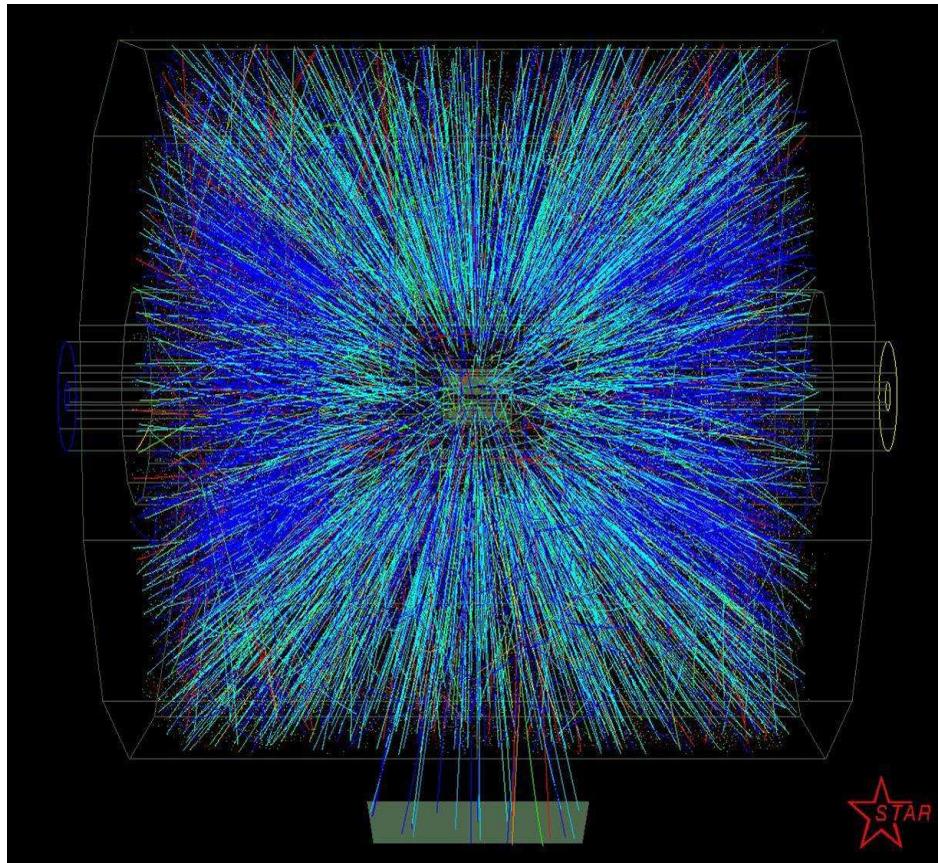
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work under progress

Plan of Talk

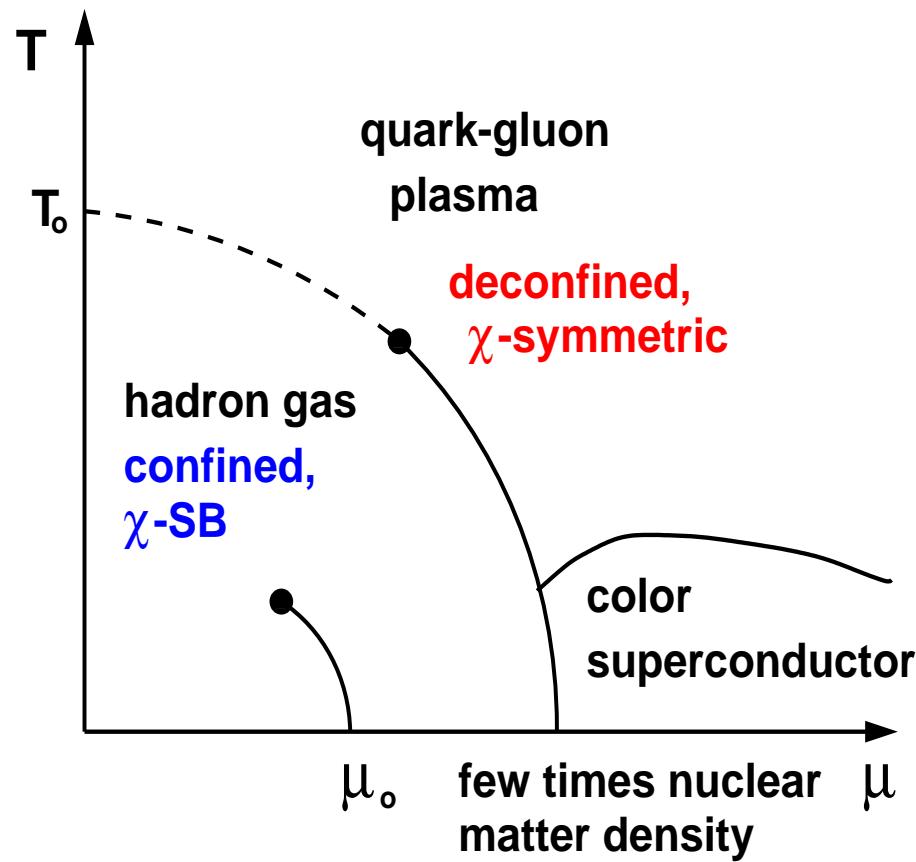
0. Motivation
1. QCD with infinite coupling constant
2. MDP Algorithm
3. Discussion

0. Motivation

- Heavy Ion Collision



- Finite T/μ QCD phase diagram



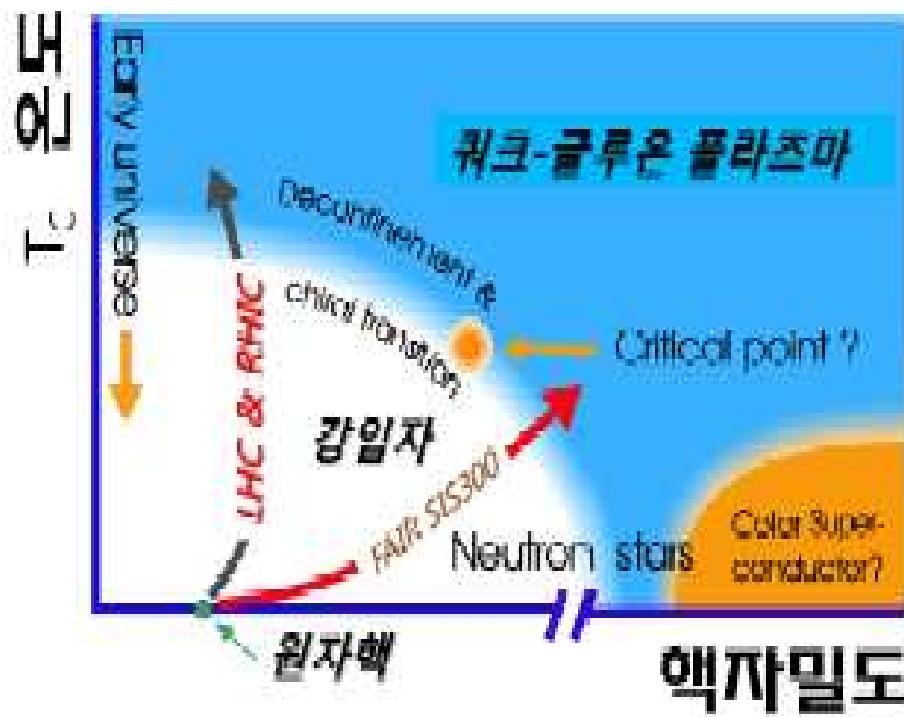


그림 2. 온도와 핵자밀도의 합수로 나타낸 핵 물질의 다양한 상(phase).

되었으나 ○
특성을 정밀
리면 명백히
을 정밀측정
적시키고 둘
데, 핵물리학
있다. LHC
지밀도가 초
입자의 수가
의 상태방전
를 결정할
히 LHC에서
배나 커서

- unlike finite T domain of QCD phase diagram, it is **difficult** to study finite μ domain systematically
- Euclidean lattice QCD action becomes complex → “**sign problem**”
- Monte Carlo simulation of lattice QCD action is unstable at best
- actually, our knowledge about finite μ domain of QCD phase diagram is **NOT** on firm ground
- → **model study**

1. QCD with infinite coupling constant

- QCD lagrangian

$$\mathcal{L} = \bar{\psi}(\gamma_\mu D_\mu + m)\psi - \frac{1}{4}F_{\mu\nu}^a F_{\mu\nu}^a \quad (1)$$

- $D_\mu = \partial_\mu + igA_\mu^a T^a$
- $F_{\mu\nu}^a = \partial_\mu A_\nu^a - \partial_\nu A_\mu^a + igf^{abc}A_\mu^b A_\nu^c$
- usually interested in weak coupling limit
 $g \rightarrow 0$ limit gives a free theory

- strong coupling limit: $g \rightarrow \infty$
- rescaling $\tilde{A}_\mu^a = g A_\mu^a$
- $D_\mu = \partial_\mu + i \tilde{A}_\mu^a T^a$
- $F_{\mu\nu}^a = \frac{1}{g} [\partial_\mu \tilde{A}_\nu^a - \partial_\nu \tilde{A}_\mu^a + i f^{abc} \tilde{A}_\mu^b \tilde{A}_\nu^c]$
- QCD lagrangian in strong coupling limit (**drop tilde**)

$$\mathcal{L} = \bar{\psi} (\gamma_\mu D_\mu + m) \psi - \frac{1}{4g^2} F_{\mu\nu}^a F_{\mu\nu}^a \quad (2)$$

- **usually** interested in strong coupling limit

$g \rightarrow \infty$ limit gives QCD string ground state

(K.G. Wilson, Phys.Rev.D10 (1974) 2445)

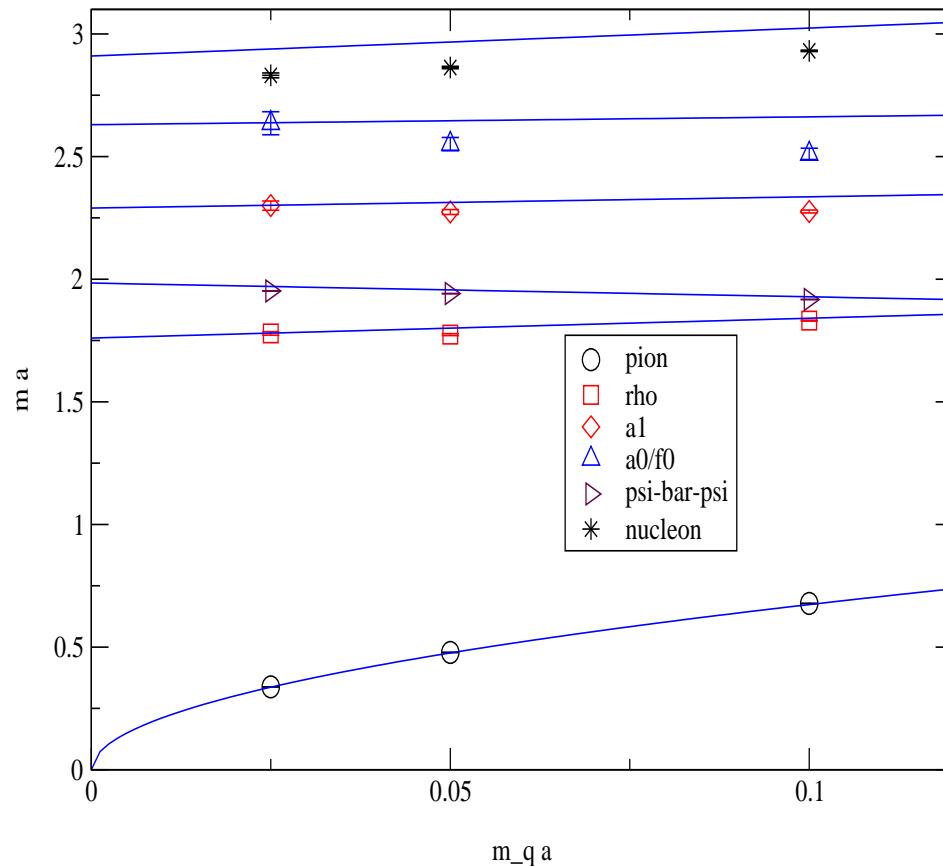
- gauge kinetic term, F^2 , drops in this limit
- gluon field becomes a **random field**
- only gauge **singlet** combination survives in the path integral

$$\int dU U_i U_j^\dagger = \delta_{ij}$$

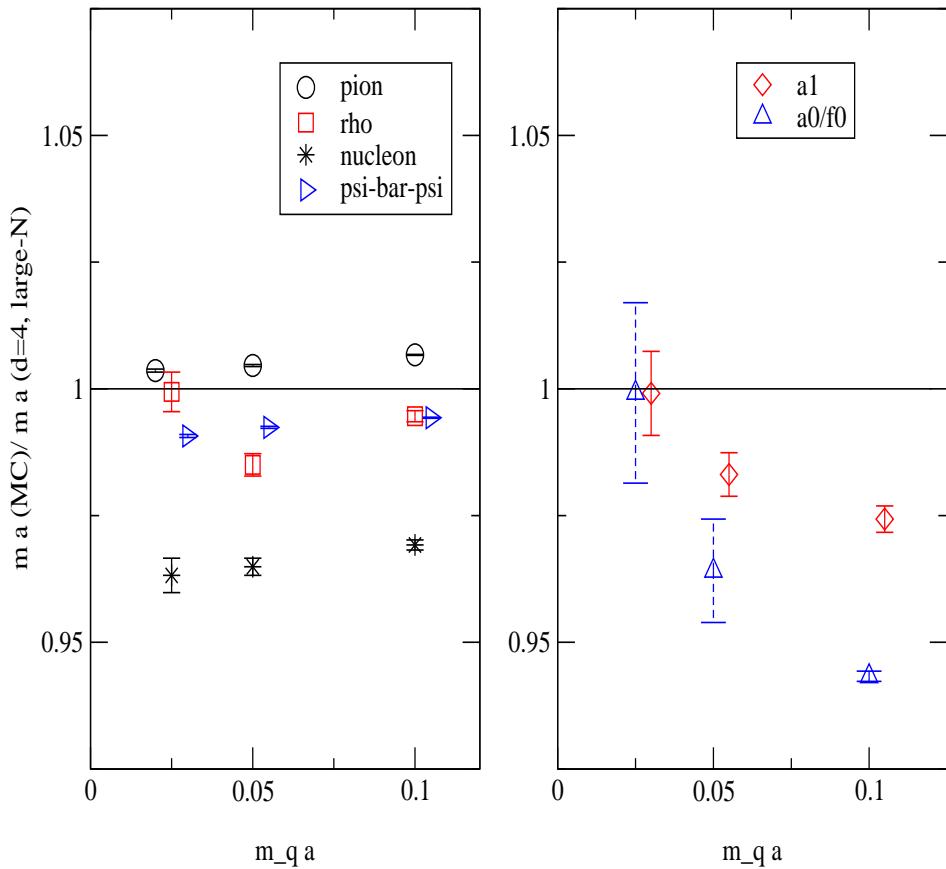
$$\int dU U_i U_j U_k = \frac{1}{3} \varepsilon_{ijk}$$

- can do analytic calculations (see e.g., N. Kawamoto and his collaborators' works)

- Comparison between analytic works and Monte Carlo result



(S.K. and Ph. de Forcrand, Phys. Lett. B645(2007) 339)



2. Monomer-Dimer-Polymer (MDP) Algorithm

- F. Karsch, K.H. Mutter, Nucl. Phys. 313 (1989) 541
- partition function of lattice QCD in strong coupling limit

$$\mathcal{Z} = \int d\bar{\psi}d\psi \int dU e^{S_F} \quad (3)$$

- $S_F = \bar{\psi}(D_0\eta_0 + D_i\eta_i + m)\psi$

$$D_i\psi = \frac{1}{2}\{U_i(x)\psi(x+i) - U_i^\dagger(x-i)\psi(x-i)\}$$

$$D_0\psi = \frac{1}{2}\{U_0(x)e^\mu\psi(x+0) - U_0^\dagger(x-0)e^{-\mu}\psi(x-0)\}$$

- ψ is staggered quark field (i.e., 1-component in spin, 3-component in color grassman field)
- each lattice site can have only $\bar{\psi}_3(x)\bar{\psi}_2(x)\bar{\psi}_1(x)\psi_1(x)\psi_2(x)\psi_3(x)$ combination due to grassmann property of quark field
- With $M(x) = \sum_{a=1,2,3} \bar{\psi}_a(x)\psi_a(x)$,
 $B(x) = \psi_1(x)\psi_2(x)\psi_3(x)$,
 $\bar{B}(x) = \bar{\psi}_3(x)\bar{\psi}_2(x)\bar{\psi}_1(x)$
- only gauge **singlet** combination survives in the path integral

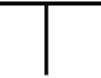
- with

$$\begin{aligned}
F(x, y) &= \int dU e^{\bar{\psi}(x)U(x,y)\psi(y)-\bar{\psi}(y)U^\dagger(y,x)\psi(x)} \\
&= 1 + \frac{1}{3}M(x)M(y) + \frac{1}{12}\{M(x)M(y)\}^2 + \frac{1}{36}\{M(x)M(y)\}^3 \\
&\quad - \eta(x, y)^3 \bar{B}(x)B(y) - \eta(y, x)^3 \bar{B}(y)B(x) \quad (4)
\end{aligned}$$

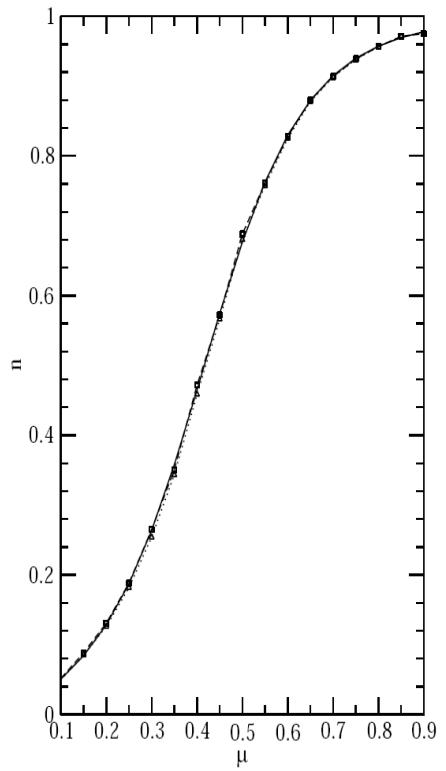
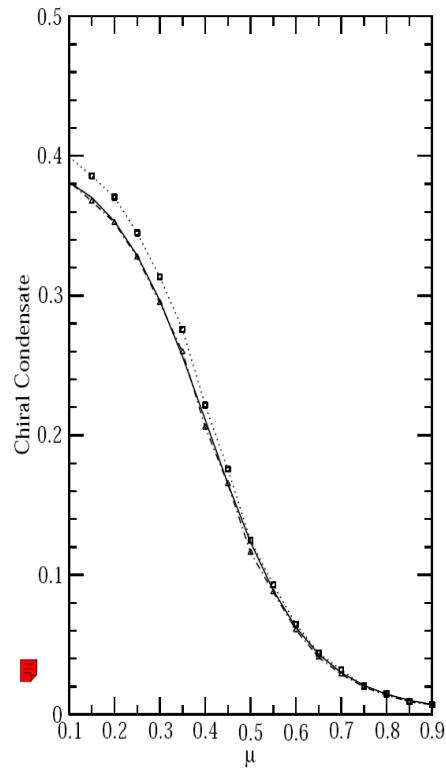
$$\mathcal{Z} = \int d\bar{\psi} d\psi e^{m \sum_x M(x)} \prod_{x,y} F(x, y) \quad (5)$$

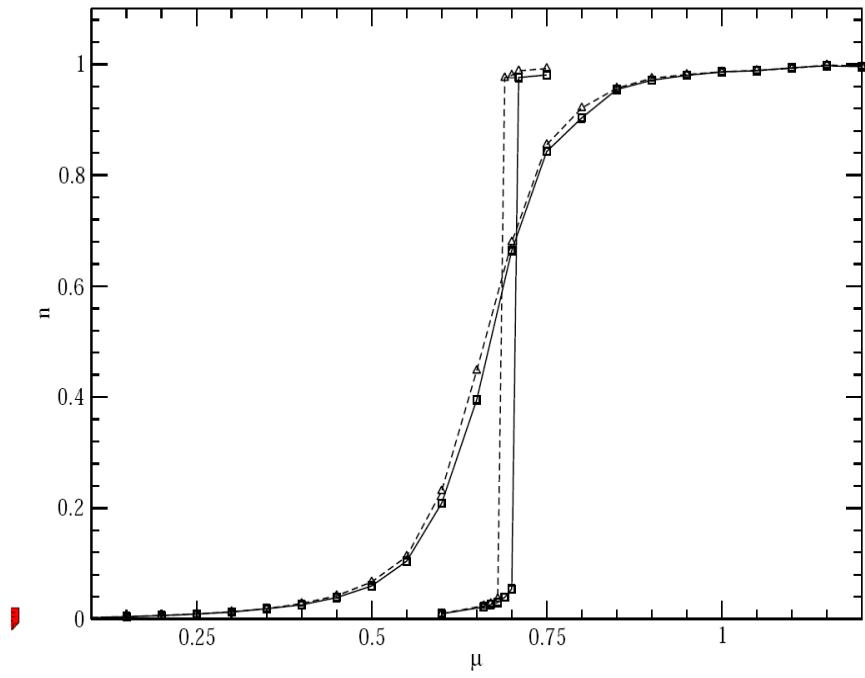
- each lattice site can have $n_M + n_D = 3$ (n_M is the number of monomer, n_D is the number of dimer)
- or occupied by baryon loop

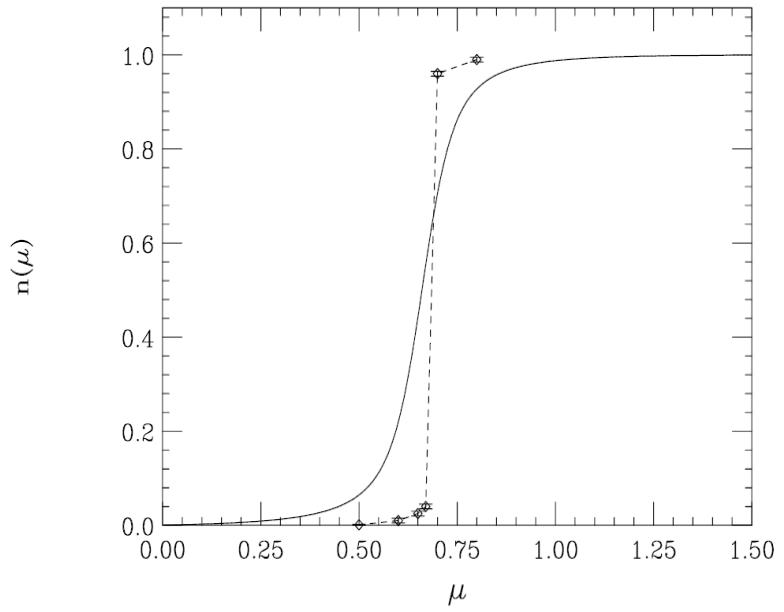
- allowed lattice site types

\mathbb{N}	0	1	2	3	4	5	6
							
$n_{D_1}(x)$	1	2	1	0	0	3	0
$n_{D_2}(x)$	1	0	0	0	1	0	0
$n_{D_3}(x)$	0	0	0	0	0	0	1
$w(x)$	3	6	3	1	3	6	1

- Metropolis algorithm
- either cut a dimer, which removes a link and add monomer at end sites
- or connect two monomers at the neighboring sites, which removes two monomers and add a link between the two sites
- throw dice to satisfy detailed balance



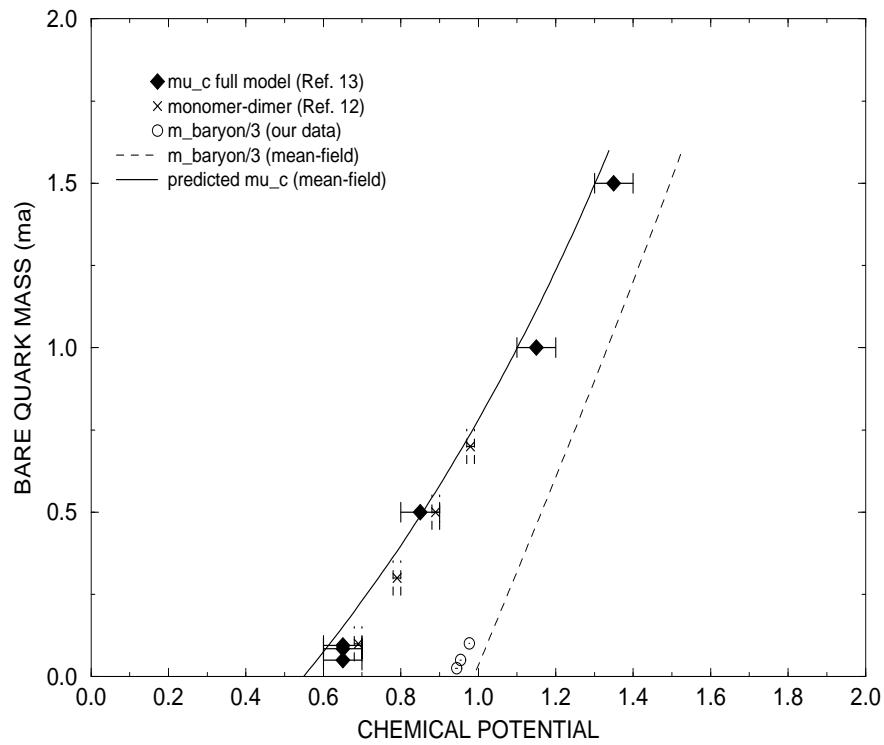




(R. Aloisio et al, Nucl. Phys. B564(2000) 489)

3. Discussion

- We could reproduce F. Karsch, K.H. Mutter, Nucl. Phys. 313 (1989) 541
- MDP algorithm has a **PROBLEM** with the chiral limit or with heavy quark mass
- further investigation under way



(S.K. and Ph. de Forcrand, Phys. Lett. B645(2007) 339)